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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.	PATH99-10	Total Pages	28729
First Named Inventor or Application Identifier	KEITH G. WEINSTOCK ET AL.		
Express Mail Label No.			

APPLICATION ELEMENTS

See MPEP Chapter 600 concerning utility patent application contents

ADDRESS TO: Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231

1. [X] Fee Transmittal Form (Submit an original, and a duplicate for fee processing)
2. [X] Specification [Total Pages 8710] (preferred arrangement set forth below)
 - Descriptive title of the Invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R&D
 - Reference to Microfiche Appendix
 - Background of the Invention
 - Brief Summary of the Invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
3. [] Drawing(s) (35 USC d113) [Total Sheets]
4. Oath or Declaration [Total Pages 3]
 a. [X] Unexecuted (original or copy)
 b. [] Copy from a prior application (37 CFR 1 63(d)) (for continuation/divisional with Box 17 completed)

 [Note Box 5 below]

 i. [] DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1 63(2) and 1 33(b)
5. [] Incorporation By Reference (useable if Box 4b is checked) The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
6. [] Microfiche Computer Program (Appendix)
7. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
 a. [X] Computer Readable Copy
 b. [X] Paper Copy (identical to computer copy)
 c. [X] Statement verifying identical of above copies

ACCOMPANYING APPLICATION PARTS

8. [] Assignment Papers (cover sheet & Documents(s))
9. [] 37 CFR 3 27(B) Statement (when there is an assignee) [] Power of Attorney
10. [] English Translation Document (if applicable)
11. [] Information Disclosure Statement (IDS)/PTO-1449 [] Copies of IDS Citations
12. [] Preliminary Amendment
13. [X] Return Receipt Postcard (MPEP 503) (Should be specifically itemized)
14. [X] Small Entity Statement(s) [] Statement filed in prior application Status still proper and desired
15. [] Certified Copy of Priority Document(s) if foreign priority is claimed)
16. [] Other:

17. If a CONTINUING APPLICATION, check appropriate box and supply the requisite information

☐ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No: /

18. CORRESPONDENCE ADDRESS

[] Customer Number or Bar Code Label or [X] Correspondence address below here)

NAME	Nina Pearlmutter, Esq.				
ADDRESS	Genome Therapeutics Corp. 100 Beaver St.				
CITY	Waltham	STATE	MA	ZIP CODE	02453
COUNTRY	United States of America	PHONE	781/398-2508	FAX	781/398-2607

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TOTAL AMOUNT OF PAYMENT ($) 725.00

Complete if Known	
Application Number	
Filing Date	
First Named Inventor	Keith G. Weinstock et al.
Examiner Name	
Group / Art Unit	
Attorney Docket No.	PATH99-10

METHOD OF PAYMENT (check one)

1. [X] The Commissioner is hereby authorized to charge indicated fees and credit any over payments to:

Deposit Account Number: 501040
Deposit Account Name: Genome Therapeutics Corp.

[X] Charge Any Additional Fee Required Under 37 CFR 1.16 and 1.17

2. [] **Payment Enclosed:** [] Check [] Money Order [] Other

FEE CALCULATION

1. BASIC FILING FEE

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
101	760	201	380	Utility filing fee	380
106	310	206	155	Design filing fee	
107	480	207	240	Plant filing fee	
108	760	208	380	Reissue filing fee	
114	150	214	75	Provisional filing fee	

SUBTOTAL (1) ($) 380.00

2. EXTRA CLAIM FEES

		Extra Claims		Fee from below	Fee Paid
Total Claims	28	-20** = 8	X	9	= 72.00
Independent Claims	10	- 3** = 7	X	39	= 273.00
Multiple Dependent					=

**or number previously paid, if greater; For Reissues, see below

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description
103	18	203	9	Claims in excess of 20
102	78	202	39	Independent claims in excess of 3
104	260	204	130	Multiple dependent claim, if not paid
109	78	209	39	** Reissue independent claims over original patent
110	18	210	9	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) ($) 345.00

FEE CALCULATION (continued)

3. ADDITIONAL FEES

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
105	130	205	65	Surcharge - late filing fee or oath	
127	50	227	25	Surcharge - late provisional filing fee or cover sheet.	
139	130	139	130	Non-English specification	
147	2,520	147	2,520	For filing a request for reexamination	
112	920*	112	920*	Requesting publication of SIR prior to Examiner action	
113	1,840*	113	1,840*	Requesting publication of SIR after Examiner action	
115	110	215	55	Extension for reply within first month	
116	380	216	190	Extension for reply within second month	
117	870	217	435	Extension for reply within third month	
118	1,360	218	680	Extension for reply within fourth month	
128	1,850	228	925	Extension for reply within fifth month	
119	300	219	150	Notice of Appeal	
120	300	220	150	Filing a brief in support of an appeal	
121	260	221	130	Request for oral hearing	
138	1,510	138	1,510	Petition to institute a public use proceeding	
140	110	240	55	Petition to revive - unavoidable	
141	1,210	241	605	Petition to revive - unintentional	
142	1,210	242	605	Utility issue fee (or reissue)	
143	430	243	215	Design issue fee	
144	580	244	290	Plant issue fee	
122	130	122	130	Petitions to the Commissioner	
123	50	123	50	Petitions related to provisional applications	
126	240	126	240	Submission of Information Disclosure Stmt	
581	40	581	40	Recording each patent assignment per property (times number of properties)	
146	760	246	380	Filing a submission after final rejection (37 CFR 1.129(a))	
149	760	249	380	For each additional invention to be examined (37 CFR 1.129(b))	

Other fee (specify) _____

Other fee (specify) _____

* Reduced by Basic Filing Fee Paid

SUBTOTAL (3) ($) 0

SUBMITTED BY

				Complete (if applicable)	
Typed or Printed Name	Nina L. Pearlmutter, Esq., Ph.D.			Reg. Number	35639
Signature		Date	10/12/99	Deposit Account User ID	

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Applicant or Patentee: Keith G. Weinstock et al.
Serial or Patent No.:
Filed: 14 October 1999
Title: **NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *ASPERGILLUS FUMIGATUS* FOR DIAGNOSTICS AND THERAPEUTICS**

Attorney's Docket No.: PATH99-10

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS (37 CFR 1.9(f) and 1.27(c)) SMALL BUSINESS CONCERN

I hereby declare that I am

[] the owner of the small business concern identified below:

[X] an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF SMALL BUSINESS CONCERN Genome Therapeutics Corporation
ADDRESS OF SMALL BUSINESS CONCERN 100 Beaver Street
Waltham, MA 02453

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.12, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees to the United States Patent and Trademark Office, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention described, entitled: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *ASPERGILLUS FUMIGATUS* FOR DIAGNOSTICS AND THERAPEUTICS by inventor(s) Keith G. Weinstock et al. described in:

[X] the specification filed herewith with title as listed above.

[] the application identified above.

[] the patent identified above.

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights in the invention is listed below * and no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.9(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d), or a nonprofit organization under 37 CFR 1.9(e).

* NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

NAME_____
ADDRESS_____
[] INDIVIDUAL [] SMALL BUSINESS CONCERN [] NONPROFIT ORGANIZATION

NAME_____
ADDRESS_____
[] INDIVIDUAL [] SMALL BUSINESS CONCERN [] NONPROFIT ORGANIZATION

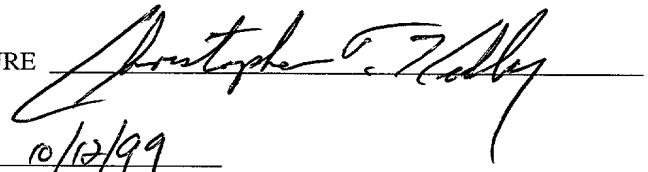
I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statement were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING Christopher T. Kelly.

TITLE OF PERSON OTHER THAN OWNER Senior Vice President of Strategic Planning/Business Development

ADDRESS OF PERSON SIGNING 100 Beaver Street, Waltham, Massachusetts 02453.

SIGNATURE 

DATE 10/12/99

Doc Code: SMALL.ENT

Title Of The Invention

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *ASPERGILLUS FUMIGATUS* FOR DIAGNOSTICS AND THERAPEUTICS

Related Applications

This application claims the benefit of U.S. Provisional Application Serial Number 60/104,683, filed October 16, 1998 and also claims the benefit of U.S. Provisional Application Serial Number 60/113,476, filed December 21, 1998, the entire teachings both of which are incorporated herein by reference.

Background Of The Invention

Significant increases in the occurrence of cases of aspergillosis have occurred since the first reported case of invasive aspergillosis in 1953 (Rankin, NE (1953) *Br. Med. J.* 183: 918-919; reviewed in Denning, DW (1998) *Clin. Infect. Dis.* 26: 781-803). This increase correlates with the increasing numbers of immunocompromised patients, including AIDS (Acquired Immune Deficiency Syndrome) and organ transplant patients taking immunosuppressant drugs to prevent organ rejection. Although *Aspergillus* is generally considered an opportunistic pathogen, invasive aspergillosis has been documented from immunocompetent patients as well (Denning DW, Stevens DA (1990) *Rev. Infect. Dis.* 12: 1147-1202; Bodey GP, Vartivarian S (1989) *Eur. J. Clin. Microbiol. Infect. Dis.* 8: 413-437). *Aspergillus* species causes a wide spectrum of disease conditions ranging from superficial cutaneous infections to life-threatening systemic mycoses. Mortality rates can approach 100% in invasive aspergillosis (Denning DW (1996) *Clin. Infect. Dis.* 23 608-615) However, only a few species of the fungal genus *Aspergillus* are found as human pathogens (Denning, DW (1998) *Clin. Infect. Dis.* 26: 781-803) and *A. fumigatus* is among the most common

of these. *A. fumigatus* is a soil-borne fungus typically associated with decaying organic matter (Mullins J, Harvey R, Seaton A. (1976) *Clin. Allergy* 6: 209-217) although it is likely that is ubiquitous in the envrionment due to the airborne distribution of its spores. A Southern hybridization study of the genetic diversity of *A. fumigatus* isolates from both clinical specimens and from the environment suggests that most if not all strains of *A. fumigatus* are capable of becoming opportunistic pathogens (Debeaupuis JP et al (1997) *Infect. Immun.* 65: 3080-3085). Potential allergen-encoding genes in *A. fumigatus* have been isolated using M13 phage display and screening with IgE from patients allergic to *A. fumigatus* (Crameri R et al (1998) *Int. Immunol.* 10: 1211-1216; Crameri R (1998) *Int. Arch. Allergy Immunol.* 115: 99-114; Crameri R, Blaser K (1996) *Int. Arch. Allergy Immunol.* 110: 41-45).

A number of molecules have been suggested to have a role in virulence. *A. fumigatus* produces a number of extracellular toxins, such as gliotoxin (Mullbacher A, Eichner RD (1984) *Proc. Natl. Acad. Sci. U.S.A.* 81: 3835-3837; Mullbacher A, Waring P, Eichner RD (1985) *J. Gen. Microbiol.* 131: 1251-1258 and restrictocin (Lamy B, Davies J (1991) *Nucl. Acids Res.* 19: 1001-1006; Lamy B, Moutaouakil M., Latge J, and Davies J (1991) *Mol. Microbiol.* 5: 1811-1815). In a mouse model, however, deletions of the *A. fumigatus* restrictocin toxin gene had no effect on virulence relative to the wild type gene (Smith JM, Davies JE, Holden DW (1993) *Mol. Microbiol.* 9:1071-1077; Holden DW, Tang CM, Smith JM (1994) *Antonie van Leeuwenhoek* 65: 251-255). Gliotoxin is known to act as an immunosuppressant *in vivo* (Sutton P, Newcombe NR, Waring P, Mullbacher A (1994) *Infect. Immun.* 62: 1192-1198) possibly through the inhibition of the activation of the transcription factor NF-kappaB (Pahl HL et al (1996) J. Exp. Med. 183: 1829-1840), but its role in pathogenesis is still unproven (Waring P, Mullbacher A (1994) *Infect. Immun.* 62: 1192-1198). Additional toxins are known from *A. fumigatus* (Moss MO (1994) in Powell KA, Perberdy JF, and Renwick A, editors. The genus *Aspergillus*. New York. Plenum Press. pp. 29-50).

Additional potential virulence factors have been suggested, including extracellular proteases (reviewed in Denning, DW (1998) *Clin. Infect. Dis.* 26: 781-803). However, deletion of AFA1, an extracellular alkaline protease with elastase activity, had no effect on pathogenicity (Holden DW, Tang CM, and Smith JM (1994) *Antonie van Leeuwenhoek* 65: 251-255). Genes encoding ATP-binding cassette proteins (AfuMDR1 and AfuMDR2) have been isolated from *A. fumigatus* using degenerate PCR primers (Tobin MB, Peery RB, Skatrud PL (1997) *Gene* 200: 11-23). These

proteins have similarities to multiple drug resistance genes from other organisms. Increased resistance to two anitfungal agents was observed when the AfuMDR1 gene was expressed in *S. cerevisiae*.

Only two antifungals, itraconazole and amphotericin B, are currently used to treat invasive aspergillosis (Denning DW (1998) *Clin. Infect. Dis.* 26: 781-803). Fluconazole, which is effective against other fungal infections including those of *Candida albicans*, is ineffective against *Aspergillus* clinical isolates (Dermoumi H (1994) *Chemotherapy* 40: 92-98). Isolates of *Aspergillus fumigatus* resistant to itraconazole have been reported (Denning DW et al (1997) *Antimicrob. Agents Chemother.* 41: 1364-1368). Resistance to amphotericin B after itraconazole therapy (Schaffner A, Bohler A (1993) *Mycoses* 36: 421-424) has also been reported and this is not due to direct antagonism between the drugs as the itraconazole treatment was stopped prior to amphotericin B treatment. *In vitro* studies demonstrate that amphotericin B-resistant strains can be readily produced in the laboratory (Manavathu EK, Alangaden GJ, Chandrasekar PH (1998) *J. Antimicrob. Chemother.* 41:615-619) and *in vivo* resistance of *A. fumigatus* to amphotericin B in mice has been demonstrated (Verweij PE (1998) *Antimicrob. Agents Chemother.* 42: 873-878).

The severity and difficulty in diagnosing *A. fumigatus* infections, the limited number of effective antifungals for treatment of infections, and the development of antifungal-resistant *A. fumigatus* strains provide the rationale for the identification of targets for more rapid and effective methods of identification, prevention, and treatment of aspergillosis. The elucidation of the genome of *A. fumigatus* would enhance the understanding of how *A. fumigatus*, as well as other fungi, causes invasive disease and how best to combat fungal infection.

Summary Of The Invention

The present invention fulfills the need for diagnostic tools and therapeutics by providing fungal-specific compositions and methods for detecting *Aspergillus* species including *A. fumigatus*, as well as compositions and methods useful for treating and preventing *Aspergillus* infection, in particular, *A. fumigatus* infection, in vertebrates including mammals.

The present invention encompasses isolated nucleic acids and polypeptides derived from *A. fumigatus* that are useful as reagents for diagnosis of fungal disease, components of effective antifungal vaccines, and/or as targets for antifungal drugs including anti-*A. fumigatus* drugs. They can also be used to detect the presence of *A. fumigatus* and other *Aspergillus* species in a sample; and in screening compounds for the ability to interfere with the *A. fumigatus* life cycle or to inhibit *A. fumigatus* infection. They also have use as biocontrol agents for plants.

In one aspect, the invention features compositions of nucleic acids corresponding to entire coding sequences of *A. fumigatus* proteins, including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *A. fumigatus* proteins to block protein translation, and methods for producing *A. fumigatus* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *A. fumigatus* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *A. fumigatus* are within the scope of this invention.

The nucleotide sequences provided in SEQ ID NO: 1 - SEQ ID NO: 22156, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 22156 may be "provided" in a variety of medias to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NO: 1 - SEQ ID NO: 22156, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 22156. Uses for and methods for providing nucleotide sequences in a variety of media is well known in the art (see e.g., EPO Publication No. EP 0 756 006).

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage media, and magnetic

tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A person skilled in the art can readily appreciate how any of the presently known computer readable media can be used to create a manufacture comprising computer readable media having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable media. A person skilled in the art can readily adopt any of the presently known methods for recording information on computer readable media to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a person skilled in the art for creating a computer readable media having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable media. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A person skilled in the art can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable media having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NO: 1 - SEQ ID NO: 22156, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to SEQ ID NO: 1 - SEQ ID NO: 22156 in computer readable form, a person skilled in the art can routinely access the coding sequence information for a variety of purposes. Computer software is publicly available which allows a person skilled in the art to access sequence information provided in a computer readable media. Examples of such computer software include programs of the "Staden Package", "DNA

Star", "MacVector", GCG "Wisconsin Package" (Genetics Computer Group, Madison, WI) and "NCBI Toolbox" (National Center For Biotechnology Information). Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Computer algorithms enable the identification of *A. fumigatus* open reading frames (ORFs) within SEQ ID NO: 1 - SEQ ID NO: 22156 which contain homology to ORFs or proteins from other organisms. Examples of such similarity-search algorithms include the BLAST [Altschul et al., J. Mol. Biol. 215:403-410 (1990)] and Smith-Waterman [Smith and Waterman (1981) Advances in Applied Mathematics, 2:482-489] search algorithms. Suitable search algorithms are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). Such algorithms are utilized on computer systems as exemplified below. The ORFs so identified represent protein encoding fragments within the *A. fumigatus* genome and are useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *A. fumigatus* genome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A person skilled in the art can readily appreciate that any one of the currently available computer-based systems is suitable for use in the present

invention. The computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *A. fumigatus* genome which are similar to, or "match", a particular target sequence or target motif. A variety of known algorithms are known in the art and have been disclosed publicly, and a variety of commercially available software for conducting homology-based similarity searches are available and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, FASTA (GCG Wisconsin Package), Bic_SW (Compugen Bioccelerator), BLASTN2, BLASTP2, BLASTX2 (NCBI) and Motifs (GCG). Suitable software programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). A person skilled in the art can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A person skilled in the art can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100

amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that many genes are longer than 500 amino acids, or 1.5 kb in length, and that commercially important fragments of the *A. fumigatus* genome, such as sequence fragments involved in gene expression and protein processing, will often be shorter than 30 nucleotides.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a specific functional domain or three-dimensional configuration which is formed upon the folding of the target polypeptide. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites, membrane-spanning regions, and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *A. fumigatus* genome possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a person skilled in the art with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *A. fumigatus* genome. In the present examples, implementing software which implement the BLASTP2 and bic_SW algorithms (Altschul et al., J Mol. Biol. 215:403-410 (1990); Compugen Biocellerator) was used to identify open reading frames within the *A. fumigatus* genome. A person skilled in the art can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski,

The Internet and the New Biology: Tools for Genomic and Molecular Research, American Society for Microbiology, Washington, D.C. (1997).

The invention features *A. fumigatus* polypeptides, preferably a substantially pure preparation of an *A. fumigatus* polypeptide, or a recombinant *A. fumigatus* polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acid residues in length; the polypeptide includes at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least about 50, 100, or 150 contiguous amino acid residues of the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *A. fumigatus* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

In preferred embodiments: the *A. fumigatus* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained in the Sequence Listing.

In a preferred embodiment, the subject *A. fumigatus* polypeptide differs in amino acid sequence at about 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *A. fumigatus* polypeptide exhibits an *A. fumigatus* biological activity, e.g., the *A. fumigatus* polypeptide retains a biological activity of a naturally occurring *A. fumigatus* enzyme.

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

In yet other preferred embodiments, the *A. fumigatus* polypeptide is a recombinant fusion protein having a first *A. fumigatus* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *A. fumigatus* . The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

In a preferred embodiment, the encoded *A. fumigatus* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at about 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *A. fumigatus* encoded polypeptide exhibits an *A. fumigatus* biological activity, e.g., the encoded *A. fumigatus* enzyme retains a biological activity of a naturally occurring *A. fumigatus* .

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

The *A. fumigatus* strain, ND158, from which genomic sequences have been sequenced, has been deposited in the American Type Culture Collection and assigned the ATCC designation # 201795.

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridize under high or low stringency conditions to a nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *A. fumigatus* polypeptides, especially by antisera to an active site or binding domain of *A. fumigatus* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *A. fumigatus* polypeptide analogs or variants.

The invention further provides nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

In preferred embodiments, the subject *A. fumigatus* nucleic acid will include a transcriptional regulatory sequence, e.g., at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *A. fumigatus* gene sequence, e.g., to render the *A. fumigatus* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *A. fumigatus* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least about 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 12 consecutive nucleotides of the invention contained in the Sequence Listing; still more preferably to at least about 20 consecutive nucleotides of the invention contained in the Sequence Listing; most preferably to at least about 40 consecutive nucleotides of the invention contained in the Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *A. fumigatus* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at

least about 60%, 70%, 80%, 90%, 95%, 98% or 99% homologous to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least about 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *A. fumigatus* polypeptide or an *A. fumigatus* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *A. fumigatus* polypeptide or *A. fumigatus* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating *an A. fumigatus* or *A. fumigatus* polypeptide variant, e.g., from the cell or from the cell culture medium.

One embodiment of the invention is directed to substantially isolated nucleic acids. Nucleic acids of the invention include sequences comprising at least about 8 nucleotides in length, more preferably at least about 12 nucleotides in length, even more preferably at least about 15-20 nucleotides in length, that correspond to a subsequence of any one of SEQ ID NO: 1 - SEQ ID NO: 22156 or complements thereof. Alternatively, the nucleic acids comprise sequences contained within any ORF (open reading frame), including a complete protein-coding sequence, of which any of SEQ ID NO: 1 - SEQ ID NO: 22156 forms a part. The invention encompasses sequence-conservative variants and function-conservative variants of these sequences. The nucleic acids may be DNA, RNA, DNA/RNA duplexes, protein-nucleic acid (PNA), or derivatives thereof.

In another aspect, the invention features a purified recombinant nucleic acid having at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence of the invention contained in the Sequence Listing

The invention also encompasses recombinant DNA (including DNA cloning and expression vectors) comprising these *A. fumigatus* -derived sequences; host cells comprising such DNA, including fungal, bacterial, yeast, plant, insect, and mammalian host cells; and methods for producing expression products comprising RNA and polypeptides encoded by the *A. fumigatus* sequences. These methods are carried out by incubating a host cell comprising an *A. fumigatus* -derived nucleic acid sequence under conditions in which the sequence is expressed. The host cell may be native or recombinant. The polypeptides can be obtained by (a) harvesting the incubated cells to produce a cell fraction and a medium fraction; and (b) recovering the *A. fumigatus* polypeptide from the cell fraction, the medium fraction, or both. The polypeptides can also be made by *in vitro* translation.

In another aspect, the invention features nucleic acids capable of binding mRNA of *A. fumigatus* . Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *A. fumigatus* . A further aspect features a nucleic acid which is capable of binding specifically to an *A. fumigatus* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *A. fumigatus* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *A. fumigatus* nucleic acid.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *A. fumigatus* polypeptide or an *A. fumigatus* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *A. fumigatus* polypeptide or *A. fumigatus* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *A. fumigatus* or *A. fumigatus* polypeptide variant, e.g., from the cell or from the cell culture medium.

In yet another embodiment of the invention encompasses reagents for detecting fungal infection, including *A. fumigatus* infection, which comprise at least one *A. fumigatus* -derived nucleic acid defined by any one of SEQ ID NO: 1 - SEQ ID NO: 22156, or sequence-conservative or function-conservative variants thereof. Alternatively, the diagnostic reagents comprise nucleotide sequences that are contained within any open reading frames (ORFs), including preferably complete protein-coding sequences, contained within any of SEQ ID NO: 1 - SEQ ID NO: 22156, or polypeptide sequences contained within any of SEQ ID NO: 22157 - SEQ ID NO: 44266, or polypeptides of which any of the above sequences forms a part, or antibodies directed against any of the above peptide sequences or function-conservative variants and/or fragments thereof.

The invention further provides antibodies, preferably monoclonal antibodies, which specifically bind to the polypeptides of the invention. Methods are also provided for producing antibodies in a host animal. The methods of the invention comprise immunizing an animal with at least one *A. fumigatus* -derived immunogenic component, wherein the immunogenic component comprises one or more of the polypeptides encoded by any one of SEQ ID NO: 1 - SEQ ID NO: 22156 or sequence-conservative or function-conservative variants thereof; or polypeptides that are contained within any ORFs, including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 22156 forms a part; or polypeptide sequences contained within any of SEQ ID NO: 22157 - SEQ ID NO: 44266; or polypeptides of which any of SEQ ID NO: 22157 - SEQ ID NO: 44266 forms a part. Host animals include any warm blooded animal, including without limitation mammals and birds. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *A. fumigatus* -specific antigens.

In yet another aspect, the invention provides diagnostic methods for detecting *A. fumigatus* antigenic components or anti-*A. fumigatus* antibodies in a sample. *A. fumigatus* antigenic components may be detected by known processes, including but not limited to detection by a process comprising: (i) contacting a sample suspected to contain a fungal antigenic component with a fungal-specific antibody, under conditions in which a stable antigen-antibody complex can form

between the antibody and fungal antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of at least one fungal antigenic component in the sample. In different embodiments of this method, the antibodies used are directed against a sequence encoded by any of SEQ ID NO: 1 - SEQ ID NO: 22156 or sequence-conservative or function-conservative variants thereof, or against a polypeptide sequence contained in any of SEQ ID NO: 22157 - SEQ ID NO: 44266 or function-conservative variants thereof.

In yet another aspect, the invention provides a method for detecting antifungal-specific antibodies in a sample, which comprises: (i) contacting a sample suspected to contain antifungal-specific antibodies with an *A. fumigatus* antigenic component, under conditions in which a stable antigen-antibody complex can form between the *A. fumigatus* antigenic component and antifungal antibodies in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of antifungal antibodies in the sample. In different embodiments of this method, the antigenic component is encoded by a sequence contained in any of SEQ ID NO: 1 - SEQ ID NO: 22156 or sequence-conservative and function-conservative variants thereof, or is a polypeptide sequence contained in any of SEQ ID NO: 22157 - SEQ ID NO: 44266 or function-conservative variants thereof.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *A. fumigatus* . The method includes: immunizing a subject with an *A. fumigatus* polypeptide, e.g., a surface or secreted polypeptide, or a combination of such peptides or active portion(s) thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *A. fumigatus* polypeptide. The method includes contacting the compound to be evaluated with an *A. fumigatus* polypeptide and determining if the compound binds or otherwise interacts with the *A. fumigatus*

polypeptide. Compounds which bind or otherwise interact with *A. fumigatus* polypeptides are candidates as modulators, including activators and inhibitors, of the fungal life cycle. These assays can be performed *in vitro* or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *A. fumigatus* nucleic acid, e.g., DNA or RNA. The method includes contacting the compound to be evaluated with an *A. fumigatus* nucleic acid and determining if the compound binds or otherwise interacts with the *A. fumigatus* nucleic acid. Compounds which bind *A. fumigatus* are candidates as modultors, including activators and inhibitors, of the fungal life cycle. These assays can be performed *in vitro* or *in vivo*.

A particularly preferred embodiment of the invention is directed to a method of screening test compounds for anti-fungal activity, which method comprises: selecting as a target a fungal specific sequence, which sequence is essential to the viability of a fungal species; contacting a test compound with said target sequence; and selecting those test compounds which bind to said target sequence as potential anti-fungal candidates. In one embodiment, the target sequence selected is specific to a single species, or even a single strain, such as, for example, the strain *A. fumigatus* ND128. In a second embodiment, the target sequence is common to at least two species of bacteria. In a third embodiment, the target sequence is common to a family of bacteria. The target sequence may be a nucleic acid sequence or a polypeptide sequence. Methods employing sequences common to more than one species of microorganism may be used to screen candidates for broad spectrum anti-fungal activity.

The invention also provides methods for preventing or treating disease caused by certain bacteria, including *A. fumigatus* , which are carried out by administering to an animal in need of such treatment, in particular a warm-blooded vertebrate, including but not limited to birds and mammals, a compound that specifically inhibits or interferes with the function of a fungal

polypeptide or nucleic acid. In a particularly preferred embodiment, the mammal to be treated is human.

DETAILED DESCRIPTION OF THE INVENTION

The sequences of the present invention include the specific nucleic acid and amino acid sequences set forth in the Sequence Listing that forms a part of the present specification, and which are designated SEQ ID NO: 1 - SEQ ID NO: 44266. Use of the terms "SEQ ID NO: 1 - SEQ ID NO: 22156 ", " SEQ ID NO: 22157 - SEQ ID NO: 44266, "the sequences depicted in Table 2", etc., is intended, for convenience, to refer to each individual SEQ ID NO *individually*, and is not intended to refer to the genus of these sequences unless such reference would be indicated. In other words, it is a shorthand for listing all of these sequences individually. The invention encompasses each sequence individually, as well as any combination thereof.

Definitions

"Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, i.e., DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

A nucleic acid or polypeptide sequence that is "derived from" a designated sequence refers to a sequence that corresponds to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants." For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the

amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native polypeptide, including, but not limited to, replacement of an amino acid with one having similar physico-chemical properties (such as, for example, acidic, basic, hydrophobic, and the like). "Function-conservative" variants also include any polypeptides that have the ability to elicit antibodies specific to a designated polypeptide.

An "*A. fumigatus* -derived" nucleic acid or polypeptide sequence may or may not be present in other fungal species, and may or may not be present in all *A. fumigatus* strains. This term is intended to refer to the source from which the sequence was originally isolated. Thus, an *A. fumigatus* -derived polypeptide, as used herein, may be used, e.g., as a target to screen for a broad spectrum antifungal agent, to search for homologous proteins in other species of bacteria or in eukaryotic organisms such asbacteria humans, etc.

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least about 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains sufficient polypeptide to allow protein sequencing; at least about 1, 10, or preferably 100 mg of polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least about 10%, more preferably at least about 50%, of the subject cells.

A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous

(i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *A. fumigatus* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise

dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

"Homologous" refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the

sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C) require correspondingly less overall complementarity between the hybridizing sequences. (1X SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

A polypeptide has *A. fumigatus* biological activity if it has one, two or preferably more of the following properties: (1) if when expressed in the course of an *A. fumigatus* infection, it can promote, or mediate the attachment of *A. fumigatus* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *A. fumigatus* protein; (3) the gene which encodes it can rescue a lethal mutation in an *A. fumigatus* gene. A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *A. fumigatus* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *A. fumigatus* polypeptides, e.g., one or more of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO (Chinese Hamster Ovary) cells. Because peptides such as *A. fumigatus* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *A. fumigatus* fragment or *A. fumigatus* analog is one which exhibits a biological activity in any biological assay for *A. fumigatus* activity. The fragment or analog possesses about 10%, preferably about 40%, more

preferably about 60%, 70%, 80% or 90% or greater of the activity of *A. fumigatus* , in any *in vivo* or *in vitro* assay.

Analogs can differ from naturally occurring *A. fumigatus* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogs include *A. fumigatus* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *A. fumigatus* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

TABLE 1

CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β-Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met

Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *A. fumigatus* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *A. fumigatus* polypeptides can be generated by methods known to those skilled in the art. The ability of an *Aspergillus* fragment to exhibit a biological activity of *A. fumigatus* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *A. fumigatus* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

An "immunogenic component" as used herein is a moiety, such as an *A. fumigatus* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *A. fumigatus* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *A. fumigatus* polypeptides.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of increased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been

used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

The "metabolism" of a substance, as used herein, means any aspect of the expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isloated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph,

tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present invention pertains, unless otherwise defined. Reference is made herein to various methodologies known to those of skill in the art. Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full. The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See e.g.*, Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.); *PCR*-A *Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991); *Immunology*, 2d Edition, 1989, Roitt *et al.*, C.V. Mosby Company, and New York; *Advanced Immunology*, 2d Edition, 1991, Male *et al.*, Grower Medical Publishing, New York.; *DNA Cloning:* A *Practical Approach*, Volumes I and II, 1985 (D.N. Glover ed.); *Oligonucleotide Synthesis,* 1984, (M.L. Gait ed); *Transcription and Translation*, 1984 (Hames and Higgins eds.); *Animal Cell Culture*, 1986 (R.I. Freshney ed.); *Immobilized Cells and Enzymes*, 1986 (IRL Press); Perbal, 1984, A *Practical Guide to Molecular Cloning*; *Gene Transfer Vectors for Mammalian Cells*, 1987 (J. H. Miller and M. P. Calos eds., Cold Spring Harbor Laboratory); Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Any suitable materials and/or methods known to those of skill can be utilized in carrying out the present invention; however, preferred materials and/or methods are described. Materials, reagents and the like to which reference is made in the following description and examples are obtainable from commercial sources, unless otherwise noted.

A. fumigatus Genomic Sequence

This invention provides nucleotide sequences of the genome of *A. fumigatus* which, in a preferred embodiment, comprises a DNA sequence library of *A. fumigatus* genomic DNA. The detailed description that follows provides nucleotide sequences of *A. fumigatus*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are methods of using the disclosed *A. fumigatus* sequences in methods including diagnostic and therapeutic applications. Furthermore, one or more libraries according to the present invention can be used as a database for identification and comparison of medically important sequences in this and other strains of *A. fumigatus*.

A. fumigatus DNA was isolated from cultures grown on Sabouraud Dextrose medium (Difco Manual, Tenth Edition (1984) Difco Laboratories Incorporated, Detroit, p.768). The isolation protocol included an initial polytron homogenization, repeated freezing and boiling of the extract followed by glass bead homogenization and phenol:chloroform:iso-amyl alcohol extraction (e.g., *Methods. Enzymol.* Guide to Yeast Genetics and Molecular Biology, Volume 194, Guthrie C and Fink GR, editors, Academic Press, Inc., Boston, Cold Spring Harbor, New York). The final extract was ethanol-precipitated, centrifuged, and the DNA pellet redissolved.

All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. Only major modifications to the protocols are highlighted. Briefly, the library was transformed into DH5á competent cells (Gibco/BRL, DH5á transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and IPTG/Xgal. The plates were incubated overnight at 37^0C. Successful transformants were then used for plating of clones and picking for sequencing. The cultures were grown overnight at 37 ^{0}C. DNA was purified using a

silica bead DNA preparation (Engelstein, 1996) method. In this manner, 25 ug of DNA was obtained per clone.

These purified DNA samples were then sequenced using ABI dye-terminator chemistry. The ABI dye terminator sequence reads were run on ABI377 machines and the data was transferred to UNIX machines following lane tracking of the gels. All reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. (1996)) with default parameters and quality scores. The initial assembly was done at 2-fold coverage and yielded 11522 contigs. Following the initial assembly, missing mates (sequences from clones that only gave one strand reads) are identified and sequenced with ABI technology to allow the identification of additional overlapping contigs. Primers for walking are selected using Pick_primer (GTC program) near the ends of the clones to facilitate gap closure. These walks are sequenced using the selected clones and primers. These data are then reassembled with PHRAP. For additional cloning and sequencing techniques please see the Exemplification.

A variety of approaches are used to order the contigs so as to obtain a continuous sequence representing the entire *A. fumigatus* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libaries of *A. fumigatus* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *A. fumigatus* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *A. fumigatus* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *A. fumigatus* polypeptide. Such start codons within the ORFs provided herein were identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *A. fumigatus* polypeptide is within the scope of this invention.

For example, within the ORFs a codon such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis were identified and the portion of an ORF to corresponding to a naturally-occurring *A. fumigatus* polypeptide was recognized. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program GENEMARK™ (Borodovsky and McIninch, 1993, *Comp.* . 17:123).

Each predicted ORF amino acid sequence was compared with all sequences found in current GENBANK, SWISS-PROT, and PIR databases using the BLAST algorithm. BLAST identifies local alignments occurring by chance between the ORF sequence and the sequence in the databank (Altschal et al., 1990, L Mol. Biol. 215:403-410). Homologous ORFs (probabilities less than 10^{-5} by chance) andORF's that are probably non-homologous (probabilities greater than 10^{-5} by chance) but have good codon usage were identified. Both homologous, sequences and non-homologous sequences with good codon usage, are likely to encode proteins and are encompassed by the invention.

A. fumigatus Nucleic Acids

The present invention provides a library of *A. fumigatus* -derived nucleic acid sequences. The libraries provide probes, primers, and markers which are used as markers in epidemiological studies. The present invention also provides a library of *A. fumigatus* -derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

The nucleic acids of this invention may be obtained directly from the DNA of the above referenced *A. fumigatus* strain by using the polymerase chain reaction (PCR). See "*PCR,* A *Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK, 1991) for details about the PCR. High fidelity PCRis used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products is verified by conventional sequencing methods. Clones carrying the desired sequences described in this invention may also be obtained by screening

the libraries by means of the PCR or by hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning,* A *Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *A. fumigatus* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *A. fumigatus* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *A. fumigatus* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

In another example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 764:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Nucleic acids isolated or synthesized in accordance with features of the present invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to

such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products) of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

Probes

A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *A. fumigatus* . With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *A. fumigatus* , and extraneous nucleic acids likely to be encountered during hybridization conditions. More preferably, the sequence will comprise at least about twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the invention contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Aspergillus* species using appropriate stringency hybridization conditions as described herein.

Capture Ligand

For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more nucleotides in a

sequence of the invention contained in the Sequence Listing have utility to separate *A. fumigatus* nucleic acid from one strain from the nucleic acid of other another strain as well as from other organisms. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Aspergillus* species from each other and from other organisms. Preferably, the sequence will comprise at least about twenty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility as primers for the amplification of *A. fumigatus* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Aspergillus* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of $\geq$ 10-15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *A. fumigatus* nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *A. fumigatus* and/or other *Aspergillus* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail herein.

The nucleic acids of the present invention find use as templates for the recombinant production of *A. fumigatus* -derived peptides or polypeptides

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *A. fumigatus* genes. These sequences also have utility as antisense agents to prevent expression of genes of other *Aspergillus* species.

In one embodiment, nucleic acid or derivatives corresponding to *A. fumigatus* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and fungal nucleic acid and/or fungal messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

The present invention encompasses isolated polypeptides and nucleic acids derived from *A. fumigatus* that are useful as reagents for diagnosis of fungal infection, components of effective anti-fungal vaccines, and/or as targets for anti-fungal drugs, including anti-*A. fumigatus* drugs.

Expression of *A. fumigatus* Nucleic Acids

Table 2, which is appended herewith and which forms part of the present specification, provides a list of open reading frames (ORFs) in both strands and a putative

identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. An ORF is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and was determined from stop to stop codons. The first column contains a designation for the ORF ("ORF Name"). The second and third columns list the SEQ ID numbers for the nucleic acid ("NT ID") and amino acid ("AA ID") sequences corresponding to each ORF, respectively. The fourth and fifth columns list the length of the nucleic acid ORF ("NT LN") and the length of the amino acid ORF ("AA LN"), respectively. The nucleotide sequence corresponding to each ORF begins at the first nucleotide immediately following a stop codon and ends at the nucleotide immediately preceding the next downstream stop codon in the same reading frame. It will be recognized by one skilled in the art that the natural translation initiation sites will correspond to ATG, GTG, or TTG codons located within the ORFs. The natural initiation sites depend not only on the sequence of a start codon but also on the context of the DNA sequence adjacent to the start codon. Usually, a recognizable ribosome binding site is found within 20 nucleotides upstream from the initiation codon. In some cases where genes are translationally coupled and coordinately expressed together in "operons", ribosome binding sites are not present, but the initiation codon of a downstream gene may occur very close to, or overlap, the stop codon of the an upstream gene in the same operon. The correct start codons can be generally identified without undue experimentation because only a few codons need be tested. It is recognized that the translational machinery in bacteria initiates all polypeptide chains with the amino acid methionine, regardless of the sequence of the start codon. In some cases, polypeptides are post-translationally modified, resulting in an N-terminal amino acid

other than methionine *in vivo*. Using the BLASTP2 algorithm as is in known in the art in determining gene similarity, each ORF's relative match was identified and is contained within the description frame ("Description"). These proteins in the Description were identified when the designated ORF was compared against a non-redundant comprehensive protein database. If a BLASTP2 score of less than 100 was obtained, no value is reported in the table. The Description provides, where available, the Swissprot accession number (SP), the locus name (LN), the Organism (OR), Source of variant (SR), E.C. number (EC), the gene name (GN), the product name (PN), the Function Description (FN), Left End (LE), Right End (RE), Coding Direction (DI), and the description (DE) or notes (NT) for each ORF. This information allows one of ordinary skill in the art to determine a potential use for each identified coding sequence and, as a result, allows to use the polypeptides of the present invention for commercial and industrial purposes.

Using the information provided in SEQ ID NO: 1 - SEQ ID NO: 22156, SEQ ID NO: 22157 - SEQ ID NO: 44266 and in Table 2 together with routine cloning and sequencing methods, one of ordinary skill in the art will be able to clone and sequence all the nucleic acid fragments of interest including open reading frames (ORFs) encoding a large variety of proteins of *A. fumigatus*.

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in SEQ ID NO: 1 - SEQ ID NO: 22156 and in Table 2 or fragments of said nucleic acid encoding active portions of *A. fumigatus* polypeptides can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large

quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the same gene product(s). This includes, but is not limited to, Eucaryotic species such as the yeast *Saccharomyces cerevisiae, Methanobacterium* strains or other Archaea, and Eubacteria such as *E. coli*, *B. Subtilis, S. Aureus, S. Pneumonia* or *Pseudomonas putida*. In some cases the expression host will utilize the natural *A. fumigatus* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *A. fumigatus* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning:

A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press (1989)), and other laboratory textbooks.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *A. fumigatus* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Chromatographic techniques which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *A. fumigatus* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding an *A. fumigatus* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

The present invention provides a library of *A. fumigatus* -derived nucleic acid sequences. The libraries provide probes, primers, and markers which can be used as markers in epidemiological studies. The present invention also provides a library of *A. fumigatus* -derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

Nucleic acids comprising any of the sequences disclosed herein or sub-sequences thereof can be prepared by standard methods using the nucleic acid sequence information provided in SEQ ID NO: 1 - SEQ ID NO: 22156. For example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 764:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Of course, due to the degeneracy of the genetic code, many different nucleotide sequences can encode polypeptides having the amino acid sequences defined by SEQ ID NO: 22157 - SEQ ID NO: 44266 or sub-sequences thereof. The codons can be selected for optimal expression in prokaryotic or eukaryotic systems. Such degenerate variants are also encompassed by this invention.

Insertion of nucleic acids (typically DNAs) encoding the polypeptides of the invention into a vector is easily accomplished when the termini of both the DNAs and the vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-stranded DNA overhangs generated by restriction

endonuclease cleavage to produce blunt ends, or to achieve the same result by filling in the single-stranded termini with an appropriate DNA polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki *et al.*, 1988, *Science* 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

The nucleic acids of the invention may be isolated directly from cells. Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or genomic material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

The nucleic acids of the present invention may be flanked by natural *A. fumigatus* regulatory sequences, or may be associated with heterologous sequences, including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3'-noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also included. The nucleic acid may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage.

Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

The invention also provides nucleic acid vectors comprising the disclosed *A. fumigatus* - derived sequences or derivatives or fragments thereof. A large number of vectors, including plasmid and bacterial vectors, have been described for replication and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for cloning or protein expression.

The encoded *A. fumigatus* polypeptides may be expressed by using many known vectors, such as pUC plasmids, pET plasmids (Novagen, Inc., Madison, WI), or pRSET or pREP (Invitrogen, San Diego, CA), and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

Recombinant cloning vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, e.g. antibiotic resistance, and one or more expression cassettes. The inserted *A. fumigatus* coding sequences may be synthesized by standard methods, isolated from natural sources, or prepared as hybrids, etc. Ligation of the *A. fumigatus* coding sequences to transcriptional regulatory elements and/or to other amino acid coding sequences may be achieved by known methods. Suitable host cells may be transformed/transfected/infected as appropriate by any suitable method including electroporation, $CaCl_2$ mediated DNA uptake, fungal infection, microinjection, microprojectile, or other established methods.

Appropriate host cells include bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *A. fumigatus* , *E. coli, B. Subtilis, Saccharomyces cerevisiae, Saccharomyces carlsbergensis, Schizosaccharomyces pombi, SF9* cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include

M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced *A. fumigatus* -derived peptides and polypeptides.

Advantageously, vectors may also include a transcription regulatory element (i.e., a promoter) operably linked to the *A. fumigatus* portion. The promoter may optionally contain operator portions and/or ribosome binding sites. Non-limiting examples of bacterial promoters compatible with *E. coli* include: b-lactamase (penicillinase) promoter; lactose promoter; tryptophan (trp) promoter; araBAD (arabinose) operon promoter; lambda-derived P$_L$ promoter and N gene ribosome binding site; and the hybrid tac promoter derived from sequences of the trp and lac UV5 promoters. Non-limiting examples of yeast promoters include 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactoepimerase promoter, and alcohol dehydrogenase (ADH) promoter. Suitable promoters for mammalian cells include without limitation viral promoters such as that from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences, polyA addition sequences and enhancer sequences to increase expression. Sequences which cause amplification of the gene may also be desirable. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or prohormone pro region sequences, may also be included. These sequences are well described in the art.

Nucleic acids encoding wild-type or variant *A. fumigatus* -derived polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence

with substantial identity to the gene. Other recombination-based methods such as nonhomologous recombinations or deletion of endogenous genes by homologous recombination may also be used.

The nucleic acids of the present invention find use as templates for the recombinant production of *A. fumigatus* -derived peptides or polypeptides.

Identification and Use of *A. fumigatus* Nucleic Acid Sequences

The disclosed *A. fumigatus* polypeptide and nucleic acid sequences, or other sequences that are contained within ORFs, including complete protein-coding sequences, of which any of the disclosed *A. fumigatus* -specific sequences forms a part, are useful as target components for diagnosis and/or treatment of *A. fumigatus* - caused infection

It will be understood that the sequence of an entire protein-coding sequence of which each disclosed nucleic acid sequence forms a part can be isolated and identified based on each disclosed sequence. This can be achieved, for example, by using an isolated nucleic acid encoding the disclosed sequence, or fragments thereof, to prime a sequencing reaction with genomic *A. fumigatus* DNA as template; this is followed by sequencing the amplified product. The isolated nucleic acid encoding the disclosed sequence, or fragments thereof, can also be hybridized to *A. fumigatus* genomic libraries to identify clones containing additional complete segments of the protein-coding sequence of which the shorter sequence forms a part. Then, the entire protein-coding sequence, or fragments thereof, or nucleic acids encoding all or part of the sequence, or sequence-conservative or function-conservative variants thereof, may be employed in practicing the present invention.

Preferred sequences are those that are useful in diagnostic and/or therapeutic applications. Diagnostic applications include without limitation nucleic-acid-based and antibody-based methods for detecting fungal infection. Therapeutic applications include without limitation vaccines, passive immunotherapy, and drug treatments directed against gene products that are both unique to bacteria and essential for growth and/or replication of bacteria.

Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *A. fumigatus*

The disclosed *A. fumigatus* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *A. fumigatus* . Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

Homology to known sequences:

Computer-assisted comparison of the disclosed *A. fumigatus* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *A. fumigatus* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-

coding sequence. Identification of such a feature in an *A. fumigatus* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antifungal drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal peptides and hydrophobic transmembrane domains. *A. fumigatus* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

Targets for therapeutic drugs according to the invention include, but are not limited to, polypeptides of the invention, whether unique to *A. fumigatus* or not, that are essential for growth and/or viability of *A. fumigatus* under at least one growth condition. Polypeptides essential for growth and/or viability can be determined by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout". Alternatively, genetic footprinting can be used (Smith *et al.*, 1995, *Proc. Natl. Acad. Sci. USA* 92:5479-6433; Published International Application WO 94/26933; U.S. Patent No. 5,612,180). Still other methods for assessing essentiality includes the ability to isolate conditional lethal mutations in the specific gene (e.g., temperature sensitive mutations). Other useful targets for therapeutic drugs, which include polypeptides that are not essential for growth or viability *per se* but lead to loss of viability of the cell, can be used to target therapeutic agents to cells.

Strain-specific sequences:

Because of the evolutionary relationship between different *A. fumigatus* strains, it is believed that the presently disclosed *A. fumigatus* sequences are useful for identifying, and/or discriminating between, previously known and new *A. fumigatus* strains. It is believed that other *A. fumigatus* strains will exhibit at least about 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *A. fumigatus* strains, and comparison with the present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all

A. fumigatus strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *A. fumigatus* . Strain-specific components can also be identified functionally by their ability to elicit or react with antibodies that selectively recognize one or more *A. fumigatus* strains.

In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *A. fumigatus* strains but are not found in other fungal species.

A. fumigatus Polypeptides

This invention encompasses isolated *A. fumigatus* polypeptides encoded by the disclosed *A. fumigatus* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least about 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding an *A. fumigatus* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *A. fumigatus* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the present invention, including function-conservative variants of the disclosed ORFs, may be isolated from wild-type or mutant *A. fumigatus* cells, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) including *A. fumigatus* into which an *A. fumigatus* -derived protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

A. fumigatus polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein , including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, *J. Am. Chem. Soc.* 85:2149. The synthesis is carried out with amino acids that are protected at the alpha-amino terminus. Trifunctional amino acids with labile side-chains are also protected with suitable groups to prevent undesired chemical reactions from occurring during the assembly of the polypeptides. The alpha-amino protecting group is selectively removed to allow subsequent reaction to take place at the amino-terminus. The conditions for the removal of the alpha-amino protecting group do not remove the side-chain protecting groups.

Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the *A. fumigatus* protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against an *A. fumigatus* protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The present invention also encompasses derivatives and homologues of *A. fumigatus* - encoded polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

To identify *A. fumigatus* -derived polypeptides for use in the present invention, essentially the complete genomic sequence of a virulent, methicillin-resistant isolate of *Aspergillus mirabilis* isolate was analyzed. While, in very rare instances, a nucleic acid sequencing error may be revealed, resolving a rare sequencing error is well within the art, and such an occurrence will not prevent one skilled in the art from practicing the invention.

Also encompassed are any *A. fumigatus* polypeptide sequences that are contained within the open reading frames (ORFs), including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 22156 forms a part. Table 2, which is appended herewith and which forms part of the present specification, provides a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. As a result, one skilled in the art can use the polypeptides of the present invention for commercial and industrial purposes consistent with the type of putative identification of the polypeptide.

The present invention provides a library of *A. fumigatus* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences that are contemplated for use as components of vaccines. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended herewith and which forms part of the present specification.

The present invention also provides a library of *A. fumigatus* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides,

wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences lacking homology to any known prokaryotic or eukaryotic sequences. Such libraries provide probes, primers, and markers which can be used to diagnose *A. fumigatus* infection, including use as markers in epidemiological studies. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended hereto and part hereof.

The present invention also provides a library of *A. fumigatus* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise targets for therapeutic drugs.

Specific Example: Determination Of *Aspergillus* Protein Antigens For Antibody And Vaccine Development

The selection of Aspergillus protein antigens for vaccine development can be derived from the nucleic acids encoding *A. fumigatus* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities lower than $1x10^{-6}$ that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible

functions can be provided to *A. fumigatus* genes based on sequence homology to genes cloned in other organisms.

Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

Production of Fragments and Analogs of *A. fumigatus* Nucleic Acids and Polypeptides

Based on the discovery of the *A. fumigatus* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed structure of *A. fumigatus* genes, e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *A. fumigatus* polypeptides. Such screens are useful for the identification of inhibitors of *A. fumigatus* .

Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases

can thus generate DNAs which encode an array of fragments. DNAs which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

Alteration of Nucleic Acids and Polypeptides: Random Methods

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

Saturation Mutagenesis

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique

includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro,* and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results

achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

Alanine Scanning Mutagenesis

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

Oligonucleotide-Mediated Mutagenesis

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA.

Generally, oligonucleotides of at least about 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci.* USA, 75: 5765[1978]).

Cassette Mutagenesis

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related

proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

Other Modifications of *A. fumigatus* Nucleic Acids and Polypeptides

It is possible to modify the structure of an *A. fumigatus* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). A modified *A. fumigatus* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *A. fumigatus* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *A. fumigatus* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *A. fumigatus* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Sehon and co-workers (Wie et al., supra) to produce a protein conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *A. fumigatus* proteins include reduction/alkylation (Tarr, *Methods of Protein*

Microcharacterization, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, supra); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of an *A. fumigatus* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *A. fumigatus* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *A. fumigatus* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below

is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

Two Hybrid Systems

Two hybrid assays such as the system described below (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *A. fumigatus* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *A. fumigatus* protein. (The *A. fumigatus* domain is used as the bait protein and the library of variants are expressed as prey fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind an *A. fumigatus* polypeptide.

Display Libraries

In one approach to screening assays, the Aspergillus peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the

surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages, M13, fd., and f1, are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH_2-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines 91*, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface

proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus* protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull *et al.* (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stablely associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.*A. 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their

C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.*A. 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7-10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the

ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated though one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics of *A. fumigatus* Polypeptides

The invention also provides for reduction of the protein binding domains of the subject *A. fumigatus* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *A. fumigatus* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *A. fumigatus* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *A. fumigatus* -derived peptidomimetics which competitively or noncompetitively inhibit binding of the *A. fumigatus* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *A. fumigatus* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *A. fumigatus* polypeptide to an interacting polypeptide and thereby interfere with the function of *A. fumigatus* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gama lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), b-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans*

1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and et al. (1986) *Biochem Biophys Res Commun* 134:71).

Vaccine Formulations for *A. fumigatus* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against infection by *A. fumigatus* or for treatment of *A. fumigatus* infection. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *A. fumigatus* , or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *A. fumigatus* surface proteins. Any nucleic acid encoding an immunogenic *A. fumigatus* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against infection by *A. fumigatus* which contains at least one immunogenic fragment of an *A. fumigatus* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *A. fumigatus* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are

thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *A. fumigatus* peptide in association with appropriate MHC molecules to T cells in conjunction with the necessary co-stimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ^{3}H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

Vaccine compositions of the invention containing immunogenic components (e.g., *A. fumigatus* polypeptide or fragment thereof or nucleic acid encoding an *A. fumigatus* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *A. fumigatus* polypeptides, the polypeptide is co-administered with a suitable adjuvant.

It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *A. fumigatus* . Cain et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl--L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to a MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycoloate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *A. fumigatus* polypeptide with cholera toxin or its B subunit, procholeragenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*A. fumigatus* fungal lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immuno-stimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 mg to 50 mg, for example 10 mg to 35 mg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *A. fumigatus* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N $NaHCO_3$ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *A. fumigatus* in an infected host,

or as a therapeutic agent in the aim to induce an immune response in a susceptible host to prevent infection by *A. fumigatus* . The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 mg to 10 g, preferably 10 mg to 100 mg. A suitable dosage for adults will also be in the range of 5 mg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *A. fumigatus* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *A. fumigatus* infection, some are useful only for treating *A. fumigatus* infection, and some are useful for both preventing and treating *A. fumigatus* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *A. fumigatus* infection by stimulating humoral and/or cell-mediated immunity against *A. fumigatus* . It should be understood that amelioration of any of the symptoms of *A. fumigatus* infection is a

desirable clinical goal, including a lessening of the dosage of medication used to treat *A. fumigatus* -caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

Antibodies Reactive With *A. fumigatus* Polypeptides

The invention also includes antibodies specifically reactive with the subject *A. fumigatus* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies:* A *Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *A. fumigatus* polypeptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *A. fumigatus* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least about 95% homologous). In yet a further preferred embodiment of the invention, the anti-*A. fumigatus* antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most preferred embodiment, there is no cross-reactivity between fungal and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *A. fumigatus* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, $F(ab')_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab')_2$ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*A. fumigatus* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *A. fumigatus* polypeptides or *A. fumigatus* polypeptide variants, and antibody fragments such as Fab` and $F(ab`)_2$, can be used to block the action of *A. fumigatus* polypeptide and allow the study of the role of a particular *A. fumigatus* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *A. fumigatus* and by microinjection of anti-*A. fumigatus* polypeptide antibodies of the present invention.

Antibodies which specifically bind *A. fumigatus* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *A. fumigatus* antigens. Anti-*A. fumigatus* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *A. fumigatus* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *A. fumigatus* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *A. fumigatus* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*A. fumigatus* antibodies can include, for example, immunoassays designed to aid in early diagnosis of *A. fumigatus* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *A. fumigatus* antigens.

Another application of anti-*A. fumigatus* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λgt11, λgt18-23, λZAP, and λORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λgt11 will produce fusion proteins whose amino termini consist of ß-galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *A. fumigatus* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*A. fumigatus* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *A. fumigatus* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

Bio chip Technology

The nucleic acid sequence of the present invention may be used to detect *A. fumigatus* or other species of *Aspergillus* acid sequence using bio chip technology. Bio chips containing arrays of nucleic acid sequence can also be used to measure expression of genes of *A. fumigatus* or other species of *Aspergillus*. For example, to diagnose a patient with a *A. fumigatus* or other *Aspergillus* infection, a sample from a human or animal can be used as a probe on a bio chip containing an array of nucleic acid sequence from the present invention. In addition, a sample from a disease state can be compared to a sample from a non-disease state which would help identify a gene that is up-regulated or expressed in the disease state. This would provide valuable insight as to the mechanism by which the disease manifests. Changes in gene expression can also be used to identify critical pathways involved in drug transport or metabolism, and may enable the identification of novel targets involved in virulence or host cell interactions involved in maintenance of an infection. Procedures using such techniques have been described by Brown *et al.*, 1995, *Science* 270: 467-470.

Bio chips can also be used to monitor the genetic changes of potential therapeutic compounds including, deletions, insertions or mismatches. Once the therapeutic is added to the patient, changes to the genetic sequence can be evaluated for its efficacy. In addition, the nucleic acid sequence of the present invention can be used to determine essential genes in cell cycling. As described in Iyer *et al.*, 1999 (*Science*, 283:83-87) genes essential in the cell cycle can be identified using bio chips. Furthermore, the present invention provides nucleic acid sequence which can be used with bio chip technology to understand regulatory networks in bacteria, measure the response to environmental signals or drugs as in drug screening, and study virulence induction. (Mons *et al.*, 1998, *Nature Biotechnology*, 16: 45-48. Patents teaching this technology include U.S. Patents 5445934, 5744305, and 5800992.

Drug Screening Assays Using *A. fumigatus* Polypeptides

By making available purified and recombinant *A. fumigatus* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *A. fumigatus* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *A. fumigatus* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the person skilled in the art.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *A. fumigatus* polypeptide.

Screening assays can be constructed *in vitro* with a purified *A. fumigatus* polypeptide or fragment thereof, such as an *A. fumigatus* polypeptide having enzymatic activity, such that the activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *A. fumigatus* polypeptide. Some of these active compounds may

directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *A. fumigatus* cells.

Overexpression Assays

Overexpression assays are based on the premise that overproduction of a protein would lead to a higher level of resistance to compounds that selectively interfere with the function of that protein. Overexpression assays may be used to identify compounds that interfere with the function of virtually any type of protein, including without limitation enzymes, receptors, DNA- or RNA-binding proteins, or any proteins that are directly or indirectly involved in regulating cell growth.

Typically, two bacterial strains are constructed. One contains a single copy of the gene of interest, and a second contains several copies of the same gene. Identification of useful inhibitory compounds of this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of the two strains. The method involves constructing a nucleic acid vector that directs high level expression of a particular target nucleic acid. The vectors are then transformed into host cells in single or multiple copies to produce strains that express low to moderate and high levels of protein encoding by the target sequence (strain A and B, respectively). Nucleic acid comprising sequences encoding the target gene can, of course, be directly integrated into the host cell.

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on the growth of the two strains. Agents which interfere with an unrelated target equally inhibit the growth of both strains. Agents which interfere with the function of the target at high concentration should inhibit the growth of both strains. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit the growth of strain A at a concentration of the compound that allows strain B to grow.

Alternatively, a bacterial strain is constructed that contains the gene of interest under the control of an inducible promoter. Identification of useful inhibitory agents using this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of this strain under both inducing and non-inducing conditions. The method involves constructing a nucleic acid vector that directs high-level expression of a particular target nucleic acid. The vector is then transformed into host cells that are grown under both non-inducing and inducing conditions (conditions A and B, respectively).

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on growth under these two conditions. Agents that interfere with the function of the target should inhibit growth under both conditions. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit growth under condition A at a concentration that allows the strain to grow under condition B.

Ligand-binding Assays

Many of the targets according to the invention have functions that have not yet been identified. Ligand-binding assays are useful to identify inhibitor compounds that interfere with the function of a particular target, even when that function is unknown. These assays are designed to detect binding of test compounds to particular targets. The detection may involve direct measurement of binding. Alternatively, indirect indications of binding may involve stabilization of protein structure or disruption of a biological function. Non-limiting examples of useful ligand-binding assays are detailed below.

A useful method for the detection and isolation of binding proteins is the Biomolecular Interaction Assay (BIAcore) system developed by Pharmacia Biosensor and described in the manufacturer's protocol (LKB Pharmacia, Sweden). The BIAcore system uses an affinity purified anti-GST antibody to immobilize GST-fusion proteins onto a sensor chip. The sensor utilizes

surface plasmon resonance which is an optical phenomenon that detects changes in refractive indices. In accordance with the practice of the invention, a protein of interest is coated onto a chip and test compounds are passed over the chip. Binding is detected by a change in the refractive index (surface plasmon resonance).

A different type of ligand-binding assay involves scintillation proximity assays (SPA, described in U.S. Patent No. 4,568,649).

Another type of ligand binding assay, also undergoing development, is based on the fact that proteins containing mitochondrial targeting signals are imported into isolated mitochondria *in vitro* (Hurt *et al.*, 1985, *Embo J.* 4:2061-2068; Eilers and Schatz, *Nature*, 1986, 322:228-231). In a mitochondrial import assay, expression vectors are constructed in which nucleic acids encoding particular target proteins are inserted downstream of sequences encoding mitochondrial import signals. The chimeric proteins are synthesized and tested for their ability to be imported into isolated mitochondria in the absence and presence of test compounds. A test compound that binds to the target protein should inhibit its uptake into isolated mitochondria *in vitro*.

Another ligand-binding assay is the yeast two-hybrid system (Fields and Song, 1989, *Nature* 340:245-246). The yeast two-hybrid system takes advantage of the properties of the GAL4 protein of the yeast *Saccharomyces cerevisiae*. The GAL4 protein is a transcriptional activator required for the expression of genes encoding enzymes of galactose utilization. This protein consists of two separable and functionally essential domains: an N-terminal domain which binds to specific DNA sequences (UAS_G); and a C-terminal domain containing acidic regions, which is necessary to activate transcription. The native GAL4 protein, containing both domains, is a potent activator of transcription when yeast are grown on galactose media. The N-terminal domain binds to DNA in a sequence-specific manner but is unable to activate transcription. The C-terminal domain contains the activating regions but cannot activate transcription because it fails to be localized to UAS_G. In the two-hybrid system, a system of two hybrid proteins containing parts of GAL4: (1) a GAL4 DNA-binding domain fused to a protein 'X' and (2) a GAL4 activation region fused to a protein 'Y'.

If X and Y can form a protein-protein complex and reconstitute proximity of the GAL4 domains, transcription of a gene regulated by UAS_G occurs. Creation of two hybrid proteins, each containing one of the interacting proteins X and Y, allows the activation region of UAS_G to be brought to its normal site of action.

The binding assay described in Fodor *et al.*, 1991, *Science* 251:767-773, which involves testing the binding affinity of test compounds for a plurality of defined polymers synthesized on a solid substrate, may also be useful.

Compounds which bind to the polypeptides of the invention are potentially useful as antifungal agents for use in therapeutic compositions.

Pharmaceutical formulations suitable for antifungal therapy comprise the antifungal agent in conjunction with one or more biologically acceptable carriers. Suitable biologically acceptable carriers include, but are not limited to, phosphate-buffered saline, saline, deionized water, or the like. Preferred biologically acceptable carriers are physiologically or pharmaceutically acceptable carriers.

The antifungal compositions include an antifungal effective amount of active agent. Antifungal effective amounts are those quantities of the antifungal agents of the present invention that afford prophylactic protection against fungal infections or which result in amelioration or cure of an existing fungal infection. This antifungal effective amount will depend upon the agent, the location and nature of the infection, and the particular host. The amount can be determined by experimentation known in the art, such as by establishing a matrix of dosages and frequencies and comparing a group of experimental units or subjects to each point in the matrix.

The antifungal active agents or compositions can be formed into dosage unit forms, such as for example, creams, ointments, lotions, powders, liquids, tablets, capsules, suppositories, sprays, aerosols or the like. If the antifungal composition is formulated into a dosage unit form, the dosage unit form may contain an antifungal effective amount of active agent. Alternatively, the dosage unit form may include less than such an amount if multiple dosage unit forms or multiple dosages are to

be used to administer a total dosage of the active agent. Dosage unit forms can include, in addition, one or more excipient(s), diluent(s), disintegrant(s), lubricant(s), plasticizer(s), colorant(s), dosage vehicle(s), absorption enhancer(s), stabilizer(s), bactericide(s), or the like.

For general information concerning formulations, see, e.g., Gilman et al. (eds.), 1990, *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*, 8th ed., Pergamon Press; and *Remington's Pharmaceutical Sciences*, 17th ed., 1990, Mack Publishing Co., Easton, PA; Avis et al. (eds.), 1993, *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York; Lieberman et al (eds.), 1990, *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York.

The antifungal agents and compositions of the present invention are useful for preventing or treating *A. fumigatus* infections. Infection prevention methods incorporate a prophylactically effective amount of an antifungal agent or composition. A prophylactically effective amount is an amount effective to prevent *A. fumigatus* infection and will depend upon the specific fungal strain, the agent, and the host. These amounts can be determined experimentally by methods known in the art and as described above.

A. fumigatus infection treatment methods incorporate a therapeutically effective amount of an antifungal agent or composition. A therapeutically effective amount is an amount sufficient to ameliorate or eliminate the infection. The prophylactically and/or therapeutically effective amounts can be administered in one administration or over repeated administrations. Therapeutic administration can be followed by prophylactic administration, once the initial fungal infection has been resolved.

The antifungal agents and compositions can be administered topically or systemically. Topical application is typically achieved by administration of creams, ointments, lotions, or sprays as described above. Systemic administration includes both oral and parental routes. Parental routes include, without limitation, subcutaneous, intramuscular, intraperitoneal, intravenous, transdermal, inhalation and intranasal administration.

EXEMPLIFICATION

Cloning and Sequencing *A. fumigatus* Genomic Sequence

This invention provides nucleotide sequences of the genome of *A. fumigatus* which thus comprises a DNA sequence library of *A. fumigatus* genomic DNA. The detailed description that follows provides nucleotide sequences of *A. fumigatus* , and also describes how the sequences were obtained and how ORFs (Open Reading Frames) and protein-coding sequences can be identified. Also described are methods of using the disclosed *A. fumigatus* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *A. fumigatus* as well as other species of *Aspergillus*.

Chromosomal DNA from strain ND158 of *A. fumigatus* DNA was isolated from cultures grown on Sabouraud Dextrose medium (Difco Manual, Tenth Edition (1984) Difco Laboratories Incorporated, Detroit, p.768). The isolation protocol included an initial polytron homogenization, repeated freezing and boiling of the extract followed by glass bead homogenization and phenol:chloroform:iso-amyl alcohol extraction (e.g., *Methods. Enzymol.* Guide to Yeast Genetics and Molecular Biology, Volume 194, Guthrie C and Fink GR, editors, Academic Press, Inc., Boston, Cold Spring Harbor, New York). The final extract was ethanol-precipitated, centrifuged, and the DNA pellet redissolved. Genomic *A. fumigatus* DNA was hydrodynamically sheared in an HPLC and then separated on a standard 1% agarose gel. Fractions corresponding to 2500-3000 bp in length were excised from the gel and purifed by the GeneClean procedure (Bio101, Inc.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique *Bst*XI-linker adapters (5'-GTCTTCACCACGGGG-3' and 5'-GTGGTGAAGAC-3' in 100-1000 fold molar excess). These linkers are complimentary to the

*Bst*XI-cut pGTC vector, while the overhang is not self-complimentary. Therefore, the linkers will not concatermerize nor will the cut-vector religate itself easily. The linker-adapted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adapted inserts were then ligated to *Bst*XI-cut vector to construct a "shotgun" sublclone libraries.

Only major modifications to the protocols are highlighted. Briefly, the library was then transformed into DH5α competent cells (Gibco/BRL, DH5á transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Transformants were then used for plating of clones and picking for sequencing. The cultures were grown overnight at 37°C. DNA was purified using a silica bead DNA preparation (Engelstein, 1996) method. In this manner, 25 μg of DNA was obtained per clone.

These purified DNA samples were then sequenced using primarily ABI dye-terminator chemistry. All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The ABI dye terminator sequence reads were run on ABI377 machines and the data was transferred to UNIX machines following lane tracking of the gels. Base calls and quality scores were determined using the program PHRED (Ewing et al., 1998, Genome Res. 8: 175-185; Ewing and Green, 1998, Genome Res. 8: 685-734). Reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157) with default program parameters and quality scores. The initial assembly was done at 2-fold coverage and yielded 11522 ordered contigs.

Finishing can follow the initial assembly. Missing mates (sequences from clones that only gave reads from one end of the *Aspergillus* DNA inserted in the plasmid) can be identified and sequenced with ABI technology to allow the identification of additional overlapping contigs.

End-sequencing of randomly picked genomic lambda was also performed. Sequencing on a both sides was done for all lambda sequences. The lambda library backbone

helped to verify the integrity of the assembly and allowed closure of some of the physical gaps. Primers for walking off the ends of contigs would be selected using pick_primer (a GTC program) near the ends of the clones to facilitate gap closure. These walks can be sequenced using the selected clones and primers. These data are then reassembled with PHRAP. Additional sequencing using PCR-generated templates and screened and/or unscreened lambda templates can be done in addition.

To identify *A. fumigatus* polypeptides the complete genomic sequence of *A. fumigatus* were analyzed essentially as follows: First, all possible stop-to- stop open reading frames (ORFs) greater than 180 nucleotides in all six reading frames were translated into amino acid sequences. Second, the identified ORFs were analyzed for homology to known (archeabacter, prokaryotic and eukaryotic) protein sequences. Third, the coding potential of non-homologous sequences were evaluated with the program GENEMARKTM (Borodovsky and Mclninch, 1993, Comp. Chem. 17:123).

Identification, Cloning and Expression of *A. fumigatus* Nucleic Acids

Expression and purification of the *A. fumigatus* polypeptides of the invention can be performed essentially as outlined below.

To facilitate the cloning, expression and purification of membrane and secreted proteins from *A. fumigatus* , a gene expression system, such as the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, is selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, is fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end is selected for fusion in order to avoid alteration of any 5' terminal signal sequence.

PCR Amplification and Cloning of Nucleic Acids Containing ORF's Encoding Enzymes

Nucleic acids chosen (for example, from the nucleic acids set forth in SEQ ID NO: 1 - SEQ ID NO: 22156 for cloning from the ND158 strain of *A. fumigatus* are prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers specific for the 5/ and 3/ ends of open reading frames (ORFs) are designed and purchased from GibcoBRL Life Technologies (Gaithersburg, MD, USA). All forward primers (specific for the 5/ end of the sequence) are designed to include an NcoI cloning site at the extreme 5/ terminus. These primers are designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *A. fumigatus* DNA sequence. All reverse primers (specific for the 3/ end of any *A. fumigatus* ORF) include a EcoRI site at the extreme 5/ terminus to permit cloning of each *A. fumigatus* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids including six histidine residues (at the extreme C-terminus), which comprise the His-Tag.

Genomic DNA prepared from the ND158 strain of *A. fumigatus* is used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *A. fumigatus* ORF, genomic DNA (50 nanograms) is introduced into a reaction vial containing 2 mM $MgCl_2$, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *A. fumigatus* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters.

Upon completion of thermal cycling reactions, each sample of amplified DNA is washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples are subjected to digestion with the restriction endonucleases, e.g., NcoI and EcoRI (New England BioLabs, Beverly, MA, USA)(Current Protocols in Molecular Biology, John

Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples are then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA is visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel is purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

Cloning of *A. fumigatus* Nucleic Acids Into an Expression Vector

The pET-28b vector is prepared for cloning by digestion with restriction endonucleases, e.g., NcoI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). The pET-28a vector, which encodes a His-Tag that can be fused to the 5′ end of an inserted gene, is prepared by digestion with appropriate restriction endonucleases.

Following digestion, DNA inserts are cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector. Products of the ligation reaction are then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

Transformation Of Competent Bacteria With Recombinant Plasmids

Competent bacteria, *E coli* strain BL21 or *E. coli* strain BL21(DE3), are transformed with recombinant pET expression plasmids carrying the cloned *A. fumigatus* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction is mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples are incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10

mM MgCl2, 10 mM MgSO4 and 20, mM glucose) at 37°C with shaking for 1 hour. Samples are then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 are then picked and analyzed to evaluate cloned inserts as described below.

Identification Of Recombinant Expression Vectors With *A. fumigatus* Nucleic Acids

Individual BL21 clones transformed with recombinant pET-28b *A. fumigatus* ORFs are analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *A. fumigatus* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verifies the integration of the *A. fumigatus* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of Nucleic Acids From Transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *A. fumigatus* ORFs are picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA is isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Expression Of Recombinant *A. fumigatus* Sequences In *E. coli*

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are

lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *A. fumigatus* sequences, 50 nanograms of plasmid DNA isolated as described above is used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-galactosidase) is expressed in the pET-System as described for the *A. fumigatus* recombinant constructions. Transformed cells are cultured in SOC medium for 1 hour, and the culture is then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies are pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nM of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *A. fumigatus* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria are pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4^{O}C. Pellets are resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells are then centrifuged at 2000 x g for 20 min at 4^{O}C. Wet pellets are weighed and frozen at -80^{O}C until ready for protein purification.

A variety of methodologies known in the art can be utilized to purify the isolated proteins. (Current Protocols in Protein Science, John Wiley and Sons, Inc., J. *E.* Coligan et al., eds., 1995). For example, the frozen cells may be thawed, resupended in buffer and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate may be centrifuged to yield a clear supernatant (crude extract) and following filtration the crude extract may be fractionated over columns. Fractions may be monitored by absorbance at OD_{280} nm. and peak fractions may analyzed by SDS-PAGE

The concentrations of purified protein preparations may be quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations are also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels of various concentrations may be purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers may include rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. The specific embodiments described herein are offered by way of example only, and the invention is to limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

TABLE 2

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725228	1	22157	597	199

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725234	2	22158	645	214

Description

GTC ORF with score 676 to: (sr:thale cress) (db:genpept-pln1) (ec:4.1.1.15) (de:arabidopsis thaliana columbia glutamate decarboxylase (gad) mrna,complete cds.) (nt:gad1 isoform; similar to the gad2 isoform of) (le:1) (re:1509) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725235	3	22159	240	80

Description

6500724556 yzfa:ybfs hypothetical protein:similar to phosphotransferase system enzyme ii (gtcfc:1.1:1.5:1.6:7.1:7.2:14.1) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfS ybfS Bacillus subtilis 1423 -11528414 7500896725 ybfs (ec:2.7.1.69) (de:intergenic region,) (db:swissprot) YBFS_BACSU P39816 BACILLUS SUBTILIS 1423 -11528414 7000694423 ybfs phosphotransferase system enzyme ii homolog ybfs (cl:phosphotransferase system n-acetylglucosamine-specific enzyme ii:phosphotransferase system glucose-specific enzyme ii, factor ii homology:phosphotransferase system glucose-specific enzyme ii, factor iii homology) (db:pir2.dat) D69750 D69750 Bacillus subtilis 1423 -11528414 7500896727 ybfs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: yzfa; similar to) (le:60246) (re:62141) (di:complement) BSUB0002 Z99105 g2632521 Bacillus subtilis 1423 -11528414 7500896728 ybfs (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:57897) (re:59792) (di:complement) AB006424 AB006424 g3599657 Bacillus subtilis 1423 -11528414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725236	4	22160	411	136

Description

6500724557 ldh:lcte l-lactate dehydrogenase (gtcfc:1.1:1.10:1.8:5.12:5.13:5.5) (ec:1.1.1.27) (keggfc:1.1:1.8:1.10:5.5:5.12:5.13) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) lctE lctE Bacillus subtilis 1423 -11528415 7000694150 lcte l-lactate dehydrogenase (cl:l-lactate dehydrogenase) (ec:1.1.1.27) (db:pir2.dat) E69649 E69649 Bacillus subtilis 1423 -11528415 222571 lcte l-lactate dehydrogenase (db:genpept-bct1) (ec:1.1.1.27) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:134680) (re:135645) (di:direct) BSUB0002 Z99105 g2632591 Bacillus subtilis 1423 -11528415 7500964884 lcte l-lactate dehydrogenase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:8982) (re:9947) (di:direct) D50453 D50453 g1805377 Bacillus subtilis 1423 -11528415

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725810	5	22161	231	76

Description

6500724558 phosphotransferase system:pts mannitol-specific enzyme iiabc component:pts system:mannitol-specific iiabc component:eiiabc-mtl:mannitol-permease iiabc component:phosphotransferase enzyme ii:abc component:eii-mtl (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) mtlA mtlA Bacillus subtilis 1423 -11528416 7000694469 mtla pts mannitol-specific enzyme iiabc component mtla:mannitol-specific phosphotransferase (cl:phosphotransferase system mannitol-specific enzyme ii:phosphotransferase system mannitol-specific enzyme ii factor ii homology:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (db:pir2.dat) E69661 E69661 Bacillus subtilis 1423 -11528416 222661 mtla phosphotransferase system pts (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:46554) (re:48386) (di:direct) BSUB0003 Z99106 g2632699 Bacillus subtilis 1423 -11528416 7500954125 mlta homologue of mannitol transport protein of b. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:128957) (re:130789) (di:direct) D50453 D50453 g1805467 Bacillus subtilis 1423 -11528416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725818	6	22162	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725827	7	22163	336	112

Description

6500724559 treb:trep phosphotransferase system:pts trehalose-specific enzyme iibc component:probable pts system:trehalose-specific iibc component:eiibc-tre:trehalose-permease iibc component:phosphotransferase enzyme ii:bc component:eii-tre (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) treP treP Bacillus subtilis 1423 -11528417 7000694470 trep:treb phosphotransferase system enzyme ii:phosphoenolpyruvate-dependent:trehalose-specific (cl:phosphotransferase system sucrose-specific enzyme ii, factor ii) (ec:2.7.1.69) (db:pir2.dat) C69725 C69725 Bacillus subtilis 1423 -11528417 5500687889 trep phosphotransferase system pts (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: treb) (le:47054) (re:48466) (di:direct) BSUB0005 Z99108 g2633104 Bacillus subtilis 1423 -11528417 6000690326 trep (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:19455) (re:20867) (di:complement) D83967 D83967 g2626831 Bacillus subtilis 1423 -11528417 7500954126 trep (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:56) (re:1468) (di:complement) D86417 D86417 g2443218 Bacillus subtilis 1423 -11528417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725830	8	22164	402	133

Description

6500724560 yfib:glvcb:glv-2:glvc phosphotransferase system:pts arbutin-like enzyme iibc component:pts system:arbutin-like iibc component:phosphotransferase enzyme ii:bc component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) glvC glvC Bacillus subtilis 1423 -11528418 92205 glvc:glvcb:glv-2 (ec:2.7.1.69) (de:ii, bc component),) (db:swissprot) PTIB_BACSU P54715 BACILLUS SUBTILIS 1423 -11528418 7000686218 glvc pts arbutin-like enzyme iibc component glvc (db:pir2.dat) G69635 G69635 Bacillus subtilis 1423 -11528418 222683 glvc phosphotransferase system pts arbutin-like (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfib) (le:88901) (re:90484) (di:direct) BSUB0005 Z99108 g2633144 Bacillus subtilis 1423 -11528418 7500888972 glv-2 unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:2577) (re:4160) (di:direct) D50543 D50543 g1486243 Bacillus subtilis 1423 -11528418 5000688494 (de:(glvcb) (pn:pts system, arbutin-like iibc component:phosphotransferase enzyme ii, bc component) (gn:glv-2) (gtcfc:7.01:7.02) (ec:2.7.1.69) (ptib_bacsu) (keggfc:1.1:1.5:1.6:4.4:7.1) (db:gtc-bacillus subtilis)) glvCB glvCB Bacillus subtilis 1423 10034238

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725863	9	22165	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725865	10	22166	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725882	11	22167	192	63

Description

6500724561 hypothetical protein:similar to phosphoglycerate mutase:glycolysis (gtcfc:1.1:14.1) (ec:5.4.2.1) (keggfc:1.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfR yhfR Bacillus subtilis 1423 -11528419 7000694413 yhfr phosphoglycerate mutase glycolysis homolog yhfr (cl:phosphoglycerate mutase homology) (db:pir2.dat) G69831 G69831 Bacillus subtilis 1423 -11528419 4000714651 yhfr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to phosphoglycerate mutase (glycolysis)) (le:108708) (re:109289) (di:complement) BSUB0006 Z99109 g2633370 Bacillus subtilis 1423 -11528419 7500965072 yhfr hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to a hypothetical protein o215b from) (le:3136) (re:3717) (di:complement) BSY14084 Y14084 g2226254 Bacillus subtilis 1423 -11528419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725885	12	22168	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725887	13	22169	261	86

Description

6500724562 ptsx:crr:ptsg phosphotransferase system:pts glucose-specific enzyme iiabc component:pts system:glucose-specific iiabc component:eiiabc-glc:glucose-permease iiabc component:phosphotransferase enzyme ii:abc component:eii-glc / eiii-glc (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) ptsG ptsG Bacillus subtilis 1423 -11528420 219356 ptsg:ptsx:crr (ec:2.7.1.69) (de:component), (eii-glc / eiii-glc)) (db:swissprot) PTGA_BACSU P20166 BACILLUS SUBTILIS 1423 -11528420 123815 ptsg phosphotransferase system enzyme ii::glucose-specific:factor ii:glucose permease:phosphoenolpyruvate:glucose phosphotransferase system enzyme ii:glucose-specific:protein-npi-phosphohistidine--sugar phosphotransferase:glucose-specific:factor ii:pts glucose-specific enzyme iiabc component ptsg (cl:phosphotransferase system n-acetylglucosamine-specific enzyme ii:phosphotransferase system glucose-specific enzyme ii, factor ii homology:phosphotransferase system glucose-specific enzyme ii, factor iii homology) (ec:2.7.1.69) (db:pir1.dat) WQBSGS S25083 Bacillus subtilis 1423 -11528420 5000688500 ptsg iiglc (fn:glucose transport and phosphorylation) (db:genpept-bct1) (de:b.subtilis ptsg gene for iiglc.) (nt:enzyme iiglucose of the phosphotransferase system) (le:452) (re:2551) (di:direct) BSIIGLCG Z11744 g39956 Bacillus subtilis 1423 -11528420 7500888945 ptsg phosphotransferase system pts glucose-specific (fn:glucose transport and phosphorylation) (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ptsx, crr) (le:61864) (re:63963) (di:direct) BSUB0008 Z99111 g2633760 Bacillus subtilis 1423 -11528420 92161 ptsg:ptsx:crr (ec:2.7.1.69) (de:component), (eii-glc / eiii-glc)) (db:swissprot) PTGA_BACSU P20166 BACILLUS SUBTILIS 1423 -11528420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725910	14	22170	435	144

Description

6500724563 phosphotransferase system:pts fructose-specific enzyme iibc component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) fruA fruA Bacillus subtilis 1423 -11528421 7000694468 frua pts fructose-specific enzyme iibc component frua (cl:phosphotransferase system enzyme ii, fructose-specific:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (db:pir2.dat) H69626 H69626 Bacillus subtilis 1423 -11528421 7500965118 frua fructose pts iiabc (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to fructose-specific pts system iibc) (le:14359) (re:16266) (di:direct) AF012285 AF012285 g3282125 Bacillus subtilis 1423 -11528421 7500965117 frua phosphotransferase system pts (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:113871) (re:115778) (di:direct) BSUB0008 Z99111 g2633811 Bacillus subtilis 1423 -11528421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725916	15	22171	603	201

Description

6500724564 acea:pdha pyruvate dehydrogenase:e1 alpha subunit:pyruvate dehydrogenase e1 component:alpha subunit:s complex:42 kd subunit (gtcfc:1.1:1.11:1.8:5.7) (ec:1.2.4.1) (keggfc:1.1:1.8:1.11:5.7) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pdhA pdhA Bacillus subtilis 1423 -11528422 7500953837 pdha pyruvate decarboxylase e-1 alpha subunit (db:genpept-bct1) (ec:1.2.4.1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to pyruvate decarboxylase (e-1) alpha) (le:33429) (re:34544) (di:direct) AF012285 AF012285 g3282142 Bacillus subtilis 1423 -11528422 220081 pdha pyruvate dehydrogenase e1 alpha subunit (db:genpept-bct1) (ec:1.2.4.1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: acea) (le:132941) (re:134056) (di:direct) BSUB0008 Z99111 g2633829 Bacillus subtilis 1423 -11528422 7000694482 pdha pyruvate dehydrogenase e1 alpha subunit pdha (cl:pyruvate dehydrogenase (lipoamide) alpha chain:thiamine pyrophosphate-binding domain homology) (db:pir) H69673 H69673 Bacillus subtilis 1423 -11528422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725934	16	22172	537	179

Description

6500724565 aceb:pdhb pyruvate dehydrogenase:e1 beta subunit:pyruvate dehydrogenase e1 component:beta subunit:s complex:36 kd subunit (gtcfc:1.1:1.11:1.8:5.7) (ec:1.2.4.1) (keggfc:1.1:1.8:1.11:5.7) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pdhB pdhB Bacillus subtilis 1423 -11528423 7000694483 pdhb pyruvate dehydrogenase lipoamide:e1 beta chain precursor pdhb (cl:pyruvate dehydrogenase (lipoamide) beta chain) (ec:1.2.4.1) (db:pir2.dat) C36718 C36718 Bacillus subtilis 1423 -11528423 220082 pdhb pyruvate decarboxylase e-1 beta subunit (db:genpept-bct1) (ec:1.2.4.1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to pyruvate decarboxylase (e-1) beta) (le:34548) (re:35525) (di:direct) AF012285 AF012285 g3282143 Bacillus subtilis 1423 -11528423 7500965123 pdhb pyruvate decarboxylase e-1 beta subunit (sr:b.subtilis (strain 168) brb1 (saca321 metb5) cell line dna, clone) (db:genpept-bct1) (ec:1.2.4.1) (de:b.subtilis pyruvate dehydrogenase complex genes, complete cds;pal-related lipoprotein (slp) gene, complete cds, lysinedecarboxylase (cad) gene, pa... BACPYDHY M57435 g143378 Bacillus subtilis 1423 -11528423 216547 pdhb pyruvate dehydrogenase e1 beta subunit (db:genpept-bct1) (ec:1.2.4.1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:134060) (re:135037) (di:direct) BSUB0008 Z99111 g2633830 Bacillus subtilis 1423 -11528423 170473 pdhb pyruvate dehydrogenase lipoamide:e1 beta chain precursor pdhb (ec:1.2.4.1) (db:pir) C36718 C36718 Bacillus subtilis 1423 -11528423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725935	17	22173	444	147

Description

6500724566 acec:pdhc pyruvate dehydrogenase:dihydrolipoamide acetyltransferase e2 subunit:dihydrolipoamide acetyltransferase component:e2 of pyruvate dehydrogenase complex:s complex:48 kd subunit (gtcfc:1.1:1.8) (ec:2.3.1.12) (keggfc:1.1:1.8) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pdhC pdhC Bacillus subtilis 1423 -11528424 7000689069 pdhc dihydrolipoamide s-acetyltransferase:precursor:pyruvate dehydrogenase complex:e2 component (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.12) (db:pir2.dat) D36718 D36718 Bacillus subtilis 1423 -11528424 220083 pdhc dihydrolipoamide acetyltransferase e2 (db:genpept-bct1) (ec:2.3.1.12) (de:bacillus subtilis moba-npre gene region.) (nt:similar to dihydrolipoamide acetyltransferase e2) (le:35640) (re:36968) (di:direct) AF012285 AF012285 g3282144 Bacillus subtilis 1423 -11528424 7500953991 pdhc dihydrolipoamide acetyltransferase e2 subunit (sr:b.subtilis (strain 168) brb1 (saca321 metb5) cell line dna, clone) (db:genpept-bct1) (ec:2.3.1.12) (de:b.subtilis pyruvate dehydrogenase complex genes, complete cds;pal-related lipoprotein (slp) gene, complete cds, lysinedecarboxylase (cad) gene, p... BACPYDHY M57435 g143379 Bacillus subtilis 1423 -11528424 216548 pdhc pyruvate dehydrogenase dihydrolipoamide (db:genpept-bct1) (ec:2.3.1.12) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:135152) (re:136480) (di:direct) BSUB0008 Z99111 g2633831 Bacillus subtilis 1423 -11528424 137904 pdhc dihydrolipoamide s-acetyltransferase:precursor:pyruvate dehydrogenase complex:e2 component (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.12) (db:pir) D36718 D36718 Bacillus subtilis 1423 -11528424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725936	18	22174	390	129

Description

6500724567 citl:aced:pdhd dihydrolipoamide dehydrogenase e3 subunit of both pyruvate dehydrogenase and 2-oxoglutarate d...:lipoamide dehydrogenase component:e3 of pyruvate dehydrogenase complex:dihydrolipoamide dehydrogenase:s complex:50 kd subunit (gtcfc:1.1:1.2:1.8:5.3) (ec:1.8.1.4) (keggfc:1.1:1.2:1.8:5.3) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pdhD pdhD Bacillus subtilis 1423 -11528425 68728 pdhd:aced:citl (ec:1.8.1.4) (de:subunit)) (db:swissprot) DLD1_BACSU P21880 BACILLUS SUBTILIS 1423 -11528425 7000685060 pdhd dihydrolipoamide dehydrogenase::2-oxoglutarate dehydrogenase complex chain e3:branched-chain 2-oxoacid dehydrogenase complex chain e3:lipoamide dehydrogenase:pyruvate dehydrogenase complex chain e3:s-complex 50k chain (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.8.1.4) (db:pir1.dat) E36718 E36718 Bacillus subtilis 1423 -11528425 220084 pdhd dihydrolipoamide dehydrogenase e3 (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to dihydrolipoamide dehydrogenase e3) (le:36973) (re:38385) (di:direct) AF012285 AF012285 g3282145 Bacillus subtilis 1423 -11528425 7500880351 pdhd dihydrolipoamide dehydrogenase e3 subunit (sr:b.subtilis (strain 168) brb1 (saca321 metb5) cell line dna, clone) (db:genpept-bct1) (ec:1.8.1.4) (de:b.subtilis pyruvate dehydrogenase complex genes, complete cds;pal-related lipoprotein (slp) gene, complete cds, lysinedecarboxylase (cad) gene, pa... BACPYDHY M57435 g143380 Bacillus subtilis 1423 -11528425 216549 pdhd dihydrolipoamide dehydrogenase e3 subunit of (db:genpept-bct1) (ec:1.8.1.4) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: citl) (le:136485) (re:137897) (di:direct) BSUB0008 Z99111 g2633832 Bacillus subtilis 1423 -11528425 122788 pdhd dihydrolipoamide dehydrogenase::2-oxoglutarate dehydrogenase complex chain e3:branched-chain 2-oxoacid dehydrogenase complex chain e3:lipoamide dehydrogenase:pyruvate dehydrogenase complex chain e3:s-complex 50k chain (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.8.1.4) (db:pir) E36718 E36718 Bacillus subtilis 1423 -11528425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725974	19	22175	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501725991	20	22176	507	168

Description

GTC ORF with score 168 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone t6k22 (essaiiproject).) (nt:similarity to antifreeze-like protein (af70) -) (le:8793:9026:9305:9603) (re:8918:9217:9512:9986) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726002	21	22177	321	106

Description

6500724568 hypothetical protein:hypothetical phosphotransferase enzyme ii:a component in pona-cotd intergenic region:f143 (gtcfc:1.1:1.5:1.6:7.1:7.2:14.1) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypqE ypqE Bacillus subtilis 1423 -11528426 115672 ypqe (ec:2.7.1.69) (de:intergenic region, (f143)) (db:swissprot) YPQE_BACSU P50829 BACILLUS SUBTILIS 1423 -11528426 7000688260 ypqe phosphotransferase system enzyme ii::factor iii (cl:phosphotransferase system glucose-specific enzyme ii, factor iii:phosphotransferase system glucose-specific enzyme ii, factor iii homology) (ec:2.7.1.69) (db:pir2.dat) H69940 H69940 Bacillus subtilis 1423 -11528426 216496 ypqe phosphotransferase system glucose-specific (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:40.5% of ide... BACPONAYPP L47838 g1146177 Bacillus subtilis 1423 -11528426 7500952279 ypqe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phosphotransferase system enzyme ii) (le:140635) (re:141141) (di:complement) BSUB0012 Z99115 g2634642 Bacillus subtilis 1423 -11528426 5000688503 (de:(ypqe) (pn:hypothetical phosphotransferase enzyme ii, a component in pona-cotd intergenic region:f143) (gtcfc:7.01:7.02) (ec:2.7.1.69) (ypqe_bacsu) (keggfc:1.1:1.5:1.6:4.4:7.1) (db:gtc-bacillus subtilis)) ypqE ypqE Bacillus subtilis 1423 10057398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726003	22	22178	234	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726007	23	22179	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726019	24	22180	294	98

Description

6500724569 hypothetical protein:similar to dihydrolipoamide dehydrogenase (gtcfc:1.1:1.2:1.8:5.3:14.1) (ec:1.8.1.4) (keggfc:1.1:1.2:1.8:5.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiV yqiV Bacillus subtilis 1423 -11528427 7000692919 yqiv dihydrolipoamide dehydrogenase homolog yqiv (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (db:pir2.dat) D69962 D69962 Bacillus subtilis 1423 -11528427 216185 yqiv (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:218115) (re:219488) (di:direct) BACJH642 D84432 g1303941 Bacillus subtilis 1423 -11528427 7500963937 yqiv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to dihydrolipoamide dehydrogenase) (le:104131) (re:105504) (di:complement) BSUB0013 Z99116 g2634840 Bacillus subtilis 1423 -11528427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726021	25	22181	642	214

Description

6500724570 alcohol dehydrogenase (gtcfc:1.1:1.8:2.2:3.2:3.5:5.12:8.1) (keggfc:1.1:1.8:2.2:3.2:3.5:5.12:8.1) (bsorffc:2.6.1) (db:gtc-bacillus subtilis) adhB adhB Bacillus subtilis 1423 -11528428 7000692164 adhb alcohol dehydrogenase:adhb (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.1) (db:pir2.dat) D69583 D69583 Bacillus subtilis 1423 -11528428 1500695697 adhb nad alcohol dehydrogenase (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:13725) (re:14861) (di:complement) BS233DEG X92868 g2108273 Bacillus subtilis 1423 -11528428 7500953776 adhb alcohol dehydrogenase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:153270) (re:154406) (di:direct) BSUB0014 Z99117 g2635142 Bacillus subtilis 1423 -11528428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726045	26	22182	435	144

Description

GTC ORF with score 121 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726053	27	22183	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726071	28	22184	447	149

Description

6500724571 nadp-dependent alcohol dehydrogenase (gtcfc:1.1:1.4:2.2:8.1) (ec:1.1.1.2) (keggfc:1.1:1.4:8.1) (bsorffc:2.6.1) (db:gtc-bacillus subtilis) adhA adhA Bacillus subtilis 1423 -11528429 7000694310 adha alcohol dehydrogenase nadp+ (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.2) (db:pir2.dat) C69583 C69583 Bacillus subtilis 1423 -11528429 1500695692 adha nadp-dependent alcohol dehydrogenase (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:10953) (re:12002) (di:complement) BS233DEG X92868 g2108268 Bacillus subtilis 1423 -11528429 7500953777 adha nadp-dependent alcohol dehydrogenase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:156129) (re:157178) (di:direct) BSUB0014 Z99117 g2635147 Bacillus subtilis 1423 -11528429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726089	29	22185	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726145	30	22186	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726156	31	22187	408	135

Description

6500724572 sacl:leve phosphotransferase system:pts fructose-specific enzyme iib component:pts system:fructose-specific iib component:eiib-fru:fructose-permease iib component:phosphotransferase enzyme ii:b component:p18 (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) levE levE Bacillus subtilis 1423 -11528430 1500695690 leve fructose-specific iib component (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:5918) (re:6406) (di:direct) BS233DEG X92868 g2108263 Bacillus subtilis 1423 -11528430 7500965116 leve phosphotransferase system pts (fn:levanase operon) (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: sacl) (le:161725) (re:162213) (di:complement) BSUB0014 Z99117 g2635152 Bacillus subtilis 1423 -11528430 7000694467 leve pts fructose-specific enzyme iib component leve (db:pir) F69650 F69650 Bacillus subtilis 1423 -11528430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726163	32	22188	363	120

Description

GTC ORF with score 196 to: (sr:schizosaccharomyces pombe dna) (db:genpept-pln1) (de:yeast dna for bfr2+ protein/pad1+ protein/sks1+ protein, orf n313,orf n150, complete cds, and for orf n118, partial cds.) (le:6171) (re:7112) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726164	33	22189	483	160

Description

6500724573 sacl:levd phosphotransferase system:pts fructose-specific enzyme iia component:pts system:fructose-specific iia component:eiia-fru:fructose-permease iia component:phosphotransferase enzyme ii:a component:p16 (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) levD levD Bacillus subtilis 1423 -11528431 219371 levd:sacl (ec:2.7.1.69) (de:(ec 2.7.1.69) (p16)) (db:swissprot) PTFA_BACSU P26379 BACILLUS SUBTILIS 1423 -11528431 7000686214 levd pts fructose-specific enzyme iia component levd (db:pir2.dat) S11398 S11398 Bacillus subtilis 1423 -11528431 7500888936 levd fructose-specific iia component (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:5478) (re:5918) (di:direct) BS233DEG X92868 g2108262 Bacillus subtilis 1423 -11528431 5000688495 levd p16 (db:genpept-bct1) (de:b.subtilis levanase operon levd, leve, levf, levg and sacc(partial) genes for fructose phosphotransferase system polypeptidesp16,18,28,30 and levanase.) (le:79) (re:519) (di:direct) BSLEVANOP X56098 g39978 Bacillus subtilis 1423 -11528431 1500685440 levd phosphotransferase system pts (fn:levanase operon) (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: sacl) (le:162213) (re:162653) (di:complement) BSUB0014 Z99117 g2635153 Bacillus subtilis 1423 -11528431 92147 levd:sacl (ec:2.7.1.69) (de:(ec 2.7.1.69) (p16)) (db:swissprot) PTFA_BACSU P26379 BACILLUS SUBTILIS 1423 -11528431 170318 levd pts fructose-specific enzyme iia component levd (db:pir) S11398 S11398 Bacillus subtilis 1423 -11528431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726203	34	22190	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726211	35	22191	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726222	36	22192	339	113

Description

6500724574 glyceraldehyde-3-phosphate dehydrogenase (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) gapB gapB Bacillus subtilis 1423 -11528432 7500881947 gapb (ec:1.2.1.12) (de:glyceraldehyde 3-phosphate dehydrogenase 2, (gapdh)) (db:swissprot) G3P2_BACSU O34425 BACILLUS SUBTILIS 1423 -11528432 7000693058 gapb glyceraldehyde-3-phosphate dehydrogenase:gapb (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir2.dat) G69628 G69628 Bacillus subtilis 1423 -11528432 4000714271 gapb glyceraldehyde-3-p-dehydrogenase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:211069) (re:212091) (di:direct) AF008220 AF008220 g2293277 Bacillus subtilis 1423 -11528432 7500881950 gapb glyceraldehyde-3-phosphate dehydrogenase (fn:glycolysis) (db:genpept-bct1) (ec:1.2.1.12) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:170976) (re:171998) (di:complement) BSUB0015 Z99118 g2635367 Bacillus subtilis 1423 -11528432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726223	37	22193	273	90

Description

6500724575 pyruvate kinase (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (keggfc:1.1:1.8:2.3) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pykA pykA Bacillus subtilis 1423 -11528433 7500884718 pyk:pyka (ec:2.7.1.40) (de:pyruvate kinase, (pk) (vegetative protein 17) (veg17)) (db:swissprot) KPYK_BACSU P80885 BACILLUS SUBTILIS 1423 -11528433 7000694484 pyka pyruvate kinase pyka (cl:pyruvate kinase) (db:pir2.dat) G69685 G69685 Bacillus subtilis 1423 -11528433 4000714259 pyka pyruvate kinase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:192579) (re:194336) (di:direct) AF008220 AF008220 g2293265 Bacillus subtilis 1423 -11528433 7500884721 pyka pyruvate kinase (fn:glycolysis) (db:genpept-bct1) (ec:2.7.1.40) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:188731) (re:190488) (di:complement) BSUB0015 Z99118 g2635383 Bacillus subtilis 1423 -11528433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726224	38	22194	234	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726252	39	22195	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726256	40	22196	648	216

Description

6500724576 6-phosphofructokinase (gtcfc:1.1:1.3:1.4:1.5:1.6) (ec:2.7.1.11) (keggfc:1.1:1.3:1.5:1.6) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) pfk pfk Bacillus subtilis 1423 -11528434 7500884425 pfka:pfk (ec:2.7.1.11) (de:(phosphohexokinase)) (db:swissprot) K6PF_BACSU O34529 BACILLUS SUBTILIS 1423 -11528434 7000692070 pfk 6-phosphofructokinase pfk (cl:6-phosphofructokinase:6-phosphofructokinase 1 homology) (db:pir2.dat) A69675 A69675 Bacillus subtilis 1423 -11528434 4000714258 pfk 6-phosphofructokinase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:191577) (re:192536) (di:direct) AF008220 AF008220 g2293264 Bacillus subtilis 1423 -11528434 7500884428 pfk 6-phosphofructokinase (fn:glycolysis) (db:genpept-bct1) (ec:2.7.1.11) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:190531) (re:191490) (di:complement) BSUB0015 Z99118 g2635384 Bacillus subtilis 1423 -11528434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726257	41	22197	615	205

Description

GTC ORF with score 413 to: (fn:catalyzes nadph dependent reduction of) (db:genpept) (de:cochliobolus lunatus 17beta-hydroxysteroid dehydrogenase mrna,complete cds.) (nt:short chain alcohol dehydrogenase/reductase family) (le:58) (re:870) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726306	42	22198	624	207

Description

6500724577 alcohol dehydrogenase (gtcfc:1.1:2.2:3.2:3.5:5.12:8.1) (ec:1.1.1.1) (keggfc:1.1:3.2:3.5:5.12:8.1) (bsorffc:2.6.1) (db:gtc-bacillus subtilis) gbsB gbsB Bacillus subtilis 1423 -11528435 7000692165 gbsb alcohol dehydrogenase gbsb (cl:lactaldehyde reductase homology) (db:pir2.dat) B69629 B69629 Bacillus subtilis 1423 -11528435 7500963387 gbsb alcohol dehydrogenase (fn:glycine betaine synthesis (osmoprotection)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:185167) (re:186378) (di:complement) BSUB0016 Z99119 g2635589 Bacillus subtilis 1423 -11528435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726309	43	22199	570	189

Description

6500724578 enolase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate hydro-lyase (gtcfc:1.1) (ec:4.2.1.11) (keggfc:1.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) eno eno Bacillus subtilis 1423 -11528436 7000692965 eno phosphopyruvate hydratase::enolase (cl:enolase) (ec:4.2.1.11) (db:pir2.dat) B69620 B69620 Bacillus subtilis 1423 -11528436 7500954419 eno enolase (fn:glycolysis) (db:genpept-bct1) (ec:4.2.1.11) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:76068) (re:77360) (di:complement) BSUB0018 Z99121 g2635903 Bacillus subtilis 1423 -11528436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726321	44	22200	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726342	45	22201	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726352	46	22202	273	90

Description

6500724579 phosphoglycerate mutase:2:3-bisphosphoglycerate-independent phosphoglycerate mutase:phosphoglyceromutase:bpg-independent pgam (gtcfc:1.1:1.4) (ec:5.4.2.1) (keggfc:1.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) pgm pgm Bacillus subtilis 1423 -11528437 7000694414 pgm phosphoglycerate mutase::2:3-diphosphoglycerate-independent (cl:phosphoglycerate mutase, 2, 3-bisphosphoglycerate-independent) (ec:5.4.2.1) (db:pir2.dat) D69675 D69675 Bacillus subtilis 1423 -11528437 7500954462 pgm phosphoglycerate mutase (fn:glycolysis) (db:genpept-bct1) (ec:5.4.2.1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:77390) (re:78925) (di:complement) BSUB0018 Z99121 g2635904 Bacillus subtilis 1423 -11528437

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726353	47	22203	222	73

Description

6500724580 tim:tpi triose phosphate isomerase:triosephosphate isomerase:tim (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) tpi tpi Bacillus subtilis 1423 -11528438 7000694830 tpi triose-phosphate isomerase (cl:triose-phosphate isomerase) (ec:5.3.1.1) (db:pir2.dat) A69725 A69725 Bacillus subtilis 1423 -11528438 7500954450 tpi triose phosphate isomerase (fn:glycolysis) (db:genpept-bct1) (ec:5.3.1.1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: tim) (le:78918) (re:79679) (di:complement) BSUB0018 Z99121 g2635905 Bacillus subtilis 1423 -11528438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726387	48	22204	567	188

Description

6500724581 phosphoglycerate kinase (gtcfc:1.1:2.4) (ec:2.7.2.3) (keggfc:1.1:2.3) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pgk pgk Bacillus subtilis 1423 -11528439 7500887927 pgk (ec:2.7.2.3) (de:phosphoglycerate kinase,) (db:swissprot) PGK_BACSU P40924 BACILLUS SUBTILIS 1423 -11528439 7000694412 pgk phosphoglycerate kinase:pgk (cl:phosphoglycerate kinase) (ec:2.7.2.3) (db:pir2.dat) C69675 C69675 Bacillus subtilis 1423 -11528439 7500887929 pgk phosphoglycerate kinase (fn:glycolysis) (db:genpept-bct1) (ec:2.7.2.3) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:79710) (re:80894) (di:complement) BSUB0018 Z99121 g2635906 Bacillus subtilis 1423 -11528439

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726402	49	22205	456	152

Description

6500724582 glyceraldehyde-3-phosphate dehydrogenase:glyceraldehyde 3-phosphate dehydrogenase:gapdh (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) gap gap Bacillus subtilis 1423 -11528440 122638 gap glyceraldehyde-3-phosphate dehydrogenase (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir1.dat) DEBSG S02754 Bacillus subtilis 1423 -11528440 219224 (db:genpept-bct1) (de:bacillus subtilis dna for glyceraldehyde-3-phosphate dehydrogenase(ec 1.2.1.12).) (nt:glyceraldehyde-3-phosphate dehydrogenase (aa 1 -) (le:197) (re:1204) (di:direct) BSGAP X13011 g39921 Bacillus subtilis 1423 -11528440 324755 gap glyceraldehyde-3-phosphate dehydrogenase (fn:glycolysis) (db:genpept-bct1) (ec:1.2.1.12) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:81211) (re:82218) (di:complement) BSUB0018 Z99121 g2635907 Bacillus subtilis 1423 -11528440 7502851491 tac-gap expre...::module (db:genpept-pat) (de:nucleotide sequence of the tac-gap expression module.) (nt:tac-promoter and gap-gene) (le:125) (re:1132) (di:direct) A06409 A06409 g412859 unidentified 32644 -11528440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726403	50	22206	555	185

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726415	51	22207	213	70

Description

6500724583 tsr:fba:fba1:fbaa fructose-1:6-bisphosphate aldolase:probable fructose-bisphosphate aldolase 1 (gtcfc:1.1:1.3:1.5:2.4) (ec:4.1.2.13) (keggfc:1.1:1.3:1.5:2.3) (bsorffc:2.4.2) (db:gtc-bacillus subtilis) fbaA fbaA Bacillus subtilis 1423 -11528441 6000684487 fbaa:fba:fba1:tsr (ec:4.1.2.13) (de:probable fructose-bisphosphate aldolase 1,) (db:swissprot) ALF1_BACSU P13243 BACILLUS SUBTILIS 1423 -11528441 125512 fbaa fructose-bisphosphate aldolase:fbaa:30k phosphoprotein orfy-tsr:fructose-1:6-bisphosphate aldolase (cl:fructose-bisphosphate aldolase ii) (ec:4.1.2.13) (db:pir1.dat) D32354 S55426 Bacillus subtilis 1423 -11528441 216855 orfy-tsr fructose-bisphosphate aldolase (sr:bacillus subtilis (strains jh642 and uot0550) dna) (db:genpept-bct1) (ec:4.1.2.13) (de:bacillus subtillis spo0f, ctp synthetase (ctra), andfructose-bisphosphate aldolase (orfy-tsr) genes, complete cds.) (le:3270) (re:4127) (di:direct) BACSPO0FA M22039 g460911 Bacillus subtilis 1423 -11528441 5000688381 tsr fructose biphosphate aldolase (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:12411) (re:13268) (di:direct) BSDNA320D Z49782 g853765 Bacillus subtilis 1423 -11528441 219142 fbaa fructose-1:6-bisphosphate aldolase (fn:glycolysis) (db:genpept-bct1) (ec:4.1.2.13) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: tsr, fba) (le:210475) (re:211332) (di:complement) BSUB0019 Z99122 g2636237 Bacillus subtilis 1423 -11528441 304114 fbaa fructose-1:6-bisphosphate aldolase (fn:glycolysis) (db:genpept-bct1) (ec:4.1.2.13) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: tsr, fba) (le:9165) (re:10022) (di:complement) BSUB0020 Z99123 g2636249 Bacillus subtilis 1423 -11528441 59120 fbaa:fba:fba1:tsr (ec:4.1.2.13) (de:probable fructose-bisphosphate aldolase 1,) (db:swissprot) ALF1_BACSU P13243 BACILLUS SUBTILIS 1423 -11528441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726416	52	22208	597	198

Description

6500724584 ipa-49d:sacp phosphotransferase system:pts sucrose-specific enzyme iibc component:pts system:sucrose-specific iibc component:eiibc-scr:sucrose-permease iibc component:phosphotransferase enzyme ii:bc component:eii-scr (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) sacP sacP Bacillus subtilis 1423 -11528442 216663 sacp:ipa-49d (ec:2.7.1.69) (de:(ec 2.7.1.69) (eii-scr)) (db:swissprot) PTSB_BACSU P05306 BACILLUS SUBTILIS 1423 -11528442 7000686233 sacp phosphotransferase system enzyme ii::sucrose-specific sacp:pts sucrose-specific enzyme iibc component sacp (cl:phosphotransferase system sucrose-specific enzyme ii, factor ii) (ec:2.7.1.69) (db:pir2.dat) A39938 A39938 Bacillus subtilis 1423 -11528442 7500889004 (sr:b.subtilis (strain marburg 168) dna, clone pbsg8-10) (db:genpept-bct1) (de:b.subtilis sact gene, complete cds, enzyme ii (sacp) gene (of thesucrose phosphotransferase system), complete cds, and sucrase gene,5' end.) (nt:enzyme ii (sacp)) (le:2008) ... BACSACP J03006 g143489 Bacillus subtilis 1423 -11528442 5000688501 ipa-49d::sacp (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:52535) (re:53917) (di:direct) BSGENR X73124 g413973 Bacillus subtilis 1423 -11528442 219286 sacp phosphotransferase system pts sucrose-specific (fn:sucrose transport) (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-49d) (le:104045) (re:105427) (di:complement) BSUB0020 Z99123 g2636340 Bacillus subtilis 1423 -11528442 92317 sacp:ipa-49d (ec:2.7.1.69) (de:(ec 2.7.1.69) (eii-scr)) (db:swissprot) PTSB_BACSU P05306 BACILLUS SUBTILIS 1423 -11528442 138892 sacp phosphotransferase system enzyme ii::sucrose-specific sacp:pts sucrose-specific enzyme iibc component sacp (cl:phosphotransferase system sucrose-specific enzyme ii, factor ii) (ec:2.7.1.69) (db:pir) A39938 A39938 Bacillus subtilis 1423 -11528442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726418	53	22209	504	168

Description

5000688491 celc:lica phosphotransferase system:pts lichenan-specific enzyme iia component:pts system:cellobiose-specific iia component:eiia-cel:cellobiose-permease iia component:phosphotransferase enzyme ii:a component:eiii-cel (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) licA licA Bacillus subtilis 1423 -11528443 7500888930 celc:lica (ec:2.7.1.69) (de:(ec 2.7.1.69) (eiii-cel)) (db:swissprot) PTCA_BACSU P46319 BACILLUS SUBTILIS 1423 -11528443 7000686208 lica pts lichenan-specific enzyme iia component lica:probable cellobiose phosphotransferase enzyme iii (cl:phosphotransferase system lactose-specific enzyme ii, factor iii) (db:pir2.dat) D69651 D69651 Bacillus subtilis 1423 -11528443 301561 celc putative cellobiose phosphotransferase enzyme (db:genpept-bct1) (de:b.subtilis cela, celb, celc, celd and ywaa genes.) (nt:gtg start codon) (le:3941) (re:4273) (di:direct) BSCELABCD Z49992 g895750 Bacillus subtilis 1423 -11528443 219051 lica phosphotransferase system pts (fn:lichenan degradation products utilization) (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: celc) (le:160235) (re:160567) (di:complement) BSUB0020 Z99123 g2636392 Bacillus subtilis 1423 -11528443 7502851492 celc cellobiose phosphotransferase enzyme iii (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:63898) (re:64230) (di:direct) D83026 D83026 g1783268 Bacillus subtilis 1423 -11528443 92137 celc:lica (ec:2.7.1.69) (de:(ec 2.7.1.69) (eiii-cel)) (db:swissprot) PTCA_BACSU P46319 BACILLUS SUBTILIS 1423 -11528443 170453 lica pts lichenan-specific enzyme iia component lica:probable cellobiose phosphotransferase enzyme iii (db:pir) D69651 D69651 Bacillus subtilis 1423 -11528443 222894 celc cellobiose phosphotransferase enzyme iii (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:63898) (re:64230) (di:direct) D83026 D83026 g1783268 Bacillus subtilis 1423 -11528443 6500724585 celc phosphotransferase system:pts lichenan-specific enzyme iia component:pts system:cellobiose-specific iia component:eiia-cel:cellobiose-permease iia component:phosphotransferase enzyme ii:a component:eiii-cel (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) licA licA Bacillus subtilis 1423 -11528443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726446	54	22210	606	201

Description

GTC ORF with score 95 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid f33h1, complete sequence.) (nt:cdna est yk318d5.5 comes from this gene; cdna est) (le:23827:24142:26253:27416) (re:24089:25973:27220:28342) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726451	55	22211	288	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726476	56	22212	408	135

Description

5000688490 cela:licb phosphotransferase system:pts lichenan-specific enzyme iib component:pts system:cellobiose-specific iib component:eiib-cel:cellobiose-permease iib component:phosphotransferase enzyme ii:b component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) licB licB Bacillus subtilis 1423 -11528444 7500888931 cela:licb (ec:2.7.1.69) (de:(ec 2.7.1.69)) (db:swissprot) PTCB_BACSU P46318 BACILLUS SUBTILIS 1423 -11528444 7000686210 licb pts lichenan-specific enzyme iib component licb:probable cellobiose phosphotransferase enzyme ii (cl:phosphotransferase system enzyme ii cellobiose-specific factor iib) (db:pir2.dat) E69651 E69651 Bacillus subtilis 1423 -11528444 301559 cela putative cellobiose phosphotransferase enzyme (db:genpept-bct1) (de:b.subtilis cela, celb, celc, celd and ywaa genes.) (le:2240) (re:2548) (di:direct) BSCELABCD Z49992 g895748 Bacillus subtilis 1423 -11528444 219049 licb phosphotransferase system pts (fn:lichenan degradation products utilization) (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: cela) (le:161960) (re:162268) (di:complement) BSUB0020 Z99123 g2636394 Bacillus subtilis 1423 -11528444 7502851493 cela cellobiose phosphotransferase enzyme ii (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:62197) (re:62505) (di:direct) D83026 D83026 g1783266 Bacillus subtilis 1423 -11528444 92139 cela:licb. (ec:2.7.1.69) (de:(ec 2.7.1.69)) (db:swissprot) PTCB_BACSU P46318 BACILLUS SUBTILIS 1423 -11528444 170451 licb pts lichenan-specific enzyme iib component licb:probable cellobiose phosphotransferase enzyme ii (db:pir) E69651 E69651 Bacillus subtilis 1423 -11528444 222892 cela cellobiose phosphotransferase enzyme ii (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:62197) (re:62505) (di:direct) D83026 D83026 g1783266 Bacillus subtilis 1423 -11528444 6500724586 cela phosphotransferase system:pts lichenan-specific enzyme iib component:pts system:cellobiose-specific iib component:eiib-cel:cellobiose-permease iib component:phosphotransferase enzyme ii:b component (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) licB licB Bacillus subtilis 1423 -11528444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726478	57	22213	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726493	58	22214	345	114

Description

6500724587 syta:n17c:bglp phosphotransferase system:pts beta-glucoside-specific enzyme iiabc component:pts system:beta-glucosides-specific iiabc component:eiiabc-bgl:beta-glucosides-permease iiabc component:phosphotransferase enzyme ii:abc component:eii-bgl (gtcfc:1.1:1.4:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (bsorffc:1.1.2:2.1.1) (db:gtc-bacillus subtilis) bglP bglP Bacillus subtilis 1423 -11528445 215872 n17c hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (nt:homologous to phosphotransferase enzyme ii,) (le:13719) (re:15548) (di:direct) BACHUTWAPA D31856 g603778 Bacillus subtilis 1423 -11528445 215887 hypothetical 64.7-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (nt:homologous to phosphotransferase enzyme ii) (le:1823) (re:3652) (di:direct) BACHYPTP D29985 g849025 Bacillus subtilis 1423 -11528445 7500965115 bglp phosphotransferase system pts (db:genpept-bct1) (ec:2.7.1.69) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: syta) (le:33287) (re:35116) (di:complement) BSUB0021 Z99124 g2636473 Bacillus subtilis 1423 -11528445 7000694465 bglp pts beta-glucoside-specific enzyme iiabc component bglp (db:pir) A69594 A69594 Bacillus subtilis 1423 -11528445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726537	59	22215	837	279

Description

6500724588 gcaa:ybxd:glms glucosamine--fructose-6-phosphate aminotransferase:isomerizing:hexosephosphate aminotransferase:d-fructose-6-phosphate amidotransferase:gfat:l-glutamine-d-fructose-6-phosphate amidotransferase:glucosamine-6-phosphate synthase (gtcfc:1.1:5.1) (ec:2.6.1.16) (keggfc:5.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) glmS glmS Bacillus subtilis 1423 -11528446 7000694147 glms l-glutamine-d-fructose-6-phosphate amidotransferase glms (cl:glutamine--fructose-6-phosphate aminotransferase (isomerizing)) (db:pir2.dat) B69633 B69633 Bacillus subtilis 1423 -11528446 219869 gcaa l-glutamine-d-fructose-6-phosphate (db:genpept-bct1) (de:bacillus subtilis l-glutamine-d-fructose-6-phosphateamidotransferase (gcaa) gene, complete cds.) (le:312) (re:2114) (di:direct) BSU21932 U21932 g726480 Bacillus subtilis 1423 -11528446 6000689878 glms l-glutamine-d-fructose-6-phosphate (db:genpept-bct1) (ec:2.6.1.16) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: gcaa, ybxd) (le:200263) (re:202065) (di:direct) BSUB0001 Z99104 g2632445 Bacillus subtilis 1423 -11528446 7500964882 glms l-glutamine-d-fructose-6-phosphate (db:genpept-bct1) (ec:2.6.1.16) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: gcaa, ybxd) (le:5613) (re:7415) (di:direct) BSUB0002 Z99105 g2632463 Bacillus subtilis 1423 -11528446 7500964883 gcaa l-glutamine-d-fructose-6-phosphate amido (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:3246) (re:5048) (di:direct) AB006424 AB006424 g3599596 Bacillus subtilis 1423 -11528446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726538	60	22216	441	146

Description

6500724589 yfjk:acoa acetoin dehydrogenase e1 component:tpp-dependent alpha subunit (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) acoA acoA Bacillus subtilis 1423 -11528447 7000692125 acoa acetoin dehydrogenase e1 component tpp-dependent alpha subuni acoa (cl:pyruvate dehydrogenase (lipoamide) alpha chain:thiamine pyrophosphate-binding domain homology) (db:pir2.dat) D69581 D69581 Bacillus subtilis 1423 -11528447 7000692126 acoa tpp-dependent acetoin dehydrogenase:e1 (db:genpept-bct1) (de:bacillus subtilis acetoin dehydrogenase enzyme system gene cluster,ribosomal protein 16-like protein gene, partial cds, tpp-dependentacetoin dehydrogenase, e1 alpha-subunit (acoa), tpp-dependentacetoin dehydrogenase, e1 beta-subun... AF006075 AF006075 g2957146 Bacillus subtilis 1423 -11528447 7000692127 acoa acetoin dehydrogenase e1 component (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfjk) (le:75688) (re:76689) (di:direct) BSUB0005 Z99108 g2633130 Bacillus subtilis 1423 -11528447 7500953838 yfjk (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:9636) (re:10637) (di:complement) D78509 D78509 g2780395 Bacillus subtilis 1423 -11528447

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726539	61	22217	561	187

Description

6500724590 yfjj:acob acetoin dehydrogenase e1 component:tpp-dependent beta subunit (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) acoB acoB Bacillus subtilis 1423 -11528448 7000692128 acob acetoin dehydrogenase e1 component tpp-dependent beta subunit acob (cl:pyruvate dehydrogenase (lipoamide) beta chain) (db:pir2.dat) E69581 E69581 Bacillus subtilis 1423 -11528448 4000714036 acob tpp-dependent acetoin dehydrogenase:e1 (db:genpept-bct1) (de:bacillus subtilis acetoin dehydrogenase enzyme system gene cluster,ribosomal protein 16-like protein gene, partial cds, tpp-dependentacetoin dehydrogenase, e1 alpha-subunit (acoa), tpp-dependentacetoin dehydrogenase, e1 beta-subun... AF006075 AF006075 g2245638 Bacillus subtilis 1423 -11528448 7000692129 acob acetoin dehydrogenase e1 component (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfjj) (le:76693) (re:77721) (di:direct) BSUB0005 Z99108 g2633131 Bacillus subtilis 1423 -11528448 7500963364 yfjj (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:8604) (re:9632) (di:complement) D78509 D78509 g2780394 Bacillus subtilis 1423 -11528448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726540	62	22218	831	277

Description

6500724591 yfji:acoc acetoin dehydrogenase e2 component:dihydrolipoamide acetyltransferase (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) acoC acoC Bacillus subtilis 1423 -11528449 7000692130 acoc acetoin dehydrogenase e2 component dihydrolipoamide acetyltra acoc (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (db:pir2.dat) F69581 F69581 Bacillus subtilis 1423 -11528449 7000692131 acoc acetoin dehydrogenase e2 component (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfji) (le:77735) (re:78931) (di:direct) BSUB0005 Z99108 g2633132 Bacillus subtilis 1423 -11528449 7500963365 yfji (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:7394) (re:8590) (di:complement) D78509 D78509 g2780393 Bacillus subtilis 1423 -11528449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726541	63	22219	567	188

Description

6500724592 yfjh:acol acetoin dehydrogenase e3 component:dihydrolipoamide dehydrogenase (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) acoL acoL Bacillus subtilis 1423 -11528450 7000692132 acol acetoin dehydrogenase e3 component dihydrolipoamide dehydroge acol (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (db:pir2.dat) G69581 G69581 Bacillus subtilis 1423 -11528450 4000714038 acol dihydrolipoamide dehydrogenase (db:genpept-bct1) (de:bacillus subtilis acetoin dehydrogenase enzyme system gene cluster,ribosomal protein 16-like protein gene, partial cds, tpp-dependentacetoin dehydrogenase, e1 alpha-subunit (acoa), tpp-dependentacetoin dehydrogenase, e1 beta-subun... AF006075 AF006075 g2245640 Bacillus subtilis 1423 -11528450 7000692133 acol acetoin dehydrogenase e3 component (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfjh) (le:78952) (re:80328) (di:direct) BSUB0005 Z99108 g2633133 Bacillus subtilis 1423 -11528450 7500963366 yfjh (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:5997) (re:7373) (di:complement) D78509 D78509 g2780392 Bacillus subtilis 1423 -11528450

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726544	64	22220	831	276

Description

6500724593 cita1:cita citrate synthase i (gtcfc:1.1:1.2:1.9) (ec:4.1.3.7) (keggfc:1.2:1.9) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) citA citA Bacillus subtilis 1423 -11528451 64658 cita (ec:4.1.3.7) (de:citrate synthase i,) (db:swissprot) CISY_BACSU P39119 BACILLUS SUBTILIS 1423 -11528451 7000684822 cita citrate synthase i cita (cl:citrate (si)-synthase) (db:pir2.dat) I40380 I40380 Bacillus subtilis 1423 -11528451 7500878759 cita citrate synthase i (db:genpept-bct1) (de:bacillus subtilis smy citrate synthase i (cita) and repressor ofcita (citr) genes, complete cds.) (le:1131) (re:2231) (di:direct) BSCITRA U05256 g452565 Bacillus subtilis 1423 -11528451 219075 cita citrate synthase i (db:genpept-bct1) (ec:4.1.3.7) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: cita1) (le:21037) (re:22137) (di:direct) BSUB0006 Z99109 g2633279 Bacillus subtilis 1423 -11528451 4000706967 cita citrate synthase i (fn:might regulate the synthesis and function of) (db:genpept-bct2) (ec:4.1.3.7) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:see subtilist bg10854, embl u05256 and swiss prot) (le:7685) (re:8785) (di:direct) BSY14082 Y14082 g2226200 Bacillus subtilis 1423 -11528451 169919 cita citrate synthase i cita (db:pir) I40380 I40380 Bacillus subtilis 1423 -11528451

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726545	65	22221	858	285

Description

6500724594 ylap:pyca pyruvate carboxylase (gtcfc:1.1) (ec:6.4.1.1) (keggfc:14.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pycA pycA Bacillus subtilis 1423 -11528452 7000694481 pyca pyruvate carboxylase pyca (cl:pyruvate carboxylase:biotin carboxylase homology:lipoyl/biotin-binding homology) (db:pir2.dat) F69685 F69685 Bacillus subtilis 1423 -11528452 7500954520 pyca pyruvate carboxylase (db:genpept-bct1) (ec:6.4.1.1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ylap) (le:158800) (re:162246) (di:direct) BSUB0008 Z99111 g2633857 Bacillus subtilis 1423 -11528452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726554	66	22222	543	181

Description

6500724595 tkta:tkt transketolase (gtcfc:1.1:1.3:2.4) (ec:2.2.1.1) (keggfc:1.3:2.3) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) tkt tkt Bacillus subtilis 1423 -11528453 7500893208 tkt:tkta (ec:2.2.1.1) (de:transketolase,) (db:swissprot) TKT_BACSU P45694 BACILLUS SUBTILIS 1423 -11528453 7000686801 tkt transketolase:tkt (cl:transketolase:thiamine pyrophosphate-binding domain homology) (ec:2.2.1.1) (db:pir2.dat) G69723 G69723 Bacillus subtilis 1423 -11528453 5000688385 tkta transketolase (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:1537) (re:3540) (di:direct) BC170DEGR Z73234 g1405446 Bacillus subtilis 1423 -11528453 217877 tkt transketolase (fn:pentose phosphate) (db:genpept-bct1) (ec:2.2.1.1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: tkta) (le:137916) (re:139919) (di:direct) BSUB0010 Z99113 g2634173 Bacillus subtilis 1423 -11528453 101621 tkt:tkta (ec:2.2.1.1) (de:transketolase,) (db:swissprot) TKT_BACSU P45694 BACILLUS SUBTILIS 1423 -11528453

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726600	67	22223	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726612	68	22224	237	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726653	69	22225	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726659	70	22226	438	145

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726660	71	22227	246	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726675	72	22228	414	137

Description

GTC ORF with score 185 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1111.) (nt:similar to saccharomyces cerevisiae glycolipid) (le:<1) (re:829) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726690	73	22229	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726691	74	22230	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726702	75	22231	831	277

Description

6500724596 aconitate hydratase:citrate hydro-lyase:aconitase (gtcfc:1.1:1.2:1.9:2.5) (ec:4.2.1.3) (keggfc:1.2:1.9:2.4) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-glyoxylate and dic... citB citB Bacillus subtilis 1423 -11528454 7000692146 citb aconitate hydratase:citb:aconitase (cl:iron-responsive element-binding protein) (ec:4.2.1.3) (db:pir2.dat) G69599 G69599 Bacillus subtilis 1423 -11528454 7500963374 citb aconitase (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:8356) (re:11085) (di:direct) BC170DEGR Z73234 g1405454 Bacillus subtilis 1423 -11528454 217885 citb aconitate hydratase (db:genpept-bct1) (ec:4.2.1.3) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:144735) (re:147464) (di:direct) BSUB0010 Z99113 g2634184 Bacillus subtilis 1423 -11528454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726721	76	22232	465	155

Description

6500724597 yoha:proj glutamate 5-kinase (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) proJ proJ Bacillus subtilis 1423 -11528455 7000693043 proj glutamate 5-kinase proj (cl:glutamate 5-kinase) (db:pir2.dat) F69682 F69682 Bacillus subtilis 1423 -11528455 4000714058 proj proj (db:genpept-bct1) (de:bacillus subtilis proh (proh) gene, partial cds, proj (proj) gene,complete cds, and lysr-type transcriptional activator of glutamatesynthase (gltc) gene, partial cds.) (nt:similar to glutamate 5-kinase) (le:297) (re:1412) (di:direct) AF006720 AF006720 g2209379 Bacillus subtilis 1423 -11528455 7500964021 proj glutamate 5-kinase (fn:proline biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yoha) (le:14819) (re:15934) (di:complement) BSUB0011 Z99114 g2634241 Bacillus subtilis 1423 -11528455

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726739	77	22233	411	137

Description

6500724598 phosphoenolpyruvate synthase (gtcfc:1.1) (ec:2.7.9.2) (keggfc:14.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pps pps Bacillus subtilis 1423 -11528456 7000694407 pps phosphoenolpyruvate synthase pps (db:pir2.dat) F69681 F69681 Bacillus subtilis 1423 -11528456 5500701886 pps pep synthase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli pep synthase (793 aa)) (le:31322) (re:33922) (di:complement) AF027868 AF027868 g2619033 Bacillus subtilis 1423 -11528456 7500965068 pps phosphoenolpyruvate synthase (db:genpept-bct1) (ec:2.7.9.2) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:50413) (re:53013) (di:complement) BSUB0011 Z99114 g2634276 Bacillus subtilis 1423 -11528456

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726740	78	22234	345	114

Description

6500724599 aldehyde dehydrogenase (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) dhaS dhaS Bacillus subtilis 1423 -11528457 7000692170 dhas aldehyde dehydrogenase dhas (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) H69614 H69614 Bacillus subtilis 1423 -11528457 5500701919 dhas aldehyde dehydrogenase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to human mitochondrial aldehyde) (le:80575) (re:82062) (di:direct) AF027868 AF027868 g2619016 Bacillus subtilis 1423 -11528457 7500953824 dhas aldehyde dehydrogenase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:99666) (re:101153) (di:direct) BSUB0011 Z99114 g2634324 Bacillus subtilis 1423 -11528457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726759	79	22235	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726760	80	22236	183	60

Description

GTC ORF with score 116 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v lambda clones 6592, 4678,4742, and 3612.) (nt:similar to hypothetical protein from s. cerevisiae,) (le:10077) (re:10466) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726763	81	22237	396	132

Description

6500724600 citm:odhb 2-oxoglutarate dehydrogenase complex:dihydrolipoamide transsuccinylase:e2 subunit:dihydrolipoamide succinyltransferase component:e2 of 2-oxoglutarate dehydrogenase complex (gtcfc:1.1:1.2) (ec:2.3.1.61) (keggfc:1.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) odhB odhB Bacillus subtilis 1423 -11528458 87466 odhb:citm (ec:2.3.1.61) (de:dehydrogenase complex, (e2)) (db:swissprot) ODO2_BACSU P16263 BACILLUS SUBTILIS 1423 -11528458 7000686035 odhb dihydrolipoamide s-succinyltransferase:odhb:2-oxoglutarate dehydrogenase complex e2 component odhb:dihydrolipoamide transsuccinylase odhb (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.61) (db:pir2.dat) B32879 B32879 Bacillus subtilis 1423 -11528458 7500887098 (sr:b.subtilis (strain 3g18) dna) (db:genpept-bct1) (de:b.subtilis 2-oxoglutarate dehydrogenase (odha) gene 3' end, anddihydrolipoamide transsuccinylase (odhb) gene, complete cds.) (nt:dihydrolipoamide transsuccinylase (odhb; ec) (le:899) (re:2152) (di... BACODHAB M27141 g143268 Bacillus subtilis 1423 -11528458 216406 odhb 2-oxoglutarate dehydrogenase complex (db:genpept-bct1) (ec:2.3.1.61) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: citm) (le:106590) (re:107843) (di:complement) BSUB0011 Z99114 g2634329 Bacillus subtilis 1423 -11528458 137899 odhb dihydrolipoamide s-succinyltransferase:odhb:2-oxoglutarate dehydrogenase complex e2 component odhb:dihydrolipoamide transsuccinylase odhb (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.61) (db:pir) B32879 B32879 Bacillus subtilis 1423 -11528458

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726778	82	22238	204	67

Description

6500724601 citk:odha 2-oxoglutarate dehydrogenase:e1 subunit:2-oxoglutarate dehydrogenase e1 component:alpha-ketoglutarate dehydrogenase (gtcfc:1.1:1.2:5.14:5.9) (ec:1.2.4.2) (keggfc:1.2:5.9:5.14) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) odhA odhA Bacillus subtilis 1423 -11528459 219433 odha:citk (ec:1.2.4.2) (de:ketoglutarate dehydrogenase)) (db:swissprot) ODO1_BACSU P23129 BACILLUS SUBTILIS 1423 -11528459 7000686033 odha oxoglutarate dehydrogenase lipoamide (cl:oxoglutarate dehydrogenase (lipoamide):thiamine pyrophosphate-binding domain homology) (ec:1.2.4.2) (db:pir2.dat) A32879 S25295 Bacillus subtilis 1423 -11528459 5000688437 odha oxoglutarate dehydrogenase nadp+ (db:genpept-bct1) (de:b. subtilis odha gene for 2-oxoglutarate dehydrogenase.) (le:291) (re:3104) (di:direct) BSODHA X54805 g40003 Bacillus subtilis 1423 -11528459 7500887095 odha 2-oxoglutarate dehydrogenase e1 subunit (db:genpept-bct1) (ec:1.2.4.2) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: citk) (le:107873) (re:110686) (di:complement) BSUB0011 Z99114 g2634330 Bacillus subtilis 1423 -11528459 87458 odha:citk (ec:1.2.4.2) (de:ketoglutarate dehydrogenase)) (db:swissprot) ODO1_BACSU P23129 BACILLUS SUBTILIS 1423 -11528459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726780	83	22239	342	114

Description

6500724602 glyc:gpsa ph-dependent glycerol-3-phosphate dehydrogenase:glycerol-3-phosphate dehydrogenase:p+:nad:ph-dependent dihydroxyacetone-phosphate reductase (gtcfc:1.1:8.1) (ec:1.1.1.94) (keggfc:8.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) gpsA gpsA Bacillus subtilis 1423 -11528460 7000694301 gpsa glycerol-3-phosphate dehydrogenase nad+:gpsa (cl:glycerol-3-phosphate dehydrogenase) (ec:1.1.1.8) (db:pir2.dat) H69636 H69636 Bacillus subtilis 1423 -11528460 7500965008 gpsa nad p h-dependent glycerol-3-phosphate (fn:synthesis of the sn-glycerol 3-phosphate) (db:genpept-bct1) (ec:1.1.1.94) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:192848) (re:193885) (di:complement) BSUB0012 Z99115 g2634701 Bacillus subtilis 1423 -11528460 216726 glyc nad+ dependent glycerol-3-phosphate (db:genpept-bct2) (ec:1.1.1.94) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ... BACSERA L47648 g1146220 Bacillus subtilis 1423 -11528460 7502851494 glyc nad+ dependent glycerol-3-phosphate (db:genpept) (ec:1.1.1.94) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb,... BACSERA L47648 g1146220 Bacillus subtilis 1423 -11528460

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726797	84	22240	354	117

Description

6500724603 succinate dehydrogenase:iron-sulfur protein:succinate dehydrogenase iron-sulfur protein (gtcfc:1.1:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycl... sdhB sdhB Bacillus subtilis 1423 -11528461 7000694640 sdhb:sdhc succinate dehydrogenase:iron-sulfur protein sdhb:fumarate reductase:fumaric hydrogenase:succinic dehydrogenase (cl:fumarate reductase iron-sulfur protein:ferredoxin 2(4fe-4s) homology:ferredoxin (2fe-2s) homology) (ec:1.3.99.1) (db:pir2.dat) B27763 B27763 Bacillus subtilis 1423 -11528461 7500965228 (sr:b.subtilis dna, clone pkim4) (db:genpept-bct1) (de:b.subtilis succinate dehydrogenase complex encoding cytochromeb-558 subunit, complete cds, and flavoprotein subunit, 5' end.) (nt:iron-sulfur protein) (le:2670) (re:3431) (di:direct) BACSDHAB M13470 g143527 Bacillus subtilis 1423 -11528461 216688 sdhb succinate dehydrogenase iron-sulfur protein (db:genpept-bct1) (ec:1.3.99.1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:109544) (re:110305) (di:complement) BSUB0015 Z99118 g2635308 Bacillus subtilis 1423 -11528461 304202 sdhb iron-sulphur subunit of succinate dehydrogenase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:iron-sulphur protein of succinate dehydrogenase) (le:59602) (re:60363) (di:direct) BSZ75208 Z75208 g1770053 Bacillus subtilis 1423 -11528461 170617 sdhb:sdhc succinate dehydrogenase:iron-sulfur protein sdhb:fumarate reductase:fumaric hydrogenase:succinic dehydrogenase (ec:1.3.99.1) (db:pir) B27763 B27763 Bacillus subtilis 1423 -11528461 220329 sdhb iron-sulphur subunit of succinate dehydrogenase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:iron-sulphur protein of succinate dehydrogenase) (le:59602) (re:60363) (di:direct) BSZ75208 Z75208 g1770053 Bacillus subtilis 1423 -11528461

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726802	85	22241	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726818	86	22242	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726821	87	22243	306	102

Description

6500724604 citf:sdha succinate dehydrogenase:flavoprotein subunit:succinate dehydrogenase flavoprotein subunit (gtcfc:1.1:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycl... sdhA sdhA Bacillus subtilis 1423 -11528462 216687 (sr:b.subtilis dna, clone pkim4) (db:genpept-bct1) (de:b.subtilis succinate dehydrogenase complex encoding cytochromeb-558 subunit, complete cds, and flavoprotein subunit, 5' end.) (nt:succinate dehydrogenase flavoprotein subunit) (le:907) (re:2667) (d... BACSDHAB M13470 g143526 Bacillus subtilis 1423 -11528462 220328 sdha succinate dehydrogenase flavoprotein subunit (db:genpept-bct1) (ec:1.3.99.1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: citf) (le:110308) (re:112068) (di:complement) BSUB0015 Z99118 g2635309 Bacillus subtilis 1423 -11528462 304201 sdha flavoprotein subunit of succinate dehydrogenase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (le:57839) (re:59599) (di:direct) BSZ75208 Z75208 g1770052 Bacillus subtilis 1423 -11528462 7000694641 sdha succinate dehydrogenase flavoprotein subunit sdha (cl:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology) (db:pir) C69704 C69704 Bacillus subtilis 1423 -11528462

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726840	88	22244	513	170

Description

6500724605 isocitrate dehydrogenase:nadp:oxalosuccinate decarboxylase:idh:nadp+-specific icdh:idp (gtcfc:1.1:1.2:2.5:6.16) (ec:1.1.1.42) (keggfc:1.2:2.4:6.9) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate ... citC citC Bacillus subtilis 1423 -11528463 78803 citc (ec:1.1.1.42) (de:decarboxylase) (idh) (nadp+-specific icdh) (idp)) (db:swissprot) IDH_BACSU P39126 BACILLUS SUBTILIS 1423 -11528463 7000685607 citc isocitrate dehydrogenase nadp+::oxalosuccinate decarboxylase (cl:isocitrate dehydrogenase (nadp)) (ec:1.1.1.42) (db:pir2.dat) I40382 I40382 Bacillus subtilis 1423 -11528463 7500883824 citc isocitrate dehydrogenase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:198137) (re:199408) (di:direct) AF008220 AF008220 g2293268 Bacillus subtilis 1423 -11528463 219077 citc isocitrate dehydrogenase (db:genpept-bct1) (de:bacillus subtilis citrate synthase ii (citz), isocitratedehydrogenase (citc) and malate dehydrogenase (cith) genes,complete cds, phop (phop) gene, partial cds.) (le:1649) (re:2920) (di:direct) BSCITZC U05257 g487434 Bacillus subtilis 1423 -11528463 4000707142 citc isocitrate dehydrogenase (db:genpept-bct1) (ec:1.1.1.42) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:183659) (re:184930) (di:complement) BSUB0015 Z99118 g2635378 Bacillus subtilis 1423 -11528463 170302 citc isocitrate dehydrogenase citc (cl:isocitrate dehydrogenase (nadp)) (db:pir) I40382 I40382 Bacillus subtilis 1423 -11528463 5000688390 (de:(citc) (pn:idh:isocitrate dehydrogenase:nadp :oxalosuccinate decarboxylase:idh:nadp) (gtcfc:2.05:6.16) (ec:1.1.1.42) (idh_bacsu) (keggfc:1.2:2.4:6.9) (bsorffc:2.4.0) (db:gtc-bacillus subtilis)) citC citC Bacillus subtilis 1423 10021139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726841	89	22245	423	140

Description

6500724606 cita2:citz citrate synthase ii (gtcfc:1.1:1.2:1.9) (ec:4.1.3.7) (keggfc:1.2:1.9) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) citZ citZ Bacillus subtilis 1423 -11528464 7500878767 citz:cita2 (ec:4.1.3.7) (de:citrate synthase ii,) (db:swissprot) CISZ_BACSU P39120 BACILLUS SUBTILIS 1423 -11528464 7000692375 citz citrate synthase ii (cl:citrate (si)-synthase) (ec:4.1.3.-) (db:pir2.dat) G69600 G69600 Bacillus subtilis 1423 -11528464 4000714262 citz citrate synthase subunit ii (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:196855) (re:197973) (di:direct) AF008220 AF008220 g2293267 Bacillus subtilis 1423 -11528464 7500878770 citz citrate synthase ii (db:genpept-bct1) (ec:4.1.3.7) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: cita2) (le:185094) (re:186212) (di:complement) BSUB0015 Z99118 g2635379 Bacillus subtilis 1423 -11528464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726843	90	22246	189	62

Description

6500724607 ppc:pcka phosphoenolpyruvate carboxykinase (gtcfc:1.1:1.2:1.8:2.4) (ec:4.1.1.49) (keggfc:1.2:1.8:2.3) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pckA pckA Bacillus subtilis 1423 -11528465 7500888344 pcka:ppc (ec:4.1.1.49) (de:phosphoenolpyruvate carboxykinase (atp),) (db:swissprot) PPCK_BACSU P54418 BACILLUS SUBTILIS 1423 -11528465 7000694406 pcka phosphoenolpyruvate carboxykinase pcka (cl:phosphoenolpyruvate carboxykinase (atp)) (db:pir2.dat) F69673 F69673 Bacillus subtilis 1423 -11528465 4000714148 pcka pep carboxykinase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to pep carboxykinase (atp) of e. coli) (le:48003) (re:49586) (di:complement) AF008220 AF008220 g2293299 Bacillus subtilis 1423 -11528465 7500888347 pcka phosphoenolpyruvate carboxykinase (db:genpept-bct1) (ec:4.1.1.49) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ppc) (le:130841) (re:132424) (di:direct) BSUB0016 Z99119 g2635540 Bacillus subtilis 1423 -11528465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726852	91	22247	201	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726860	92	22248	207	68

Description

6500724608 glycogen phosphorylase (gtcfc:1.1:7.2) (ec:2.4.1.1) (keggfc:7.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) glgP glgP Bacillus subtilis 1423 -11528466 7500888075 glgp (ec:2.4.1.1) (de:glycogen phosphorylase,) (db:swissprot) PHSG_BACSU P39123 BACILLUS SUBTILIS 1423 -11528466 7000686142 glgp glycogen phosphorylase:glgp (cl:phosphorylase) (ec:2.4.1.1) (db:pir2.dat) S40052 S40052 Bacillus subtilis 1423 -11528466 4000707250 glgp glycogen phosphorylase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:12988) (re:15384) (di:direct) AF008220 AF008220 g2293140 Bacillus subtilis 1423 -11528466 5000688514 glgp glycogen phosphorylase (fn:degrades starch and glycogen by) (db:genpept-bct1) (de:b.subtilis glycogen operon dna.) (nt:fifth and last gene of glycogen operon) (le:5979) (re:8375) (di:direct) BSGLYCGOP Z25795 g397492 Bacillus subtilis 1423 -11528466 219344 glgp glycogen phosphorylase (fn:degrades starch and glycogen by phosphorylation) (db:genpept-bct1) (ec:2.4.1.1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:165043) (re:167439) (di:complement) BSUB0016 Z99119 g2635578 Bacillus subtilis 1423 -11528466 89697 glgp (ec:2.4.1.1) (de:glycogen phosphorylase,) (db:swissprot) PHSG_BACSU P39123 BACILLUS SUBTILIS 1423 -11528466 170025 glgp glycogen phosphorylase:glgp (cl:phosphorylase) (ec:2.4.1.1) (db:pir) S40052 S40052 Bacillus subtilis 1423 -11528466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726862	93	22249	441	146

Description

6500724609 glycogen synthase:starch:bacterial glycogen synthase (gtcfc:1.1:7.2) (ec:2.4.1.21) (keggfc:7.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) glgA glgA Bacillus subtilis 1423 -11528467 7500882394 glga (ec:2.4.1.21) (de:synthase)) (db:swissprot) GLGA_BACSU P39125 BACILLUS SUBTILIS 1423 -11528467 7000685394 glga adpglucose--starch bacterial glycogen glucosyltransferase:glga:starch bacterial glycogen synthase glga (cl:starch synthase) (ec:2.4.1.21) (db:pir2.dat) S40051 S40051 Bacillus subtilis 1423 -11528467 4000707093 glga starch synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:11547) (re:13001) (di:direct) AF008220 AF008220 g2293139 Bacillus subtilis 1423 -11528467 5000688511 glga starch bacterial glycogen synthase (fn:synthesizes alpha-1,4-glucan chains using) (db:genpept-bct1) (ec:2.4.1.21) (de:b.subtilis glycogen operon dna.) (nt:fourth gene in glycogen operon) (le:4538) (re:5992) (di:direct) BSGLYCGOP Z25795 g580887 Bacillus subtilis 1423 -11528467 219343 glga starch bacterial glycogen synthase (fn:synthesizes alpha-1,4-glucan chains using) (db:genpept-bct1) (ec:2.4.1.21) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:167426) (re:168880) (di:complement) BSUB0016 Z99119 g2635579 Bacillus subtilis 1423 -11528467 73775 glga (ec:2.4.1.21) (de:synthase)) (db:swissprot) GLGA_BACSU P39125 BACILLUS SUBTILIS 1423 -11528467 206171 glga adpglucose--starch bacterial glycogen glucosyltransferase:glga:starch bacterial glycogen synthase glga (ec:2.4.1.21) (db:pir) S40051 S40051 Bacillus subtilis 1423 -11528467

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726886	94	22250	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726907	95	22251	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726936	96	22252	240	79

Description

6500724610 adp-glucose pyrophosphorylase:glycogen biosynthesis protein glgd (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) glgD glgD Bacillus subtilis 1423 -11528468 7500882406 glgd (de:glycogen biosynthesis protein glgd) (db:swissprot) GLGD_BACSU P39124 BACILLUS SUBTILIS 1423 -11528468 7000685404 glgd glycogen biosynthesis protein glgd:adp-glucose pyrophosphorylase homolog:glucose-1-phosphate adenylyltransferase homolog (db:pir2.dat) S40050 S40050 Bacillus subtilis 1423 -11528468 4000707097 glgd glgd (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:10519) (re:11550) (di:direct) AF008220 AF008220 g2293138 Bacillus subtilis 1423 -11528468 219342 glgd protein with similarity to adp-glucose (fn:unknown) (db:genpept-bct1) (de:b.subtilis glycogen operon dna.) (nt:third gene in glycogen operon) (le:3510) (re:4541) (di:direct) BSGLYCGOP Z25795 g580886 Bacillus subtilis 1423 -11528468 7502851495 glgd adp-glucose pyrophosphorylase (fn:required for the synthesis of glycogen) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:168877) (re:169908) (di:complement) BSUB0016 Z99119 g2635580 Bacillus subtilis 1423 -11528468 73803 glgd (de:glycogen biosynthesis protein glgd) (db:swissprot) GLGD_BACSU P39124 BACILLUS SUBTILIS 1423 -11528468 170016 glgd glycogen biosynthesis protein glgd:adp-glucose pyrophosphorylase homolog:glucose-1-phosphate adenylyltransferase homolog (db:pir) S40050 S40050 Bacillus subtilis 1423 -11528468

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726937	97	22253	543	181

Description

6500724611 glucose-1-phosphate adenylyltransferase:adp-glucose synthase:adp-glucose pyrophosphorylase (gtcfc:1.1:7.2) (ec:2.7.7.27) (keggfc:7.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) glgC glgC Bacillus subtilis 1423 -11528469 219341 glgc (ec:2.7.7.27) (de:synthase) (adp-glucose pyrophosphorylase)) (db:swissprot) GLGC_BACSU P39122 BACILLUS SUBTILIS 1423 -11528469 7000685400 glgc glucose-1-phosphate adenylyltransferase:glgc:adp-glucose pyrophosphorylase (cl:glucose-1-phosphate adenylyltransferase) (ec:2.7.7.27) (db:pir2.dat) S40049 S40049 Bacillus subtilis 1423 -11528469 7500882402 glgc adp-glucose pyrophosphorylase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:9353) (re:10495) (di:direct) AF008220 AF008220 g2293137 Bacillus subtilis 1423 -11528469 5000688513 glgc adp-glucose pyrophosphorylase (fn:activates glucose-1-phosphate using atp) (db:genpept-bct1) (ec:2.7.7.27) (de:b.subtilis glycogen operon dna.) (nt:second gene in glycogen operon) (le:2344) (re:3486) (di:direct) BSGLYCGOP Z25795 g397489 Bacillus subtilis 1423 -11528469 4000707096 glgc glucose-1-phosphate adenylyltransferase (fn:activates glucose-1-phosphate using atp) (db:genpept-bct1) (ec:2.7.7.27) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:169932) (re:171074) (di:complement) BSUB0016 Z99119 g2635581 Bacillus subtilis 1423 -11528469 73798 glgc (ec:2.7.7.27) (de:synthase) (adp-glucose pyrophosphorylase)) (db:swissprot) GLGC_BACSU P39122 BACILLUS SUBTILIS 1423 -11528469 139290 glgc glucose-1-phosphate adenylyltransferase:glgc:adp-glucose pyrophosphorylase (cl:glucose-1-phosphate adenylyltransferase) (ec:2.7.7.27) (db:pir) S40049 S40049 Bacillus subtilis 1423 -11528469

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726965	98	22254	276	91

Description

6500724612 1:4-alpha-glucan branching enzyme:glycogen branching enzyme (gtcfc:1.1:7.2) (ec:2.4.1.18) (keggfc:7.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) glgB glgB Bacillus subtilis 1423 -11528470 219340 glgb (ec:2.4.1.18) (de:enzyme)) (db:swissprot) GLGB_BACSU P39118 BACILLUS SUBTILIS 1423 -11528470 7000685398 glgb 1:4-alpha-glucan branching enzyme:glgb (cl:1,4-alpha-glucan branching enzyme) (ec:2.4.1.18) (db:pir2.dat) S40048 S40048 Bacillus subtilis 1423 -11528470 7500882398 glgb 1:4-alpha-glucan branching enzyme (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:7473) (re:9356) (di:direct) AF008220 AF008220 g2293136 Bacillus subtilis 1423 -11528470 5000688512 glgb 1:4-alpha-glucan branching enzyme (fn:introduces alpha-1,6-linkages in starch and) (db:genpept-bct1) (ec:2.4.1.18) (de:b.subtilis glycogen operon dna.) (nt:first gene of glycogen operon) (le:464) (re:2347) (di:direct) BSGLYCGOP Z25795 g397488 Bacillus subtilis 1423 -11528470 4000707094 glgb 1:4-alpha-glucan branching enzyme (fn:introduces alpha-1,6-linkages in starch and) (db:genpept-bct1) (ec:2.4.1.18) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:171071) (re:172954) (di:complement) BSUB0016 Z99119 g2635582 Bacillus subtilis 1423 -11528470 73782 glgb (ec:2.4.1.18) (de:enzyme)) (db:swissprot) GLGB_BACSU P39118 BACILLUS SUBTILIS 1423 -11528470 138083 glgb 1:4-alpha-glucan branching enzyme:glgb (cl:1,4-alpha-glucan branching enzyme) (ec:2.4.1.18) (db:pir) S40048 S40048 Bacillus subtilis 1423 -11528470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726967	99	22255	498	165

Description

6500724613 yugl:pgi glucose-6-phosphate isomerase (gtcfc:1.1) (ec:5.3.1.9) (keggfc:14.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) pgi pgi Bacillus subtilis 1423 -11528471 7000693040 pgi glucose-6-phosphate isomerase pgi (cl:glucose-6-phosphate isomerase) (db:pir2.dat) B69675 B69675 Bacillus subtilis 1423 -11528471 1500693690 pgi glucose-6-phosphate isomerase (fn:glycolysis) (db:genpept-bct1) (ec:5.3.1.9) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yugl) (le:22799) (re:24154) (di:complement) BSUB0017 Z99120 g2635631 Bacillus subtilis 1423 -11528471 1500693691 yugl glucose-6-phosphate isomerase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yugl to yugp.) (nt:putative) (le:132) (re:1487) (di:direct) BSZ93936 Z93936 g1934802 Bacillus subtilis 1423 -11528471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726978	100	22256	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501726989	101	22257	732	244

Description

6500724614 fumarate hydratase:fumarate hydratase:class-ii:fumarase (gtcfc:1.1:1.2:2.5) (ec:4.2.1.2) (keggfc:1.2:2.4) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-glycolysis--gluconeogenesis:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2... citG citG Bacillus subtilis 1423 -11528472 7000693014 citg fumarate hydratase (db:genpept-bct1) (ec:4.2.1.2) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:191083) (re:192471) (di:complement) BSUB0017 Z99120 g2635801 Bacillus subtilis 1423 -11528472 7500954410 citg fumarase protein:citg (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:37816) (re:39204) (di:direct) BS43KBDNA AJ223978 g2832825 Bacillus subtilis 1423 -11528472 7000693013 citg fumarate hydratase citg (cl:fumarate hydratase) (db:pir) A69600 A69600 Bacillus subtilis 1423 -11528472

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727009	102	22258	351	116

Description

6500724615 yvfn:laca beta-galactosidase (gtcfc:1.1) (ec:3.2.1.23) (keggfc:14.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) lacA lacA Bacillus subtilis 1423 -11528473 7000692261 laca beta-galactosidase laca (cl:bacillus beta-galactosidase) (db:pir2.dat) B69649 B69649 Bacillus subtilis 1423 -11528473 1500694060 laca beta-galactosidase (db:genpept-bct1) (ec:3.2.1.23) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvfn) (le:102533) (re:104596) (di:complement) BSUB0018 Z99121 g2635926 Bacillus subtilis 1423 -11528473 7500954270 yvfn hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable beta-galactosidase i) (le:77075) (re:79138) (di:direct) BSZ94043 Z94043 g1945714 Bacillus subtilis 1423 -11528473

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727012	103	22259	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727036	104	22260	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727063	105	22261	522	173

Description

6500724616 yxke:aldy aldehyde dehydrogenase (gtcfc:1.1) (keggfc:14.2) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) aldY aldY Bacillus subtilis 1423 -11528474 7000692169 aldy aldehyde dehydrogenase aldy (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) C69584 C69584 Bacillus subtilis 1423 -11528474 222870 aldy aldehyde dehydrogenase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxke) (le:186820) (re:188277) (di:direct) BSUB0020 Z99123 g2636418 Bacillus subtilis 1423 -11528474 301537 aldy (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:highly homologous to many aldehyde dehydrogenases) (le:36188) (re:37645) (di:complement) D83026 D83026 g1783244 Bacillus subtilis 1423 -11528474

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727064	106	22262	186	61

Description

5000688367 yxas:yxbe:ve7fr:aldx aldehyde dehydrogenase:probable aldehyde dehydrogenase yxas (gtcfc:1.1) (ec:1.2.1.3) (keggfc:14.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) aldX aldX Bacillus subtilis 1423 -11528475 68359 aldx:ve7fr (ec:1.2.1.3) (de:probable aldehyde dehydrogenase aldx,) (db:swissprot) DHA3_BACSU P46329 BACILLUS SUBTILIS 1423 -11528475 7000685029 aldx aldehyde dehydrogenase aldx (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) B69584 B69584 Bacillus subtilis 1423 -11528475 215748 aldx probable aldehyde dehydrogenase (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (ec:1.2.1.3) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:conserved universally; see swiss_prot acc#: p46335) (le:23763) (re:25100) (di:complement) AB005554 AB005554 g904197 Bacillus subtilis 1423 -11528475 7500880223 aldx aldehyde dehydrogenase (db:genpept-bct1) (ec:1.2.1.3) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxas, yxbe) (le:93493) (re:94830) (di:direct) BSUB0021 Z99124 g2636532 Bacillus subtilis 1423 -11528475 6500724617 yxas:yxbe:ve7fr aldehyde dehydrogenase:probable aldehyde dehydrogenase yxas (gtcfc:1.1) (ec:1.2.1.3) (keggfc:14.1) (bsorffc:2.4.1) (db:gtc-bacillus subtilis) aldX aldX Bacillus subtilis 1423 -11528475

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727069	107	22263	318	105

Description

6500724618 hypothetical protein:probable aldehyde dehydrogenase ycbd (gtcfc:1.10:1.11:1.7:1.8:3.2:3.5:5.10:5.11:5.12:5.14:5.6:5.9:6.1:8.1:14.1) (ec:1.2.1.3) (keggfc:1.7:1.8:1.10:1.11:3.2:3.5:5.6:5.9:5.10:5.11:5.12:5.14:6.1:8.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbD ycbD Bacillus subtilis 1423 -11528476 68352 ycbd (ec:1.2.1.3) (de:probable aldehyde dehydrogenase ycbd,) (db:swissprot) DHA1_BACSU P42236 BACILLUS SUBTILIS 1423 -11528476 7000685027 ycbd aldehyde dehydrogenase homolog ycbd (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) G69752 G69752 Bacillus subtilis 1423 -11528476 217116 ycbd aldehyde dehydrogenase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:2374) (re:3840) (di:direct) BACYCB20 D30808 g1479999 Bacillus subtilis 1423 -11528476 7500880221 ycbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to aldehyde dehydrogenase) (le:74188) (re:75654) (di:direct) BSUB0002 Z99105 g2632533 Bacillus subtilis 1423 -11528476 5000688364 (de:(ycbd) (pn:probable aldehyde dehydrogenase ycbd) (gtcfc:1.10:1.11:5.10:5.11:5.14) (ec:1.2.1.3) (dha1_bacsu) (keggfc:1.7:1.8:1.10:1.11:3.2:3.5:5.6:5.10:5.11:5.14:6.1:8.1) (bsorffc:2.1.0) (db:gtc-bacillus subtilis)) ycbD ycbD Bacillus subtilis 1423 10010944

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727070	108	22264	495	165

Description

6500724619 hypothetical protein:similar to 4-aminobutyrate aminotransferase (gtcfc:1.10:1.11:5.1:5.2:6.1:14.1) (ec:2.6.1.19) (keggfc:1.10:1.11:5.1:5.2:6.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnG ycnG Bacillus subtilis 1423 -11528477 7502851496 gabt (ec:2.6.1.19) (de:semialdehyde transaminase) (gaba aminotransferase)) (db:swissprot) GABT_BACSU P94427 BACILLUS SUBTILIS 1423 -11528477 7000692062 ycng 4-aminobutyrate aminotransferase homolog ycng (db:pir2.dat) C69764 C69764 Bacillus subtilis 1423 -11528477 222653 ycng (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to 4-aminobutyrate aminotransferase) (le:38401) (re:39711) (di:direct) BSUB0003 Z99106 g2632691 Bacillus subtilis 1423 -11528477 7500963306 ycng homologue of 4-aminobutyrate aminotransferase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:120804) (re:122114) (di:direct) D50453 D50453 g1805459 Bacillus subtilis 1423 -11528477

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727082	109	22265	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727086	110	22266	555	185

Description

6500724620 succinyl-coa synthetase:beta subunit (gtcfc:1.10:1.12:1.2:1.8:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-ci... sucC sucC Bacillus subtilis 1423 -11528478 7500892225 succ (ec:6.2.1.5) (de:(vegetative protein 63) (veg63)) (db:swissprot) SUCC_BACSU P80886 BACILLUS SUBTILIS 1423 -11528478 7000694644 succ succinate--coa ligase adp-forming:beta chain (cl:succinate--coa ligase (adp-forming) beta chain) (ec:6.2.1.5) (db:pir2.dat) E69719 E69719 Bacillus subtilis 1423 -11528478 7500892227 succ succinyl-coa synthetase beta subunit (db:genpept-bct1) (ec:6.2.1.5) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:81410) (re:82567) (di:direct) BSUB0009 Z99112 g2633981 Bacillus subtilis 1423 -11528478 5500687815 succ putative succinyl-coa synthetase beta chain (db:genpept-bct1) (de:bacillus subtilis ylqg to codv gene region.) (le:578) (re:1735) (di:direct) BSYLQGCOD AJ000975 g2462967 Bacillus subtilis 1423 -11528478

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727090	111	22267	366	121

Description

6500724621 succinyl-coa synthetase:alpha subunit (gtcfc:1.10:1.12:1.2:1.8:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-ci... sucD sucD Bacillus subtilis 1423 -11528479 7000694643 sucd succinate--coa ligase adp-forming:alpha chain (cl:succinate--coa ligase (adp-forming) alpha chain) (ec:6.2.1.5) (db:pir2.dat) F69719 F69719 Bacillus subtilis 1423 -11528479 5500687816 sucd succinyl-coa synthetase alpha subunit (db:genpept-bct1) (ec:6.2.1.5) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:82596) (re:83498) (di:direct) BSUB0009 Z99112 g2633982 Bacillus subtilis 1423 -11528479 7500954493 sucd putative succinyl-coa synthetase alpha chain (db:genpept-bct1) (de:bacillus subtilis ylqg to codv gene region.) (le:1764) (re:2666) (di:direct) BSYLQGCOD AJ000975 g2462968 Bacillus subtilis 1423 -11528479

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727115	112	22268	789	262

Description

6500724622 hypothetical protein:putative propionyl-coa carboxylase beta chain:pccase:propanoyl-coa:carbon dioxide ligase (gtcfc:1.10:5.6:14.1) (ec:6.4.1.3) (keggfc:1.10:5.6) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjD yqjD Bacillus subtilis 1423 -11528480 88789 yqjd (ec:6.4.1.3) (de:(propanoyl-coa:carbon dioxide ligase)) (db:swissprot) PCCB_BACSU P54541 BACILLUS SUBTILIS 1423 -11528480 7000686101 yqjd propionyl-coa carboxylase homolog yqjd (cl:propionyl-coa carboxylase beta chain) (db:pir2.dat) D69963 D69963 Bacillus subtilis 1423 -11528480 216199 yqjd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:231318) (re:232838) (di:direct) BACJH642 D84432 g1303955 Bacillus subtilis 1423 -11528480 7500887720 yqjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to propionyl-coa carboxylase) (le:90781) (re:92301) (di:complement) BSUB0013 Z99116 g2634826 Bacillus subtilis 1423 -11528480 5000688365 (de:(yqjd) (pn:putative propionyl-coa carboxylase beta chain:pccase:propanoyl-coa:carbon dioxide ligase) (gtcfc:1.10) (ec:6.4.1.3) (pccb_bacsu) (keggfc:1.10:5.6) (db:gtc-bacillus subtilis)) yqjD yqjD Bacillus subtilis 1423 10030916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727133	113	22269	330	109

Description

6500724623 yqil:mmga acetyl-coa acetyltransferase:acetoacetyl-coa thiolase (gtcfc:1.10:1.11:1.8:2.2:3.1:3.2:3.3:5.14:5.9) (ec:2.3.1.9) (keggfc:1.8:1.10:1.11:3.1:3.2:3.3:5.9:5.14) (bsorffc:2.6.1:2.6.2) (db:gtc-bacillus subtilis) mmgA mmgA Bacillus subtilis 1423 -11528481 7000692135 mmga acetyl-coa acetyltransferase mmga (cl:acetyl-coa acetyltransferase) (db:pir2.dat) B69658 B69658 Bacillus subtilis 1423 -11528481 216175 yqil (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:205608) (re:206789) (di:direct) BACJH642 D84432 g1303931 Bacillus subtilis 1423 -11528481 7500963367 mmga acetyl-coa acetyltransferase (db:genpept-bct1) (ec:2.3.1.9) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqil) (le:116830) (re:118011) (di:complement) BSUB0013 Z99116 g2634851 Bacillus subtilis 1423 -11528481

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727134	114	22270	312	103

Description

6500724624 yqhx:accc acetyl-coa carboxylase subunit:biotin carboxylase subunit:biotin carboxylase:a subunit of acetyl-coa carboxylase:acc (gtcfc:1.10:1.8:3.1:9.6) (keggfc:1.8:1.10:3.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:lipid metabolism-fatty acid biosynthesis:metabolis... accC accC Bacillus subtilis 1423 -11528482 7000692140 accc acetyl-coa carboxylase biotin carboxylase subunit accc (cl:biotin carboxylase:biotin carboxylase homology) (db:pir2.dat) A69581 A69581 Bacillus subtilis 1423 -11528482 216157 yqhx (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:187900) (re:189252) (di:direct) BACJH642 D84432 g1303913 Bacillus subtilis 1423 -11528482 7500954523 accc acetyl-coa carboxylase subunit biotin (fn:long-chain fatty acid biosynthesis) (db:genpept-bct1) (ec:6.4.1.2) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqhx) (le:134369) (re:135721) (di:complement) BSUB0013 Z99116 g2634868 Bacillus subtilis 1423 -11528482

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727135	115	22271	498	165

Description

GTC ORF with score 182 to: (sr:mice macrophage) (db:genpept-rod) (de:putative transcription regulator {clone t2, repetitive sequence}(mice, macrophage, mrna, 1263 nt).) (nt:method: conceptual translation supplied by author.) (le:55) (re:732) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727136	116	22272	627	208

Description

6500724625 fabe:yqhw:accb acetyl-coa carboxylase subunit:biotin carboxyl carrier subunit:biotin carboxyl carrier protein of acetyl-coa carboxylase:bccp (gtcfc:3.1:9.6:1.10:1.8) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:lipid metabolism-fatty acid biosynthesis:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:carbohydrate meta... accB accB Bacillus subtilis 1423 -11528483 7000692139 accb acetyl-coa carboxylase biotin carboxyl carrier subunit accb (cl:biotin carboxyl carrier protein:lipoyl/biotin-binding homology) (db:pir2.dat) H69580 H69580 Bacillus subtilis 1423 -11528483 216156 yqhw (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:187409) (re:187888) (di:direct) BACJH642 D84432 g1303912 Bacillus subtilis 1423 -11528483 7500963370 accb acetyl-coa carboxylase subunit biotin carboxyl (fn:long-chain fatty acid biosynthesis) (db:genpept-bct1) (ec:6.4.1.2) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: fabe, yqhw) (le:135733) (re:136212) (di:complement) BSUB0013 Z99116 g2634869 Bacillus subtilis 1423 -11528483

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727137	117	22273	438	145

Description

6500724626 acetyl coa carboxylase:alpha subunit (gtcfc:1.10:1.8:3.1:9.6) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:lipid metabolism-fatty acid biosynthe... accA accA Bacillus subtilis 1423 -11528484 7500876280 acca (ec:6.4.1.2) (de:(ec 6.4.1.2)) (db:swissprot) ACCA_BACSU O34847 BACILLUS SUBTILIS 1423 -11528484 7000692138 acca acetyl-coa carboxylase::carboxyltransferase alpha chain (cl:acetyl-coa carboxylase, carboxyltransferase alpha chain) (ec:6.4.1.2) (db:pir2.dat) G69580 G69580 Bacillus subtilis 1423 -11528484 4000714257 acca acetyl-coa carboxylase subunit (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:190416) (re:191393) (di:direct) AF008220 AF008220 g2293263 Bacillus subtilis 1423 -11528484 7500876283 acca acetyl coa carboxylase alpha subunit (fn:long-chain fatty acid biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:191674) (re:192651) (di:complement) BSUB0015 Z99118 g2635385 Bacillus subtilis 1423 -11528484

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727157	118	22274	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727172	119	22275	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727179	120	22276	432	144

Description

6500724627 acetate kinase:acetokinase (gtcfc:1.10:1.8) (ec:2.7.2.1) (keggfc:1.8:1.10) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) ackA ackA Bacillus subtilis 1423 -11528485 58184 acka (ec:2.7.2.1) (de:acetate kinase, (acetokinase)) (db:swissprot) ACKA_BACSU P37877 BACILLUS SUBTILIS 1423 -11528485 7000684501 acka acetate kinase:acka (cl:acetate kinase) (ec:2.7.2.1) (db:pir2.dat) B49935 B49935 Bacillus subtilis 1423 -11528485 7500876316 acka acetate kinase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:162827) (re:164014) (di:direct) AF008220 AF008220 g2293240 Bacillus subtilis 1423 -11528485 215119 acka acetate kinase (db:genpept-bct1) (ec:2.7.2.1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:16413) (re:17600) (di:complement) BSUB0016 Z99119 g2635431 Bacillus subtilis 1423 -11528485 4000706877 acka acetate kinase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct2) (de:bacillus subtilis acetate kinase (acka) gene, complete cds.) (le:698) (re:1885) (di:direct) BACACKA L17320 g405134 Bacillus subtilis 1423 -11528485 138942 acka acetate kinase:acka (cl:acetate kinase) (ec:2.7.2.1) (db:pir) B49935 B49935 Bacillus subtilis 1423 -11528485 5000688359 (de:(acka) (pn:acetate kinase:acetate kinase :acetokinase) (gtcfc:1.10) (ec:2.7.2.1) (acka_bacsu) (keggfc:1.8:1.10) (bsorffc:2.1.0) (db:gtc-bacillus subtilis)) ackA ackA Bacillus subtilis 1423 10000964

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727245	121	22277	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727246	122	22278	480	159

Description

6500724628 hypothetical protein:similar to acetate-coa ligase (gtcfc:1.10:1.8:2.5:14.1) (ec:6.2.1.1) (keggfc:1.8:1.10:2.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:energy metabolism-reductive carboxyl... ytcI ytcI Bacillus subtilis 1423 -11528486 7000692124 ytci acetate-coa ligase homolog ytci (cl:acetate--coa ligase homology) (db:pir2.dat) E69989 E69989 Bacillus subtilis 1423 -11528486 4000714223 ytci ytci (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:putative acetate coa-ligase) (le:153853) (re:155448) (di:direct) AF008220 AF008220 g2293232 Bacillus subtilis 1423 -11528486 7500963363 ytci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to acetate-coa ligase) (le:24979) (re:26574) (di:complement) BSUB0016 Z99119 g2635440 Bacillus subtilis 1423 -11528486

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727263	123	22279	222	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727265	124	22280	576	191

Description

GTC ORF with score 138 to: (sr:bodo saltans) (db:genpept-inv) (de:bodo saltans nadh dehydrogenase subunit 5 (nd5) mrna, kinetoplastgene encoding kinetoplast protein, partial cds.) (nt:partially edited mrna) (le:<1) (re:639) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727266	125	22281	456	151

Description

5000688360 acetyl-coa synthetase:acetyl-coenzyme a synthetase:acetate--coa ligase:acyl-activating enzyme:acetyl-coa synthase (gtcfc:1.10:1.8:2.5:3.2) (keggfc:1.8:1.10:2.4:3.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-pyruvate and acetyl-coa metabolism:energy metabolism-reductive carboxylate cycle ... acsA acsA Bacillus subtilis 1423 -11528487 58307 acsa (ec:6.2.1.1) (de:activating enzyme) (acetyl-coa synthase)) (db:swissprot) ACSA_BACSU P39062 BACILLUS SUBTILIS 1423 -11528487 7000684509 acsa acetate--coa ligase:acsa:acetyl-coa synthetase acsa (cl:acetate--coa ligase:acetate--coa ligase homology) (ec:6.2.1.1) (db:pir2.dat) S39646 S39646 Bacillus subtilis 1423 -11528487 7500876380 acsa acetyl-coa synthetase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:139191) (re:140909) (di:direct) AF008220 AF008220 g2293224 Bacillus subtilis 1423 -11528487 215125 acsa acetyl-coa synthetase (fn:acetate utilization) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis homologues of mota and motb genes acetoinutilization operon genes acua, acub and acuc, and acetyl-coasynthase (acsa) genes, complete cds.) (le:420... BACACUCBA L17309 g348053 Bacillus subtilis 1423 -11528487 4000706878 acsa acetyl-coa synthetase (fn:acetate utilization) (db:genpept-bct1) (ec:6.2.1.1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:39518) (re:41236) (di:complement) BSUB0016 Z99119 g2635452 Bacillus subtilis 1423 -11528487 142310 acsa acetate--coa ligase:acsa:acetyl-coa synthetase acsa (cl:acetate--coa ligase:acetate--coa ligase homology) (ec:6.2.1.1) (db:pir) S39646 S39646 Bacillus subtilis 1423 -11528487 6500724629 acetyl-coa synthetase:acetyl-coenzyme a synthetase:acetate--coa ligase:acyl-activating enzyme:acetyl-coa synthase (gtcfc:1.10:1.8:2.5:3.2) (keggfc:1.8:1.10:2.4:3.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acsA acsA Bacillus subtilis 1423 -11528487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727268	126	22282	531	176

Description

6500724630 ipa-58r:ywdh hypothetical protein:probable aldehyde dehydrogenase ywdh (gtcfc:1.10:1.11:1.7:1.8:3.2:3.5:5.10:5.11:5.12:5.14:5.6:5.9:6.1:8.1:14.1) (ec:1.2.1.3) (keggfc:1.7:1.8:1.10:1.11:3.2:3.5:5.6:5.9:5.10:5.11:5.12:5.14:6.1:8.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywdH ywdH Bacillus subtilis 1423 -11528488 7500880222 ywdh:ipa-58r (ec:1.2.1.3) (de:probable aldehyde dehydrogenase ywdh,) (db:swissprot) DHA2_BACSU P39616 BACILLUS SUBTILIS 1423 -11528488 7000685028 ywdh aldehyde dehydrogenase homolog ywdh:protein ipa-58r (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) S39713 S39713 Bacillus subtilis 1423 -11528488 5000688366 ipa-58r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:59908) (re:61281) (di:complement) BSGENR X73124 g413982 Bacillus subtilis 1423 -11528488 219295 ywdh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-58r; similar to aldehyde) (le:96681) (re:98054) (di:direct) BSUB0020 Z99123 g2636331 Bacillus subtilis 1423 -11528488 68357 ywdh:ipa-58r (ec:1.2.1.3) (de:probable aldehyde dehydrogenase ywdh,) (db:swissprot) DHA2_BACSU P39616 BACILLUS SUBTILIS 1423 -11528488 170137 ywdh aldehyde dehydrogenase homolog ywdh (db:pir) S39713 S39713 Bacillus subtilis 1423 -11528488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727270	127	22283	555	184

Description

6500724631 hypothetical protein:similar to pyruvate oxidase (gtcfc:1.11:1.12:1.8:5.7:9.5:14.1) (keggfc:1.8:1.11:1.12:5.7:9.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-pyruvat... ydaP ydaP Bacillus subtilis 1423 -11528489 7000694485 ydap pyruvate oxidase homolog ydap (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (db:pir2.dat) G69769 G69769 Bacillus subtilis 1423 -11528489 302689 ydap (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to pyruvate oxidase and acetolactate) (le:21889) (re:23613) (di:direct) AB001488 AB001488 g1881244 Bacillus subtilis 1423 -11528489 7500965124 ydap (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to pyruvate oxidase) (le:85633) (re:87357) (di:direct) BSUB0003 Z99106 g2632734 Bacillus subtilis 1423 -11528489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727271	128	22284	516	171

Description

6500724632 hypothetical protein:probable phosphate butyryltransferase:phosphotransbutyrylase (gtcfc:1.11:14.1) (ec:2.3.1.19) (keggfc:1.11) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiS yqiS Bacillus subtilis 1423 -11528490 92132 yqis (ec:2.3.1.19) (de:(phosphotransbutyrylase)) (db:swissprot) PTB_BACSU P54530 BACILLUS SUBTILIS 1423 -11528490 7000686207 yqis phosphate butyryltransferase homolog yqis (cl:phosphate acetyltransferase) (db:pir2.dat) A69962 A69962 Bacillus subtilis 1423 -11528490 216182 yqis (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:214979) (re:215878) (di:direct) BACJH642 D84432 g1303938 Bacillus subtilis 1423 -11528490 7500888927 yqis (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to phosphate butyryltransferase) (le:107741) (re:108640) (di:complement) BSUB0013 Z99116 g2634843 Bacillus subtilis 1423 -11528490 5000688378 (de:(yqis) (pn:probable phosphate butyryltransferase:phosphotransbutyrylase) (gtcfc:1.11) (ec:2.3.1.19) (ptb_bacsu) (keggfc:1.11) (db:gtc-bacillus subtilis)) yqiS yqiS Bacillus subtilis 1423 10034166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727289	129	22285	360	119

Description

6500724633 yqim:mmgb 3-hydroxybutyryl-coa dehydrogenase (gtcfc:1.11:1.8:2.2) (ec:1.1.1.157) (keggfc:1.11) (bsorffc:2.6.1:2.6.2) (db:gtc-bacillus subtilis) mmgB mmgB Bacillus subtilis 1423 -11528491 7000692045 mmgb 3-hydroxybutyryl-coa dehydrogenase mmgb (cl:3-hydroxyacyl-coa dehydrogenase:3-hydroxyacyl-coa dehydrogenase homology) (db:pir2.dat) C69658 C69658 Bacillus subtilis 1423 -11528491 216176 yqim (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:206939) (re:207673) (di:direct) BACJH642 D84432 g1303932 Bacillus subtilis 1423 -11528491 7500963296 mmgb 3-hydroxybutyryl-coa dehydrogenase (fn:(butyrate/butanol-producing pathway)) (db:genpept-bct1) (ec:1.1.1.157) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqim) (le:115946) (re:116680) (di:complement) BSUB0013 Z99116 g2634850 Bacillus subtilis 1423 -11528491

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727294	130	22286	309	102

Description

6500724634 acetolactate synthase:acetohydroxy-acid synthase:small subunit:acetolactate synthase small subunit:ahas:acetohydroxy-acid synthase small subunit:als (gtcfc:1.11:1.12:5.3:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (bsorffc:3.1.3:3.4.9) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabol... ilvN ilvN Bacillus subtilis 1423 -11528492 79273 ilvn (ec:4.1.3.18) (de:(acetohydroxy-acid synthase small subunit) (als)) (db:swissprot) ILVN_BACSU P37252 BACILLUS SUBTILIS 1423 -11528492 7000685626 ilvn acetolactate synthase small subunit ilvn (cl:acetolactate synthase small chain) (db:pir2.dat) E69644 E69644 Bacillus subtilis 1423 -11528492 215903 ilvn acetolactate synthase small subunit (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis ilvb, ilvn and ilvc genes, complete ilv-leuoperon.) (le:2438) (re:2962) (di:direct) BACILNB L03181 g143092 Bacillus subtilis 1423 -11528492 220343 ilvn acetolactate synthase acetohydroxy-acid (fn:valine/isoleucine biosynthesis) (db:genpept-bct1) (ec:4.1.3.18) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:98696) (re:99220) (di:complement) BSUB0015 Z99118 g2635295 Bacillus subtilis 1423 -11528492 304216 ilvn acetolactate synthase small subunit (db:genpept-bct1) (ec:4.1.3.18) (de:b.subtilis genomic sequence 89009bp.) (nt:acetolactate synthase (acetohydroxy-acid synthase)) (le:70687) (re:71211) (di:direct) BSZ75208 Z75208 g1770067 Bacillus subtilis 1423 -11528492 5000688373 (de:(ilvn) (pn:acetolactate synthase small subunit:ahas:als:acetolactate synthase small subunit :ahas:acetohydroxy-acid synthase small subunit:als) (gtcfc:1.11:1.12) (ec:4.1.3.18) (ilvn_bacsu) (keggfc:1.11:1.12:5.7:9.5) (bsorff) ilvN ilvN Bacillus subtilis 1423 10021601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727298	131	22287	381	126

Description

6500724635 acetolactate synthase:acetohydroxy-acid synthase:large subunit:acetolactate synthase large subunit:ahas:acetohydroxy-acid synthase large subunit:als (gtcfc:1.11:1.12:5.3:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (bsorffc:3.1.3:3.4.9) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabol... ilvB ilvB Bacillus subtilis 1423 -11528493 7000692134 ilvb acetolactate synthase:large chain (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:4.1.3.18) (db:pir2.dat) B69644 B69644 Bacillus subtilis 1423 -11528493 220342 ilvb acetolactate synthase acetohydroxy-acid (fn:valine/isoleucine biosynthesis) (db:genpept-bct1) (ec:4.1.3.18) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:99217) (re:100941) (di:complement) BSUB0015 Z99118 g2635296 Bacillus subtilis 1423 -11528493 304215 ilvb acetolactate synthase large subunit (db:genpept-bct1) (ec:4.1.3.18) (de:b.subtilis genomic sequence 89009bp.) (nt:acetolactate synthase (acetohydroxy-acid synthase)) (le:68966) (re:70690) (di:direct) BSZ75208 Z75208 g1770066 Bacillus subtilis 1423 -11528493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727324	132	22288	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727352	133	22289	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727356	134	22290	417	138

Description

6500724636 succinate dehydrogenase:cytochrome b558 subunit:succinate dehydrogenase cytochrome b-558 subunit (gtcfc:1.11:1.2:2.1:2.5:2.8) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-oxidative phosphoryl... sdhC sdhC Bacillus subtilis 1423 -11528494 68614 sdhc (de:succinate dehydrogenase cytochrome b-558 subunit) (db:swissprot) DHSC_BACSU P08064 BACILLUS SUBTILIS 1423 -11528494 122691 sdhc:sdha succinate dehydrogenase:cytochrome b558:fumarate reductase c protein (cl:succinate dehydrogenase cytochrome b558) (ec:1.3.99.1) (db:pir1.dat) (mp:70) DEBSSC A29843 Bacillus subtilis 1423 -11528494 216686 (sr:b.subtilis dna, clone pkim4) (db:genpept-bct1) (de:b.subtilis succinate dehydrogenase complex encoding cytochromeb-558 subunit, complete cds, and flavoprotein subunit, 5' end.) (nt:succinate dehydrogenase cytochrome b-558 subunit) (le:265) (re:873)... BACSDHAB M13470 g143525 Bacillus subtilis 1423 -11528494 220327 sdhc succinate dehydrogenase cytochrome b558 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:112102) (re:112710) (di:complement) BSUB0015 Z99118 g2635310 Bacillus subtilis 1423 -11528494 304200 sdhc cytochrome b558 subunit of succinate (db:genpept-bct1) (ec:1.3.99.1) (de:b.subtilis genomic sequence 89009bp.) (le:57197) (re:57805) (di:direct) BSZ75208 Z75208 g1770051 Bacillus subtilis 1423 -11528494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727382	135	22291	798	266

Description

6500724637 alpha-acetolactate decarboxylase (gtcfc:1.11:1.12:1.8:2.2) (ec:4.1.1.5) (keggfc:1.11:1.12) (bsorffc:2.6.1:2.6.2) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-pyruvate ... alsD alsD Bacillus subtilis 1423 -11528495 1500685061 alsd (ec:4.1.1.5) (de:alpha-acetolactate decarboxylase,) (db:swissprot) ALDC_BACSU Q04777 BACILLUS SUBTILIS 1423 -11528495 7000684553 alsd acetolactate decarboxylase:alsd:alpha-acetolactate decarboxylase alsd (cl:acetolactate decarboxylase) (ec:4.1.1.5) (db:pir2.dat) B47126 B47126 Bacillus subtilis 1423 -11528495 7500876743 alsd acetolactate decarboxylase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis als operon regulatory protein (alsr), ph6acetolactate synthase (alss) and acetolactate decarboxylase (alsd)genes, complete cds.) (le:3562) (re:4329) (di:direct) BACALSRD L04470 g142471 Bacillus subtilis 1423 -11528495 215158 alsd alpha-acetolactate decarboxylase (fn:acetoin biosynthesis) (db:genpept-bct1) (ec:4.1.1.5) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:110766) (re:111533) (di:complement) BSUB0019 Z99122 g2636125 Bacillus subtilis 1423 -11528495 5000688368 alsd alpha-acetolactate decarboxylase protein:alsd (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:13638) (re:14405) (di:direct) BSZ93767 Z93767 g1929341 Bacillus subtilis 1423 -11528495 59103 alsd (ec:4.1.1.5) (de:alpha-acetolactate decarboxylase,) (db:swissprot) ALDC_BACSU Q04777 BACILLUS SUBTILIS 1423 -11528495 141459 alsd acetolactate decarboxylase:alsd:alpha-acetolactate decarboxylase alsd (cl:acetolactate decarboxylase) (ec:4.1.1.5) (db:pir) B47126 B47126 Bacillus subtilis 1423 -11528495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727442	136	22292	489	163

Description

GTC ORF with score 711 to: (sr:penicillium janthinellum (strain:ifo7719) dna) (db:genpept-pln1) (ec:3.2.1.15) (de:penicillium janthinellum dna for polygalacturonase, complete cds.) (le:2005:2330:2812) (re:2241:2749:3270) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727457	137	22293	594	198

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727459	138	22294	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727460	139	22295	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727495	140	22296	588	196

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727500	141	22297	954	318

Description

6500724638 alpha-acetolactate synthase:ph6 (gtcfc:1.11:1.12:1.8:2.2:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (bsorffc:2.6.1:2.6.2) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate met... alsS alsS Bacillus subtilis 1423 -11528496 7000692179 alss acetolactate synthase (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:4.1.3.18) (db:pir2.dat) H69584 H69584 Bacillus subtilis 1423 -11528496 1500693629 alss alpha-acetolactate synthase ph6 (fn:acetoin biosynthesis) (db:genpept-bct1) (ec:4.1.3.18) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:111595) (re:113310) (di:complement) BSUB0019 Z99122 g2636126 Bacillus subtilis 1423 -11528496 7500954402 alss alpha-acetolactate synthase protein:alss (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:11861) (re:13576) (di:direct) BSZ93767 Z93767 g1929340 Bacillus subtilis 1423 -11528496

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727517	142	22298	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727520	143	22299	327	109

Description

6500724639 hypothetical protein:similar to malate dehydrogenase (gtcfc:1.2:1.8:1.9:2.4:2.5:14.1) (keggfc:1.2:1.8:1.9:2.3:2.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-pyruvate and acetyl-coa metabolism:carbohydrate metabolism-glyoxyl... yjmC yjmC Bacillus subtilis 1423 -11528497 7000694184 yjmc malate dehydrogenase homolog yjmc (cl:malate dehydrogenase ylbc) (db:pir2.dat) E69852 E69852 Bacillus subtilis 1423 -11528497 5500701566 yjmc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to malate dehydrogenase) (le:108502) (re:109515) (di:direct) BSUB0007 Z99110 g2633586 Bacillus subtilis 1423 -11528497 7500964912 yjmc malate dehydrogenase-like protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to methanococcus jannaschii malate) (le:22662) (re:23675) (di:direct) AF015825 AF015825 g2612904 Bacillus subtilis 1423 -11528497

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727575	144	22300	267	88

Description

6500724640 yqio:mmgd citrate synthase iii (gtcfc:1.2:1.8:1.9:2.2) (ec:4.1.3.7) (keggfc:1.2:1.9) (bsorffc:2.6.1:2.6.2) (db:gtc-bacillus subtilis) mmgD mmgD Bacillus subtilis 1423 -11528498 64651 mmgd (ec:4.1.3.7) (de:citrate synthase iii,) (db:swissprot) CISW_BACSU P45858 BACILLUS SUBTILIS 1423 -11528498 7000684821 mmgd citrate synthase iii mmgd (cl:citrate (si)-synthase) (db:pir2.dat) E69658 E69658 Bacillus subtilis 1423 -11528498 216178 yqio (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:208871) (re:209989) (di:direct) BACJH642 D84432 g1303934 Bacillus subtilis 1423 -11528498 219906 mmgd citrate synthase iii (db:genpept-bct1) (de:bacillus subtilis (mmga), (mmgb), (mmgc), and citrate synthase iii(mmgd) genes, complete cds, and (mmge) gene, partial cds.) (le:3545) (re:4663) (di:direct) BSU29084 U29084 g881607 Bacillus subtilis 1423 -11528498 7500878757 mmgd citrate synthase iii (db:genpept-bct1) (ec:4.1.3.7) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqio) (le:113630) (re:114748) (di:complement) BSUB0013 Z99116 g2634848 Bacillus subtilis 1423 -11528498

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727576	145	22301	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727581	146	22302	261	86

Description

6500724641 mdh:cith malate dehydrogenase (gtcfc:1.2:1.8:1.9:2.4:2.5:12.2) (ec:1.1.1.37) (keggfc:1.2:1.8:1.9:2.3:2.4) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-pyruvate and acetyl-coa metabolism:carbohydrate meta... citH citH Bacillus subtilis 1423 -11528499 7000685807 cith malate dehydrogenase:cith (cl:l-lactate dehydrogenase) (ec:1.1.1.37) (db:pir2.dat) I40383 I40383 Bacillus subtilis 1423 -11528499 4000707195 cith malate dehydrogenase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:199452) (re:200390) (di:direct) AF008220 AF008220 g2293269 Bacillus subtilis 1423 -11528499 7500964911 cith malate dehydrogenase (db:genpept-bct1) (de:bacillus subtilis citrate synthase ii (citz), isocitratedehydrogenase (citc) and malate dehydrogenase (cith) genes,complete cds, phop (phop) gene, partial cds.) (le:2964) (re:3902) (di:direct) BSCITZC U05257 g1045296 Bacillus subtilis 1423 -11528499 219078 cith malate dehydrogenase (db:genpept-bct1) (ec:1.1.1.37) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: mdh) (le:182677) (re:183615) (di:complement) BSUB0015 Z99118 g2635377 Bacillus subtilis 1423 -11528499 83303 mdh_bacsu (de:malate dehydrogenase (ec 1.1.1.37).) P49814 P49814 Bacillus subtilis 1423 -11528499 5000688380 (de:(cith) (pn:malate dehydrogenase) (gn:mdh) (gtcfc:2.04:2.05) (ec:1.1.1.37) (mdh_bacsu) (keggfc:1.2:1.8:1.9:2.3:2.4) (db:gtc-bacillus subtilis)) citH citH Bacillus subtilis 1423 10025522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727582	147	22303	306	101

Description

6500724642 ribose-phosphate pyrophosphokinase:phosphoribosyl pyrophosphate synthetase (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) prs prs Bacillus subtilis 1423 -11528500 215040 prs (ec:2.7.6.1) (de:pyrophosphate synthetase)) (db:swissprot) KPRS_BACSU P14193 BACILLUS SUBTILIS 1423 -11528500 123908 prs ribose-phosphate pyrophosphokinase:prs:phosphoribosylpyrophosphate synthetase (cl:ribose-phosphate pyrophosphokinase catalytic chain) (ec:2.7.6.1) (db:pir1.dat) KIBSRS S05372 Bacillus subtilis 1423 -11528500 7500884705 prs phosphoribosylpyrophosphate synthetase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:121345) (re:122298) (di:direct) BAC180K D26185 g467440 Bacillus subtilis 1423 -11528500 219733 (db:genpept-bct1) (de:b.subtilis prs,tms,and ctc (partial) genes for prpp synthetase andtwo undefined gene products.) (nt:prpp synthetase (aa 1-317)) (le:1615) (re:2568) (di:direct) BSTMSPRS X16518 g40218 Bacillus subtilis 1423 -11528500 7502851497 prs phosphoribosyl pyrophosphate synthetase (fn:nucleotide biosynthesis) (db:genpept-bct1) (ec:2.7.6.1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:57743) (re:58696) (di:direct) BSUB0001 Z99104 g2632318 Bacillus subtilis 1423 -11528500 81013 prs (ec:2.7.6.1) (de:pyrophosphate synthetase)) (db:swissprot) KPRS_BACSU P14193 BACILLUS SUBTILIS 1423 -11528500 7000685700 prs ribose-phosphate pyrophosphokinase:prs:phosphoribosylpyrophosphate synthetase (cl:ribose-phosphate pyrophosphokinase catalytic chain) (ec:2.7.6.1) (db:pir) KIBSRS S66081 Bacillus subtilis 1423 -11528500

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727583	148	22304	219	72

Description

6500724643 glucose 1-dehydrogenase (gtcfc:1.3:1.4) (ec:1.1.1.47) (keggfc:1.3) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) gdh gdh Bacillus subtilis 1423 -11528501 7000693031 gdh glucose 1-dehydrogenase (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.1.1.47) (db:pir2.dat) D69629 D69629 Bacillus subtilis 1423 -11528501 222656 gdh glucose 1-dehydrogenase (db:genpept-bct1) (ec:1.1.1.47) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:42174) (re:42959) (di:direct) BSUB0003 Z99106 g2632694 Bacillus subtilis 1423 -11528501 7500964013 gdh glucose dehydrogenase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:124577) (re:125362) (di:direct) D50453 D50453 g1805462 Bacillus subtilis 1423 -11528501

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727584	149	22305	420	139

Description

6500724644 hypothetical protein:similar to ribulose-5-phosphate 3-epimerase (gtcfc:1.3:1.4:2.4:14.1) (ec:5.1.3.1) (keggfc:1.3:1.4:2.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloR yloR Bacillus subtilis 1423 -11528502 7000694547 ylor ribulose-5-phosphate 3-epimerase homolog ylor (cl:yeast ribulose-5-phosphate-epimerase) (db:pir2.dat) B69879 B69879 Bacillus subtilis 1423 -11528502 5500687802 ylor (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to ribulose-5-phosphate 3-epimerase) (le:54983) (re:55636) (di:direct) BSUB0009 Z99112 g2633951 Bacillus subtilis 1423 -11528502 7500965161 ylor putative cfxe protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:16755) (re:17408) (di:direct) BSY13937 Y13937 g2337808 Bacillus subtilis 1423 -11528502

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727598	150	22306	318	105

Description

6500724645 2-keto-3-deoxygluconate kinase:2-dehydro-3-deoxygluconokinase:2-keto-3-deoxygluconokinase:3-deoxy-2-oxo-d-gluconate kinase:kdg kinase (gtcfc:1.3:1.4) (ec:2.7.1.45) (keggfc:1.3:1.4) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) kdgK kdgK Bacillus subtilis 1423 -11528503 80575 kdgk (ec:2.7.1.45) (de:deoxygluconokinase) (3-deoxy-2-oxo-d-gluconate kinase) (kdg kinase)) (db:swissprot) KDGK_BACSU P50845 BACILLUS SUBTILIS 1423 -11528503 7000685670 kdgk 2-keto-3-deoxygluconate kinase kdgk (db:pir2.dat) A69648 A69648 Bacillus subtilis 1423 -11528503 216508 kdgk 2-keto-3-deoxygluconate kinase (fn:pectin utilization) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:26... BACPONAYPP L47838 g1146189 Bacillus subtilis 1423 -11528503 7500884544 kdgk 2-keto-3-deoxygluconate kinase (fn:pectin utilization) (db:genpept-bct1) (ec:2.7.1.45) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:127303) (re:128277) (di:complement) BSUB0012 Z99115 g2634630 Bacillus subtilis 1423 -11528503

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727600	151	22307	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727617	152	22308	534	177

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727628	153	22309	237	78

Description

6500724646 yqkn:drm phosphopentomutase:phosphodeoxyribomutase (gtcfc:1.3:4.4) (ec:5.4.2.7) (keggfc:1.3) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) drm drm Bacillus subtilis 1423 -11528504 7000694405 drm phosphodeoxyribomutase drm (cl:phosphopentomutase) (db:pir2.dat) B69619 B69619 Bacillus subtilis 1423 -11528504 216239 yqkn (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:271220) (re:272404) (di:direct) BACJH642 D84432 g1303995 Bacillus subtilis 1423 -11528504 7500954459 drm phosphodeoxyribomutase (fn:conversion of ribose-1-p/deoxyribose-1-p to) (db:genpept-bct1) (ec:5.4.2.7) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqkn) (le:51215) (re:52399) (di:complement) BSUB0013 Z99116 g2634785 Bacillus subtilis 1423 -11528504

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727654	154	22310	873	290

Description

5000688474 zwf:yqjj hypothetical protein:glucose-6-phosphate 1-dehydrogenase:g6pd (gtcfc:1.3:6.16:14.1) (ec:1.1.1.49) (keggfc:1.3:6.9) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjJ yqjJ Bacillus subtilis 1423 -11528505 72776 zwf (ec:1.1.1.49) (de:protein 11) (veg11)) (db:swissprot) G6PD_BACSU P54547 BACILLUS SUBTILIS 1423 -11528505 7000685337 yqjj probable glucose-6-phosphate 1-dehydrogenase:yqjj (cl:glucose-6-phosphate dehydrogenase) (ec:1.1.1.49) (db:pir2.dat) B69964 B69964 Bacillus subtilis 1423 -11528505 216205 yqjj (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:239025) (re:240494) (di:complement) BACJH642 D84432 g1303961 Bacillus subtilis 1423 -11528505 7500881992 yqjj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to glucose-6-phosphate 1-dehydrogenase) (le:83125) (re:84594) (di:direct) BSUB0013 Z99116 g2634820 Bacillus subtilis 1423 -11528505 6500724647 zwf hypothetical protein:glucose-6-phosphate 1-dehydrogenase:g6pd (gtcfc:1.3:6.16:14.1) (ec:1.1.1.49) (keggfc:1.3:6.9) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjJ yqjJ Bacillus subtilis 1423 -11528505

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727680	155	22311	552	183

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727682	156	22312	273	90

Description

6500724648 ribokinase (gtcfc:1.3:1.4) (ec:2.7.1.15) (keggfc:1.3) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) rbsK rbsK Bacillus subtilis 1423 -11528506 7502851498 rbsk (ec:2.7.1.15) (de:ribokinase,) (db:swissprot) RBSK_BACSU P36945 BACILLUS SUBTILIS 1423 -11528506 7000694512 rbsk ribokinase (cl:ribokinase) (ec:2.7.1.15) (db:pir2.dat) D69690 D69690 Bacillus subtilis 1423 -11528506 307933 rbsk ribokinase (fn:ribose metabolism) (db:genpept-bct1) (ec:2.7.1.15) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:104360) (re:105241) (di:direct) BSUB0019 Z99122 g2636117 Bacillus subtilis 1423 -11528506 7500954065 rbsk ribokinase (db:genpept-bct1) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (nt:part of the ribose transport operon) (le:4777) (re:5658) (di:complement) BSZ92953 Z92953 g1894761 Bacillus subtilis 1423 -11528506

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727683	157	22313	216	71

Description

6500724649 deoxyribose-phosphate aldolase:phosphodeoxyriboaldolase:deoxyriboaldolase (gtcfc:1.3:4.4) (ec:4.1.2.4) (keggfc:1.3) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) dra dra Bacillus subtilis 1423 -11528507 68251 dra (ec:4.1.2.4) (de:(deoxyriboaldolase)) (db:swissprot) DEOC_BACSU P39121 BACILLUS SUBTILIS 1423 -11528507 7000685009 dra deoxyribose-phosphate aldolase (cl:deoxyribose-phosphate aldolase) (ec:4.1.2.4) (db:pir2.dat) A69619 A69619 Bacillus subtilis 1423 -11528507 222538 dra deoxyribose-phosphate aldolase (fn:nucleotide/deoxyribonucleotide catabolism) (db:genpept-bct1) (ec:4.1.2.4) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:51149) (re:51784) (di:complement) BSUB0021 Z99124 g2636488 Bacillus subtilis 1423 -11528507 7500880163 dra deoxyribose-phosphate aldolase (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:19692) (re:20327) (di:direct) D45912 D45912 g1408506 Bacillus subtilis 1423 -11528507

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727684	158	22314	258	85

Description

6500724650 gluconokinase:gluconate kinase (gtcfc:1.3:1.4) (ec:2.7.1.12) (keggfc:1.3) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) gntK gntK Bacillus subtilis 1423 -11528508 74248 gntk (ec:2.7.1.12) (de:gluconokinase, (gluconate kinase)) (db:swissprot) GNTK_BACSU P12011 BACILLUS SUBTILIS 1423 -11528508 7000685435 gntk gluconate kinase gntk (cl:xylulokinase) (db:pir2.dat) B26190 B26190 Bacillus subtilis 1423 -11528508 7500882618 gntk gluconate kinase (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (ec:2.7.1.12) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:homologs are found in e. coli and h. influenzae;) (le:2982) (re:4523) (di:complement) AB005554 AB005554 g563932 Bacillus subtilis 1423 -11528508 215718 gluconate kinase (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:b.subtilis (gluconate operon) gntr, gntk and gntp genes encodinggnt repressor, gluconate kinase and permease, and gntz gene.) (le:960) (re:2501) (di:direct) BACGNT J02584 g143015 Bacillus subtilis 1423 -11528508 215728 gntk gluconate kinase (fn:gluconate utilization) (db:genpept-bct1) (ec:2.7.1.12) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:114069) (re:115610) (di:direct) BSUB0021 Z99124 g2636553 Bacillus subtilis 1423 -11528508 170014 gntk gluconate kinase gntk (cl:xylulokinase) (db:pir) B26190 B26190 Bacillus subtilis 1423 -11528508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727701	159	22315	516	172

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727702	160	22316	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727705	161	22317	321	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727726	162	22318	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727738	163	22319	192	63

Description

6500724651 6-phosphogluconate dehydrogenase:6-phosphogluconate dehydrogenase:decarboxylating (gtcfc:1.3:1.4) (ec:1.1.1.44) (keggfc:1.3) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) gntZ gntZ Bacillus subtilis 1423 -11528509 7500876141 gntz (ec:1.1.1.44) (de:6-phosphogluconate dehydrogenase, decarboxylating,) (db:swissprot) 6PGD_BACSU P12013 BACILLUS SUBTILIS 1423 -11528509 7000684469 gntz phosphogluconate dehydrogenase decarboxylating:gntz:6-phosphogluconate dehydrogenase gntz (cl:phosphogluconate dehydrogenase (decarboxylating):3-hydroxyisobutyrate dehydrogenase homology) (ec:1.1.1.44) (db:pir2.dat) D26190 D26190 Bacillus subtilis 1423 -11528509 215726 gntz probable 6-phosphogluconate dehydrogenase (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (ec:1.1.1.44) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:conserved universally; see swiss_prot acc#:p12013) (le:178) (re:1584) (di:complement) AB005554 AB005554 g563930 Bacillus subtilis 1423 -11528509 215720 gntz (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:b.subtilis (gluconate operon) gntr, gntk and gntp genes encodinggnt repressor, gluconate kinase and permease, and gntz gene.) (nt:putative) (le:3899) (re:5305) (di:direct) BACGNT J02584 g600499 Bacillus subtilis 1423 -11528509 7502851499 gntz 6-phosphogluconate dehydrogenase (fn:gluconate utilization) (db:genpept-bct1) (ec:1.1.1.44) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:117008) (re:118414) (di:direct) BSUB0021 Z99124 g2636555 Bacillus subtilis 1423 -11528509 57626 gntz (ec:1.1.1.44) (de:6-phosphogluconate dehydrogenase, decarboxylating,) (db:swissprot) 6PGD_BACSU P12013 BACILLUS SUBTILIS 1423 -11528509 136290 gntz phosphogluconate dehydrogenase decarboxylating:gntz:6-phosphogluconate dehydrogenase gntz (cl:phosphogluconate dehydrogenase (decarboxylating):3-hydroxyisobutyrate dehydrogenase homology) (ec:1.1.1.44) (db:pir) D26190 D26190 Bacillus subtilis 1423 -11528509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727743	164	22320	699	232

Description

GTC ORF with score 261 to: (db:genpept-bct2) (de:myxococcus xanthus saframycin mx1 synthetase b (safb), saframycinmx1 synthetase a (safa), and safc genes, complete cds.) (nt:contains two putative amino acid activating) (le:5491) (re:13308) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727769	165	22321	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727772	166	22322	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727776	167	22323	480	159

Description

6500724652 hypothetical protein:similar to glucuronate isomerase (gtcfc:1.4:14.1) (ec:5.3.1.12) (keggfc:1.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmA yjmA Bacillus subtilis 1423 -11528510 7000693042 yjma glucuronate isomerase homolog yjma (db:pir2.dat) C69852 C69852 Bacillus subtilis 1423 -11528510 5500701564 yjma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to glucuronate isomerase) (le:105529) (re:106950) (di:direct) BSUB0007 Z99110 g2633584 Bacillus subtilis 1423 -11528510 7500964020 yjma hypothetical uronate isomerase (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:19689) (re:21110) (di:direct) AF015825 AF015825 g2612902 Bacillus subtilis 1423 -11528510

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727793	168	22324	645	215

Description

6500724653 hypothetical protein:similar to d-mannonate hydrolase (gtcfc:1.4:14.1) (ec:4.2.1.8) (keggfc:1.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmE yjmE Bacillus subtilis 1423 -11528511 7000692906 yjme d-mannonate hydrolase homolog yjme (db:pir2.dat) G69852 G69852 Bacillus subtilis 1423 -11528511 5500701568 yjme (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to d-mannonate hydrolase) (le:110565) (re:111644) (di:direct) BSUB0007 Z99110 g2633588 Bacillus subtilis 1423 -11528511 7500963927 yjme hypothetical d-mannonate hydratase (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:24725) (re:25804) (di:direct) AF015825 AF015825 g2612906 Bacillus subtilis 1423 -11528511

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727800	169	22325	504	168

Description

6500724654 hypothetical protein:similar to tagaturonate reductase (gtcfc:1.4:14.1) (ec:1.1.1.58) (keggfc:1.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmI yjmI Bacillus subtilis 1423 -11528512 7000694665 yjmi probable tagaturonate reductase::d-altronate:nad 3-oxidoreductase:tagaturonate dehydrogenase (cl:tagaturonate reductase) (ec:1.1.1.58) (db:pir2.dat) C69853 C69853 Bacillus subtilis 1423 -11528512 5500701572 yjmi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to tagaturonate reductase) (le:114959) (re:116401) (di:direct) BSUB0007 Z99110 g2633592 Bacillus subtilis 1423 -11528512 7500965248 yjmi hypothetical altronate oxidoreductase (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:member of the mannitol dehydrogenases family) (le:29119) (re:30561) (di:direct) AF015825 AF015825 g2612910 Bacillus subtilis 1423 -11528512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727846	170	22326	492	163

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727852	171	22327	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727885	172	22328	717	238

Description

6500724655 hypothetical protein:similar to altronate hydrolase (gtcfc:1.4:14.1) (ec:4.2.1.7) (keggfc:1.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmJ yjmJ Bacillus subtilis 1423 -11528513 7000692182 yjmj altronate hydrolase homolog yjmj (db:pir2.dat) D69853 D69853 Bacillus subtilis 1423 -11528513 5500701573 yjmj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to altronate hydrolase) (le:116398) (re:117891) (di:direct) BSUB0007 Z99110 g2633593 Bacillus subtilis 1423 -11528513 7500963396 yjmj hypothetical altronate dehydratase (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:30558) (re:32051) (di:direct) AF015825 AF015825 g2612911 Bacillus subtilis 1423 -11528513

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727896	173	22329	255	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727897	174	22330	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727912	175	22331	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727920	176	22332	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727935	177	22333	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727942	178	22334	642	213

Description

6500724656 xylose isomerase (gtcfc:1.4:1.5) (ec:5.3.1.5) (keggfc:1.4:1.5) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) xylA xylA Bacillus subtilis 1423 -11528514 7000694905 xyla xylose isomerase::xylose isomerase xyla:xylose ketol-isomerase (cl:xylose isomerase) (ec:5.3.1.5) (db:pir1.dat) ISBSXS C69735 Bacillus subtilis 1423 -11528514 220178 xyla xylose isomerase (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750124 Bacillus subtilis 1423 -11528514 7500954451 xyla xylose isomerase (fn:xylose metabolism) (db:genpept-bct1) (ec:5.3.1.5) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:109962) (re:111299) (di:direct) BSUB0010 Z99113 g2634144 Bacillus subtilis 1423 -11528514

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727977	179	22335	561	186

Description

GTC ORF with score 156 to: (sr:e.coli k12 dna) (db:genpept-bct1) (ec:2.7.1.15) (de:e.coli k12 rbsd, rbsa, rbsc, rbsb, rbsk, and rbsr genes encodingthe high affinity ribose transport system, complete cds.) (le:4128) (re:5057) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727994	180	22336	342	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501727996	181	22337	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728000	182	22338	213	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728019	183	22339	618	206

Description

6500724657 ynca:xylb xylulose kinase:xylulokinase (gtcfc:1.4) (ec:2.7.1.17) (keggfc:1.4) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) xylB xylB Bacillus subtilis 1423 -11528515 108211 xylb (ec:2.7.1.17) (de:xylulose kinase, (xylulokinase)) (db:swissprot) XYLB_BACSU P39211 BACILLUS SUBTILIS 1423 -11528515 7000687055 xylb xylulose kinase xylb (cl:xylulokinase) (db:pir2.dat) D69735 D69735 Bacillus subtilis 1423 -11528515 220179 xylb xylulose kinase (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750125 Bacillus subtilis 1423 -11528515 7500894486 xylb xylulose kinase (fn:xylose metabolism) (db:genpept-bct1) (ec:2.7.1.17) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: ynca) (le:111450) (re:112949) (di:direct) BSUB0010 Z99113 g2634145 Bacillus subtilis 1423 -11528515

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728037	184	22340	222	73

Description

6500724658 hypothetical protein:similar to utp-glucose-1-phosphate uridylyltransferase (gtcfc:1.4:1.6:4.3:7.2:14.1) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngB yngB Bacillus subtilis 1423 -11528516 7000694897 yngb utp-glucose-1-phosphate uridylyltransferas homolog yngb (cl:escherichia coli utp--glucose-1-phosphate uridylyltransferase) (db:pir2.dat) G69892 G69892 Bacillus subtilis 1423 -11528516 7500954163 yngb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to utp-glucose-1-phosphate) (le:164757) (re:165650) (di:direct) BSUB0010 Z99113 g2634201 Bacillus subtilis 1423 -11528516

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728038	185	22341	273	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728065	186	22342	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728070	187	22343	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728089	188	22344	183	60

Description

5000688417 deoxyphosphogluconate aldolase:4-hydroxy-2-oxoglutarate aldolase:2-keto-4-hydroxyglutarate aldolase:khg-aldolase / 2-dehydro-3-deoxyphosphogluconate aldolase:phospho-2-dehydro-3-deoxygluconate aldolase:phospho-2-keto-3-deoxygluconate aldolase:2-keto-3-deoxy-6-phosphogluconate aldolase:kdpg-aldolase (gtcfc:1.4:1.9:5.10) (keggfc:1.4:1.9:5.10) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) kdgA kdgA Bacillus subtilis 1423 -11528517 59189 kdga (ec:4.1.3.16:4.1.2.14) (de:(2-keto-3-deoxy-6-phosphogluconate aldolase) (kdpg-aldolase)) (db:swissprot) ALKH_BACSU P50846 BACILLUS SUBTILIS 1423 -11528517 7000684558 kdga deoxyphosphogluconate aldolase kdga (cl:2-dehydro-3-deoxyphosphogluconate aldolase) (db:pir2.dat) H69647 H69647 Bacillus subtilis 1423 -11528517 216509 kdga 2-keto-3-deoxy-6-phosphogluconate aldolase (fn:pectin utilization) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:36... BACPONAYPP L47838 g1146190 Bacillus subtilis 1423 -11528517 7500876759 kdga deoxyphosphogluconate aldolase (fn:pectin utilization) (db:genpept-bct1) (ec:4.1.2.14) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:126711) (re:127301) (di:complement) BSUB0012 Z99115 g2634629 Bacillus subtilis 1423 -11528517 6500724659 deoxyphosphogluconate aldolase:4-hydroxy-2-oxoglutarate aldolase:2-keto-4-hydroxyglutarate aldolase:khg-aldolase / 2-dehydro-3-deoxyphosphogluconate aldolase:phospho-2-dehydro-3-deoxygluconate aldolase:phospho-2-keto-3-deoxygluconate aldolase:2-keto-3-deoxy-6-phosphogluconate aldolase:kdpg-aldolase (gtcfc:1.4:1.9:5.10) (keggfc:1.4:1.9:5.10) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) kdgA kdgA Bacillus subtilis 1423 -11528517

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728090	189	22345	285	94

Description

6500724660 l-ribulose-5-phosphate 4-epimerase (gtcfc:1.4) (ec:5.1.3.4) (keggfc:1.4) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) araD araD Bacillus subtilis 1423 -11528518 4000707575 arad (ec:5.1.3.4) (de:l-ribulose-5-phosphate 4-epimerase,) (db:swissprot) ARAD_BACSU P94525 BACILLUS SUBTILIS 1423 -11528518 7000684601 arad l-ribulose-phosphate 4-epimerase (cl:l-ribulose-phosphate 4-epimerase) (ec:5.1.3.4) (db:pir2.dat) E69587 E69587 Bacillus subtilis 1423 -11528518 220292 arad l-ribulose-5-phosphate 4-epimerase (fn:l-arabinose utilization) (db:genpept-bct1) (ec:5.1.3.4) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:148955) (re:149644) (di:complement) BSUB0015 Z99118 g2635343 Bacillus subtilis 1423 -11528518 304165 arad l-ribulose-5-phosphate-4-epimerase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to arad of escherichia coli;identified on) (le:20263) (re:20952) (di:direct) BSZ75208 Z75208 g1770016 Bacillus subtilis 1423 -11528518

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728100	190	22346	873	291

Description

6500724661 l-ribulokinase (gtcfc:1.4) (ec:2.7.1.16) (keggfc:1.4) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) araB araB Bacillus subtilis 1423 -11528519 4000708983 arab (ec:2.7.1.16) (de:l-ribulokinase,) (db:swissprot) ARAB_BACSU P94524 BACILLUS SUBTILIS 1423 -11528519 7000684600 arab l-ribulokinase arab (db:pir2.dat) D69587 D69587 Bacillus subtilis 1423 -11528519 220291 arab l-ribulokinase (fn:l-arabinose utilization) (db:genpept-bct1) (ec:2.7.1.16) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:149661) (re:151343) (di:complement) BSUB0015 Z99118 g2635344 Bacillus subtilis 1423 -11528519 304164 arab l-ribulokinase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to arab of escherichia coli;identified on) (le:18564) (re:20246) (di:direct) BSZ75208 Z75208 g1770015 Bacillus subtilis 1423 -11528519

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728102	191	22347	570	190

Description

6500724662 l-arabinose isomerase (gtcfc:1.4) (ec:5.3.1.4) (keggfc:1.4) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) araA araA Bacillus subtilis 1423 -11528520 4000708982 araa (ec:5.3.1.4) (de:l-arabinose isomerase,) (db:swissprot) ARAA_BACSU P94523 BACILLUS SUBTILIS 1423 -11528520 7000684599 araa l-arabinose isomerase (cl:l-arabinose isomerase) (ec:5.3.1.4) (db:pir2.dat) C69587 C69587 Bacillus subtilis 1423 -11528520 220290 araa l-arabinose isomerase (fn:l-arabinose utilization) (db:genpept-bct1) (ec:5.3.1.4) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:151357) (re:152853) (di:complement) BSUB0015 Z99118 g2635345 Bacillus subtilis 1423 -11528520 304163 araa l-arabinose isomerase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to araa of escherichia coli; identified on) (le:17054) (re:18550) (di:direct) BSZ75208 Z75208 g1770014 Bacillus subtilis 1423 -11528520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728117	192	22348	201	67

Description

5000688521 yzwa:ytda hypothetical protein:putative utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate uridylyltransferase:uridine diphosphoglucose pyrophosphorylase (gtcfc:1.4:1.6:4.3:7.2:14.1) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytdA ytdA Bacillus subtilis 1423 -11528521 117030 ytda (ec:2.7.7.9) (de:uridylyltransferase) (uridine diphosphoglucose pyrophosphorylase)) (db:swissprot) YTDA_BACSU P42407 BACILLUS SUBTILIS 1423 -11528521 7000688612 ytda utp-glucose-1-phosphate uridylyltransferas homolog ytda (cl:escherichia coli utp--glucose-1-phosphate uridylyltransferase) (db:pir2.dat) A69990 A69990 Bacillus subtilis 1423 -11528521 219862 ytda ytda (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to utp-glucose-1-p uridylyltransferase of) (le:23566) (re:24384) (di:direct) AF008220 AF008220 g2293144 Bacillus subtilis 1423 -11528521 4000707480 (db:genpept-bct1) (de:bacillus subtilis gtab homolog (orfx) and orfq genes, complete cds.) (nt:orfx, similar to bacillus subtilis udp-glucose) (le:167) (re:985) (di:direct) BSU20447 U20447 g669000 Bacillus subtilis 1423 -11528521 7500952750 ytda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: yzwa; similar to) (le:156043) (re:156861) (di:complement) BSUB0016 Z99119 g2635569 Bacillus subtilis 1423 -11528521 6500724663 yzwa hypothetical protein:putative utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate uridylyltransferase:uridine diphosphoglucose pyrophosphorylase (gtcfc:1.4:1.6:4.3:7.2:14.1) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytdA ytdA Bacillus subtilis 1423 -11528521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728119	193	22349	225	74

Description

6500724664 utp-glucose-1-phosphate uridylyltransferase:utp--glucose-1-phosphate uridylyltransferase:udp-glucose pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate uridylyltransferase:uridine diphosphoglucose pyrophosphorylase (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (bsorffc:3.3.1) (db:gtc-bacillus subtilis) gtaB gtaB Bacillus subtilis 1423 -11528522 219382 gtab (ec:2.7.7.9) (de:(general stress protein 33) (gsp33)) (db:swissprot) GTAB_BACSU Q05852 BACILLUS SUBTILIS 1423 -11528522 139266 gtab utp--glucose-1-phosphate uridylyltransferase::udp-glucose pyrophosphorylase (cl:escherichia coli utp--glucose-1-phosphate uridylyltransferase) (ec:2.7.7.9) (db:pir1.dat) A40650 A40650 Bacillus subtilis 1423 -11528522 215814 gtab udp-glucose pyrophosphorylase (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (ec:2.7.7.9) (de:bacillus subtilis udp-glucose pyrophosphorylase (gtab) gene,complete cds.) (nt:similar to udp-glucose pyrophosphorylase of) (le:120) (re:998) (di:direct) BACGTABX L12272 g289287 Bacillus subtilis 1423 -11528522 5000688515 gtab udp-glucose pyrophosphorylase (db:genpept-bct1) (ec:2.7.7.9) (de:b.subtilis lytr, orfx, and gtab genes.) (nt:similar to other procaryotic udp-glucose) (le:1581) (re:2459) (di:direct) BSLYTGTA Z22516 g405623 Bacillus subtilis 1423 -11528522 7500882821 gtab utp-glucose-1-phosphate uridylyltransferase (fn:glucosylation of teichoic acid) (db:genpept-bct1) (ec:2.7.7.9) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:67599) (re:68477) (di:direct) BSUB0019 Z99122 g2636093 Bacillus subtilis 1423 -11528522 74819 gtab (ec:2.7.7.9) (de:(general stress protein 33) (gsp33)) (db:swissprot) GTAB_BACSU Q05852 BACILLUS SUBTILIS 1423 -11528522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728127	194	22350	555	185

Description

6500724665 ybed:glpq glycerophosphoryl diester phosphodiesterase:glycerophosphodiester phosphodiesterase (gtcfc:1.4:8.1:8.4) (ec:3.1.4.46) (keggfc:8.1:8.4) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) glpQ glpQ Bacillus subtilis 1423 -11528523 7500882513 glpq (ec:3.1.4.46) (de:(glycerophosphodiester phosphodiesterase)) (db:swissprot) GLPQ_BACSU P37965 BACILLUS SUBTILIS 1423 -11528523 7000685419 glpq glycerophosphoryl diester phosphodiesterase glpq (db:pir2.dat) I40418 I40418 Bacillus subtilis 1423 -11528523 219338 glpq glycerophosphoryl diester phosphodiesterase (fn:hydrolysis of deacylated phospholipids) (db:genpept-bct1) (de:b.subtilis glpt and glpq genes for glycerol 3-phosphate permeaseand glycerophosphoryl diester phosphodiesterase.) (le:1748) (re:2629) (di:direct) BSGLPTQ Z26522 g403373 Bacillus subtilis 1423 -11528523 7500882514 glpq glycerophosphoryl diester phosphodiesterase (fn:hydrolysis of deacylated phospholipids) (db:genpept-bct1) (ec:3.1.4.46) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ybed) (le:38353) (re:39234) (di:complement) BSUB0002 Z99105 g2632499 Bacillus subtilis 1423 -11528523 7502851500 ybed (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:36004) (re:36885) (di:complement) AB006424 AB006424 g3599635 Bacillus subtilis 1423 -11528523 74045 glpq (ec:3.1.4.46) (de:(glycerophosphodiester phosphodiesterase)) (db:swissprot) GLPQ_BACSU P37965 BACILLUS SUBTILIS 1423 -11528523 170023 glpq glycerophosphoryl diester phosphodiesterase glpq (db:pir) I40418 I40418 Bacillus subtilis 1423 -11528523

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728159	195	22351	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728165	196	22352	228	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728191	197	22353	189	62

Description

6500724666 amya:amye alpha-amylase:alpha-amylase precursor:1:4-alpha-d-glucan glucanohydrolase (gtcfc:1.4:7.2) (ec:3.2.1.1) (keggfc:7.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) amyE amyE Bacillus subtilis 1423 -11528524 219002 amye:amya (ec:3.2.1.1) (de:glucanohydrolase)) (db:swissprot) AMY_BACSU P00691 BACILLUS SUBTILIS 1423 -11528524 124481 amye alpha-amylase:amye m-type precursor:1:4-alpha-d-glucan glucanohydrolase (cl:alpha-amylase, subtilis type:alpha-amylase core homology) (ec:3.2.1.1) (db:pir1.dat) ALBS A00842 Bacillus subtilis 1423 -11528524 215181 (sr:b.subtilis dna, clones pmy100 and lambda g40 (1); clon) (db:genpept-bct1) (de:b.subtilis amylase gene, complete cds.) (nt:amylase precursor (ec.3.2.1.1)) (le:498) (re:2480) (di:direct) BACAMYLY J01547 g142507 Bacillus subtilis 1423 -11528524 5000688507 amye alpha-amylase precursor (db:genpept-bct1) (de:bacillus subtilis amylase gene, a starch degrading enzyme. (ec2.2.1.1).) (le:498) (re:2480) (di:direct) BSAMYL V00101 g39794 Bacillus subtilis 1423 -11528524 222570 amye alpha-amylase (db:genpept-bct1) (ec:3.2.1.1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: amya) (le:132521) (re:134503) (di:direct) BSUB0002 Z99105 g2632590 Bacillus subtilis 1423 -11528524 7500876904 amye alpha-amylase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:6823) (re:8805) (di:direct) D50453 D50453 g1805376 Bacillus subtilis 1423 -11528524 59504 amye:amya (ec:3.2.1.1) (de:glucanohydrolase)) (db:swissprot) AMY_BACSU P00691 BACILLUS SUBTILIS 1423 -11528524

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728200	198	22354	882	293

Description

6500724667 sorbitol dehydrogenase:l-iditol 2-dehydrogenase (gtcfc:1.4:1.5) (ec:1.1.1.14) (keggfc:1.5) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) gutB gutB Bacillus subtilis 1423 -11528525 7000689016 gutb l-iditol 2-dehydrogenase::glucitol dehydrogenase:polyol dehydrogenase:sorbitol dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.14) (db:pir1.dat) A45052 A45052 Bacillus subtilis 1423 -11528525 7500953160 gutb sorbitol dehydrogenase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (ec:1.1.1.14) (de:bacillus subtilis sorbitol dehydrogenase (gutb) gene, complete cds.) (le:87) (re:1148) (di:direct) BACGUTB M96947 g304153 Bacillus subtilis 1423 -11528525 215819 gutb sorbitol dehydrogenase (db:genpept-bct1) (ec:1.1.1.14) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:66483) (re:67544) (di:direct) BSUB0004 Z99107 g2632928 Bacillus subtilis 1423 -11528525 135985 gutb l-iditol 2-dehydrogenase::glucitol dehydrogenase:polyol dehydrogenase:sorbitol dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.14) (db:pir) A45052 A45052 Bacillus subtilis 1423 -11528525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728214	199	22355	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728215	200	22356	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728219	201	22357	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728236	202	22358	456	152

Description

GTC ORF with score 167 to: (fn:chloroquine resistance gene candidate) (sr:malaria parasite) (db:genpept-inv) (de:plasmodium falciparum strain hb3 cg2 (cg2) gene, complete cds.) (nt:detected by monoclonal antibody) (le:37) (re:8496) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728238	203	22359	573	191

Description

6500724668 pectate lyase:pectate lyase precursor:pl (gtcfc:1.4) (ec:4.2.2.2) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) pel pel Bacillus subtilis 1423 -11528526 216447 pel (ec:4.2.2.2) (de:pectate lyase precursor, (pl)) (db:swissprot) PEL_BACSU P39116 BACILLUS SUBTILIS 1423 -11528526 7000686110 pelk pectate lyase:precursor (cl:pectate lyase) (ec:4.2.2.2) (db:pir2.dat) JC2249 JC2249 Bacillus sp. 1409 -11528526 141945 pel pectate lyase:pel precursor (cl:pectate lyase) (ec:4.2.2.2) (db:pir2.dat) S39459 S39459 Bacillus subtilis 1423 -11528526 7500887792 pelk pectate lyase (sr:bacillus sp. (strain:ya-14) dna) (db:genpept-bct1) (de:bacillus sp. pelk gene for pectate lyase, complete cds.) (le:210) (re:1472) (di:direct) BACPELK D26349 g450461 Bacillus sp. 1409 -11528526 5000688481 pel pectate lyase (db:genpept-bct1) (ec:4.2.2.2) (de:b.subtilis pel gene for pectate lyase.) (le:205) (re:1467) (di:direct) BSDNAPEL X74880 g439245 Bacillus subtilis 1423 -11528526 219170 pel pectate lyase (db:genpept-bct1) (ec:4.2.2.2) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:24681) (re:25943) (di:direct) BSUB0005 Z99108 g2633080 Bacillus subtilis 1423 -11528526 5500684674 pel (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:22578) (re:23840) (di:complement) D86417 D86417 g2443242 Bacillus subtilis 1423 -11528526 88959 pel (ec:4.2.2.2) (de:pectate lyase precursor, (pl)) (db:swissprot) PEL_BACSU P39116 BACILLUS SUBTILIS 1423 -11528526 141944 pelk pectate lyase (cl:pectate lyase) (ec:4.2.2.2) (db:pir) JC2249 JC2249 Bacillus sp. 1409 -11528526

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728239	204	22360	411	136

Description

6500724669 trec:trea trehalose-6-phosphate hydrolase (gtcfc:1.4:7.2) (ec:3.2.1.93) (keggfc:7.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) treA treA Bacillus subtilis 1423 -11528527 7000694828 trea alpha:alpha-phosphotrehalase:trea:phospho alpha 1-1 glucosidase trea:phosphotrehalase:trehalose-6-phosphate hydrolase trea (cl:alpha-glucosidase:alpha-amylase core homology) (ec:3.2.1.93) (db:pir2.dat) B69725 B69725 Bacillus subtilis 1423 -11528527 6000690328 trea trehalose-6-phosphate hydrolase (db:genpept-bct1) (ec:3.2.1.93) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: trec) (le:48537) (re:50222) (di:direct) BSUB0005 Z99108 g2633105 Bacillus subtilis 1423 -11528527 7500965381 trec (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:17699) (re:19384) (di:complement) D83967 D83967 g2626830 Bacillus subtilis 1423 -11528527

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728240	205	22361	528	176

Description

5000689434 glvg:glv-1:glva 6-phospho-alpha-glucosidase:probable 6-phospho-beta-glucosidase (gtcfc:1.4) (ec:3.2.1.86) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) glvA glvA Bacillus subtilis 1423 -11528528 74187 glvg:glva:glv-1 (ec:3.2.1.122) (de:glucosidase)) (db:swissprot) GLVG_BACSU P54716 BACILLUS SUBTILIS 1423 -11528528 7000685430 glva 6-phospho-alpha-glucosidase glva (db:pir2.dat) F69635 F69635 Bacillus subtilis 1423 -11528528 222681 glva 6-phospho-alpha-glucosidase (fn:arbutin fermentation) (db:genpept-bct1) (ec:3.2.1.86) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: glvg) (le:86708) (re:88057) (di:direct) BSUB0005 Z99108 g2633142 Bacillus subtilis 1423 -11528528 7500882585 glv-1 unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:384) (re:1733) (di:direct) D50543 D50543 g1486241 Bacillus subtilis 1423 -11528528 6500724670 glvg:glv-1 6-phospho-alpha-glucosidase:probable 6-phospho-beta-glucosidase (gtcfc:1.4) (ec:3.2.1.86) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) glvA glvA Bacillus subtilis 1423 -11528528

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728268	206	22362	486	162

Description

6500724671 glycerol kinase:atp:glycerol 3-phosphotransferase:glycerokinase:gk (gtcfc:1.4:8.1) (ec:2.7.1.30) (keggfc:8.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) glpK glpK Bacillus subtilis 1423 -11528529 74036 glpk (ec:2.7.1.30) (de:(glycerokinase) (gk)) (db:swissprot) GLPK_BACSU P18157 BACILLUS SUBTILIS 1423 -11528529 7000685417 glpk glycerol kinase:glpk (cl:xylulokinase) (ec:2.7.1.30) (db:pir2.dat) (mp:75 (degrees)) B45868 B45868 Bacillus subtilis 1423 -11528529 7500882501 (sr:b.subtilis (strain w168) dna) (db:genpept-bct1) (de:b.subtilis glycerol kinase (glpk) and glycerol-3-phosphatedehydrogenase (glpd) genes, complete cds.) (nt:glycerol kinase (glpk) (ec 2.7.1.30)) (le:698) (re:2188) (di:direct) BACGLPKD M34393 g142992 Bacillus subtilis 1423 -11528529 215683 glpk glycerol kinase (fn:glycerol utilization) (db:genpept-bct1) (ec:2.7.1.30) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:200029) (re:201519) (di:direct) BSUB0005 Z99108 g2633252 Bacillus subtilis 1423 -11528529 4000707100 glpk glycerol kinase (fn:glycerol utilization) (db:genpept-bct1) (ec:2.7.1.30) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:3349) (re:4839) (di:direct) BSUB0006 Z99109 g2633264 Bacillus subtilis 1423 -11528529 6000684761 glpk glycerol kinase (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:see embl m34393 and swiss prot p18157.) (le:2997) (re:4487) (di:direct) BSY14079 Y14079 g2226137 Bacillus subtilis 1423 -11528529 138462 glpk glycerol kinase:glpk (cl:xylulokinase) (ec:2.7.1.30) (db:pir) (mp:75 (degrees)) B45868 B45868 Bacillus subtilis 1423 -11528529

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728276	207	22363	462	154

Description

5000689139 hypothetical protein:phage-like element pbsx protein xtra (gtcfc:1.4:14.1) (keggfc:14.2) (bsorffc:2.1.1:8.1.1) (db:gtc-bacillus subtilis) xtrA xtrA Bacillus subtilis 1423 -11528530 108166 xtra (de:phage-like element pbsx protein xtra) (db:swissprot) XTRA_BACSU P54344 BACILLUS SUBTILIS 1423 -11528530 7000687053 xtra pbsx prophage orf xtra (cl:hypothetical protein yqao) (db:pir2.dat) B69735 B69735 Bacillus subtilis 1423 -11528530 219482 xtra (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqao of the skin element) (le:3277) (re:3483) (di:direct) BSPBSXSE Z70177 g1225940 Bacillus subtilis 1423 -11528530 7500894482 xtra (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:129226) (re:129432) (di:direct) BSUB0007 Z99110 g2633609 Bacillus subtilis 1423 -11528530 6500724672 hypothetical protein:phage-like element pbsx protein xtra (gtcfc:1.4:14.1) (keggfc:14.2) (bsorffc:2.1.1:8.1.1) (db:gtc-bacillus subtilis) xtrA xtrA Bacillus subtilis 1423 -11528530

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728320	208	22364	303	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728339	209	22365	450	150

Description

6500724673 histidine-containing phosphocarrier protein of the phosphotransferase system:pts:hpr protein:phosphocarrier protein hpr:histidine-containing protein (gtcfc:1.4:12.1) (keggfc:14.2) (bsorffc:1.1.1:2.1.1) (db:gtc-bacillus subtilis) ptsH ptsH Bacillus subtilis 1423 -11528531 130684 ptsh phosphotransferase system phosphohistidine-containing protein:phosphocarrier protein hpr:ptsh (cl:phosphotransferase system phosphohistidine-containing protein:phosphotransferase system phosphohistidine-containing protein homology) (db:pir1.dat) WQBSPH S04177 Bacillus subtilis 1423 -11528531 219560 ptsh hpr protein (db:genpept-bct1) (de:bacillus subtilis ptsx, ptsh and ptsi genes for enzyme iii-glucose(ec 2.7.1.69), hpr protein and enzyme i (ec 2.7.3.9) of pep:sugarphosphtransferase system.) (le:1118) (re:1384) (di:direct) BSPTSXHI X12832 g48682 Bacillus subtilis 1423 -11528531 7500953600 ptsh histidine-containing phosphocarrier protein of (fn:transfers phosphate from enzyme i to specific) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:64061) (re:64327) (di:direct) BSUB0008 Z99111 g2633761 Bacillus subtilis 1423 -11528531

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728352	210	22366	384	127

Description

6500724674 lysine decarboxylase:ldc (gtcfc:1.4:5.9) (ec:4.1.1.18) (keggfc:5.9) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) cad cad Bacillus subtilis 1423 -11528532 7500880055 cad (ec:4.1.1.18) (de:lysine decarboxylase, (ldc)) (db:swissprot) DCLY_BACSU P21885 BACILLUS SUBTILIS 1423 -11528532 7000684989 cad lysine decarboxylase:cad (cl:lysine decarboxylase cad) (ec:4.1.1.18) (db:pir2.dat) A54546 A54546 Bacillus subtilis 1423 -11528532 220086 cad lysine decarboxylase (db:genpept-bct1) (ec:4.1.1.18) (de:bacillus subtilis moba-npre gene region.) (nt:similar to lysine decarboxylase encoded by genbank) (le:39382) (re:40854) (di:complement) AF012285 AF012285 g3282147 Bacillus subtilis 1423 -11528532 219046 cad lysine decarboxylase (db:genpept-bct1) (ec:4.1.1.18) (de:b.subtillis cad gene for lysine decarboxylase.) (nt:ttg initiation codon) (le:312) (re:1784) (di:direct) BSCADDNA X58433 g580835 Bacillus subtilis 1423 -11528532 7502851501 cad lysine decarboxylase (fn:cadaverine synthesis) (db:genpept-bct1) (ec:4.1.1.18) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:138894) (re:140366) (di:complement) BSUB0008 Z99111 g2633834 Bacillus subtilis 1423 -11528532 68019 cad (ec:4.1.1.18) (de:lysine decarboxylase, (ldc)) (db:swissprot) DCLY_BACSU P21885 BACILLUS SUBTILIS 1423 -11528532 170323 cad lysine decarboxylase:cad (ec:4.1.1.18) (db:pir) A54546 A54546 Bacillus subtilis 1423 -11528532

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728353	211	22367	252	83

Description

6500724675 ynak:xynb xylan beta-1:4-xylosidase (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) xynB xynB Bacillus subtilis 1423 -11528533 7000694904 xynb xylan 1:4-beta-xylosidase:xynb (ec:3.2.1.37) (db:pir2.dat) G69735 G69735 Bacillus subtilis 1423 -11528533 220176 xynb xylan beta-1:4-xylosidase (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750122 Bacillus subtilis 1423 -11528533 7500965437 xynb xylan beta-1:4-xylosidase (fn:xylan degradation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: ynak) (le:106828) (re:108429) (di:direct) BSUB0010 Z99113 g2634142 Bacillus subtilis 1423 -11528533

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728356	212	22368	465	155

Description

6500724676 egls:bglc endo-1:4-beta-glucanase (gtcfc:1.4:7.2) (ec:3.2.1.4) (keggfc:7.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) bglC bglC Bacillus subtilis 1423 -11528534 7000692958 bglc cellulase:bglc precursor:endo-1:4-beta-glucanase (ec:3.2.1.4) (db:pir2.dat) G69593 G69593 Bacillus subtilis 1423 -11528534 7500963965 egls endo-1:4-beta glucanase (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:22274) (re:23800) (di:direct) BC170DEGR Z73234 g1405465 Bacillus subtilis 1423 -11528534 217896 bglc endo-1:4-beta-glucanase (fn:cellulose degradation) (db:genpept-bct1) (ec:3.2.1.4) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: egls) (le:158653) (re:160179) (di:direct) BSUB0010 Z99113 g2634196 Bacillus subtilis 1423 -11528534

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728379	213	22369	333	110

Description

6500724677 endo-1:4-beta-xylanase:xylanase d (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) xynD xynD Bacillus subtilis 1423 -11528535 7000692963 xynd endo-1:4-beta-xylanase xynd (cl:clostridium xylanase a repeat homology) (db:pir2.dat) H69735 H69735 Bacillus subtilis 1423 -11528535 7500963969 xynd endo-1:4-beta-xylanase xylanase d (fn:xylan degradation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:162168) (re:163709) (di:complement) BSUB0010 Z99113 g2634199 Bacillus subtilis 1423 -11528535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728401	214	22370	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728410	215	22371	519	172

Description

6500724678 endo-1:4-beta-xylanase:endo-1:4-beta-xylanase a precursor:xylanase a:1:4-beta-d-xylan xylanohydrolase a (gtcfc:1.4) (ec:3.2.1.8) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) xynA xynA Bacillus subtilis 1423 -11528536 108271 xyna (ec:3.2.1.8) (de:(1,4-beta-d-xylan xylanohydrolase a)) (db:swissprot) XYNA_BACSU P18429 BACILLUS SUBTILIS 1423 -11528536 7000687057 xyna endo-1:4-beta-xylanase:a precursor:xylanase a (cl:endo-1,4-beta-xylanase:endo-1,4-beta-xylanase homology) (ec:3.2.1.8) (db:pir1.dat) (mp:175 degrees) I40569 I40569 Bacillus subtilis 1423 -11528536 217071 xyna xylanase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (le:34592) (re:35233) (di:complement) AF027868 AF027868 g2619034 Bacillus subtilis 1423 -11528536 5500684797 (sr:b.subtilis pap115 dna) (db:genpept-bct1) (de:b.subtilis xylanase gene, complete cds.) (nt:xylanase (ec 3.2.1.8)) (le:118) (re:759) (di:direct) BACXYNAB M36648 g143843 Bacillus subtilis 1423 -11528536 7500894502 xyna endo-1:4-beta-xylanase (fn:xylan degradation) (db:genpept-bct1) (ec:3.2.1.8) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:53683) (re:54324) (di:complement) BSUB0011 Z99114 g2634277 Bacillus subtilis 1423 -11528536 5000688485 (de:(xyna) (pn:endo-1,4-beta-xylanase a precursor:xylanase a:1,4-beta-d-xylan xylanohydrolase a:endo-1,4-beta-xylanase a precursor :xylanase a:1,4- beta-d-xylan xylanohydrolase a) (gtcfc:7.01) (ec:3.2.1.8) (xyna_bacsu) (keggfc:1) xynA xynA Bacillus subtilis 1423 10050003

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728425	216	22372	408	135

Description

GTC ORF with score 124 to: (sr:bodo saltans) (db:genpept-inv) (de:bodo saltans nadh dehydrogenase subunit 5 (nd5) mrna, kinetoplastgene encoding kinetoplast protein, partial cds.) (nt:partially edited mrna) (le:<1) (re:639) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728429	217	22373	498	165

Description

5000689091 2-keto-3-deoxygluconate permease:kdg permease (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) kdgT kdgT Bacillus subtilis 1423 -11528537 80589 kdgt (de:2-keto-3-deoxygluconate permease (kdg permease)) (db:swissprot) KDGT_BACSU P50847 BACILLUS SUBTILIS 1423 -11528537 7000685673 kdgt 2-keto-3-deoxygluconate permease kdgt (db:pir2.dat) C69648 C69648 Bacillus subtilis 1423 -11528537 216510 kdgt 2-keto-3-deoxygluconate permease (fn:pectin utilization) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:51... BACPONAYPP L47838 g1146191 Bacillus subtilis 1423 -11528537 7500884556 kdgt 2-keto-3-deoxygluconate permease (fn:pectin utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:125674) (re:126666) (di:complement) BSUB0012 Z99115 g2634628 Bacillus subtilis 1423 -11528537 6500724679 2-keto-3-deoxygluconate permease:kdg permease (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) kdgT kdgT Bacillus subtilis 1423 -11528537

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728430	218	22374	489	162

Description

6500724680 5-keto-4-deoxyuronate isomerase:4-deoxy-l-threo-5-hexosulose-uronate ketol-isomerase:5-keto-4-deoxyuronate isomerase:dki isomerase (gtcfc:1.4) (ec:5.3.1.17) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) kduI kduI Bacillus subtilis 1423 -11528538 80608 kdui (ec:5.3.1.17) (de:(5-keto-4-deoxyuronate isomerase) (dki isomerase)) (db:swissprot) KDUI_BACSU P50843 BACILLUS SUBTILIS 1423 -11528538 7000685678 kdui 5-keto-4-deoxyuronate isomerase kdui (cl:erwinia chrysanthemi kdui protein) (db:pir2.dat) E69648 E69648 Bacillus subtilis 1423 -11528538 216506 kdui 5-keto-4-deoxyuronate isomerase (fn:pectin utilization) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:49... BACPONAYPP L47838 g1146187 Bacillus subtilis 1423 -11528538 7500884581 kdui 5-keto-4-deoxyuronate isomerase (fn:pectin utilization) (db:genpept-bct1) (ec:5.3.1.17) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:129556) (re:130383) (di:direct) BSUB0012 Z99115 g2634632 Bacillus subtilis 1423 -11528538 5000689437 (de:(kdui) (pn:4-deoxy-l-threo-5-hexosulose-uronate ketol-isomerase:5-keto-4-deoxyuronate isomerase:dki isomerase) (gtcfc:13.07) (ec:5.3.1.17) (kdui_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) kduI kduI Bacillus subtilis 1423 10022850

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728447	219	22375	654	217

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728448	220	22376	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728453	221	22377	612	203

Description

6500724681 2-keto-3-deoxygluconate oxidoreductase:2-deoxy-d-gluconate 3-dehydrogenase:2-keto-3-deoxygluconate oxydoreductase (gtcfc:1.4) (ec:1.1.1.125) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) kduD kduD Bacillus subtilis 1423 -11528539 80605 kdud (ec:1.1.1.125) (de:deoxygluconate oxidoreductase)) (db:swissprot) KDUD_BACSU P50842 BACILLUS SUBTILIS 1423 -11528539 7000685676 kdud 2-keto-3-deoxygluconate oxidoreductase kdud (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D69648 D69648 Bacillus subtilis 1423 -11528539 216505 kdud 2-keto-3-deoxygluconate oxidoreductase (fn:pectin utilizationn) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:5... BACPONAYPP L47838 g1146186 Bacillus subtilis 1423 -11528539 7500884579 kdud 2-keto-3-deoxygluconate oxidoreductase (fn:pectin utilization) (db:genpept-bct1) (ec:1.1.1.125) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:130385) (re:131149) (di:direct) BSUB0012 Z99115 g2634633 Bacillus subtilis 1423 -11528539 5000689436 (de:(kdud) (pn:2-deoxy-d-gluconate 3-dehydrogenase:2-keto-3-deoxygluconate oxydoreductase) (gtcfc:13.07) (ec:1.1.1.125) (kdud_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) kduD kduD Bacillus subtilis 1423 10022847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728481	222	22378	318	106

Description

5000689317 yqgr:glck glucose kinase:hypothetical 33.5 kd protein in soda-comga intergenic region (gtcfc:1.4) (ec:2.7.1.2) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) glcK glcK Bacillus subtilis 1423 -11528540 115914 glck (ec:2.7.1.2) (de:glucokinase, (glucose kinase)) (db:swissprot) GLK_BACSU P54495 BACILLUS SUBTILIS 1423 -11528540 7000688409 glck glucose kinase glck (cl:glucose kinase:glucose kinase homology) (db:pir2.dat) B69632 B69632 Bacillus subtilis 1423 -11528540 216109 yqgr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:148034) (re:148999) (di:direct) BACJH642 D84432 g1303865 Bacillus subtilis 1423 -11528540 7500882437 glck glucose kinase (db:genpept-bct1) (ec:2.7.1.2) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqgr) (le:174622) (re:175587) (di:complement) BSUB0013 Z99116 g2634919 Bacillus subtilis 1423 -11528540 6500724682 yqgr glucose kinase:hypothetical 33.5 kd protein in soda-comga intergenic region (gtcfc:1.4) (ec:2.7.1.2) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) glcK glcK Bacillus subtilis 1423 -11528540

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728483	223	22379	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728521	224	22380	753	251

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728523	225	22381	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728525	226	22382	204	68

Description

6500724683 sacl:sacc levanase:levanase precursor:2:6-beta-d-fructan fructanohydrolase (gtcfc:1.4) (ec:3.2.1.65) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) sacC sacC Bacillus subtilis 1423 -11528541 97840 sacc (ec:3.2.1.65) (de:fructanohydrolase)) (db:swissprot) SACC_BACSU P05656 BACILLUS SUBTILIS 1423 -11528541 1500685537 sacc levanase precursor (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:8237) (re:10270) (di:direct) BS233DEG X92868 g2108266 Bacillus subtilis 1423 -11528541 7500891278 sacc levanase (fn:levanase operon) (db:genpept-bct1) (ec:3.2.1.65) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: sacl) (le:157861) (re:159894) (di:complement) BSUB0014 Z99117 g2635149 Bacillus subtilis 1423 -11528541 7000686547 sacc levanase sacc (db:pir) A69703 A69703 Bacillus subtilis 1423 -11528541 5000688484 (de:(sacc) (pn:levanase precursor:levanase precursor :2,6-beta-d-fructan fructanohydrolase) (gtcfc:7.01) (ec:3.2.1.65) (sacc_bacsu) (keggfc:11.1) (bsorffc:2.1.0) (db:gtc-bacillus subtilis)) sacC sacC Bacillus subtilis 1423 10039720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728530	227	22383	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728553	228	22384	390	129

Description

GTC ORF with score 155 to: (sr:soybean) (db:genpept-pln2) (ec:2.6.1.1) (de:glycine max aspartate aminotransferase glyoxysomal isozyme aat1precursor and aspartate aminotransferase cytosolic isozyme aat2(aat) mrna, complete cds.) (le:152) (re:1522) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728555	229	22385	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728556	230	22386	420	139

Description

6500724684 asd:xsa beta-xylosidase / alpha-l-arabinosidase:alpha-l-arabinofuranosidase 2:arabinosidase (gtcfc:1.4) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) xsa xsa Bacillus subtilis 1423 -11528542 4000708009 xsa:asd (ec:3.2.1.55) (de:alpha-l-arabinofuranosidase 2, (arabinosidase)) (db:swissprot) ABF2_BACSU P94552 BACILLUS SUBTILIS 1423 -11528542 7000684482 xsa beta-xylosidase / alpha-l-arabinosidase xsa (db:pir2.dat) G69734 G69734 Bacillus subtilis 1423 -11528542 220319 xsa alpha-l-arabinosidase (fn:xylan degradation) (db:genpept-bct1) (ec:3.2.1.37:3.2.1.55) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:beta-xylosidase) (le:117633) (re:119120) (di:complement) BSUB0015 Z99118 g2635316 Bacillus subtilis 1423 -11528542 304192 asd arabinosidase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology with an arabinosidase gene of bacteriodes) (le:50787) (re:52274) (di:direct) BSZ75208 Z75208 g1770043 Bacillus subtilis 1423 -11528542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728561	231	22387	381	126

Description

6500724685 alpha-l-arabinofuranosidase (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) abfA abfA Bacillus subtilis 1423 -11528543 5500684837 abfa (ec:3.2.1.55) (de:alpha-l-arabinofuranosidase 1, (arabinosidase)) (db:swissprot) ABFA_BACSU P94531 BACILLUS SUBTILIS 1423 -11528543 7000684484 abfa alpha-l-arabinofuranosidase abfa (db:pir2.dat) C69580 C69580 Bacillus subtilis 1423 -11528543 220298 abfa alpha-l-arabinofuranosidase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:142302) (re:143804) (di:complement) BSUB0015 Z99118 g2635337 Bacillus subtilis 1423 -11528543 304171 abfa alpha-l-arabinofuranosidase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (le:26103) (re:27605) (di:direct) BSZ75208 Z75208 g1770022 Bacillus subtilis 1423 -11528543

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728600	232	22388	1137	379

Description

6500724686 arabinan-endo 1:5-alpha-l-arabinase (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) abnA abnA Bacillus subtilis 1423 -11528544 7000692222 abna arabinan-endo 1:5-alpha-l-arabinase abna (db:pir2.dat) E69580 E69580 Bacillus subtilis 1423 -11528544 220289 abna arabinan-endo 1:5-alpha-l-arabinase (fn:degradation of plant cell wall polysaccharide) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:153061) (re:154002) (di:complement) BSUB0015 Z99118 g2635346 Bacillus subtilis 1423 -11528544 304162 abna arabinan-endo 1:5-alpha-l-arabinase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to abna from aspergillus niger;identified) (le:15905) (re:16846) (di:direct) BSZ75208 Z75208 g1770013 Bacillus subtilis 1423 -11528544

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728605	233	22389	606	201

Description

GTC ORF with score 131 to: (sr:baker's yeast) (db:genpept-pln1) (de:s.cerevisiae dna from chromosome xii right arm including ace2,cki1, pdc5, sls1, put1 and trna-asp genes.) (nt:internal orf of l3133 probably not coding) (le:18132) (re:18713) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728631	234	22390	783	261

Description

6500724687 levansucrase:levansucrase precursor:beta-d-fructofuranosyl transferase:sucrose 6-fructosyl transferase (gtcfc:1.4:7.2) (ec:2.4.1.10) (keggfc:7.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) sacB sacB Bacillus subtilis 1423 -11528545 7500891277 sacb (ec:2.4.1.10) (de:transferase) (sucrose 6-fructosyl transferase)) (db:swissprot) SACB_BACSU P05655 BACILLUS SUBTILIS 1423 -11528545 170315 sacb levansucrase:sacb precursor:sucrose 6-fructosyl-transferase (ec:2.4.1.10) (db:pir2.dat) A25040 S07309 Bacillus subtilis 1423 -11528545 5000688483 levansucrase (db:genpept-bct1) (de:bacillus subtilis sacb gene for levansucrase.) (le:464) (re:1885) (di:direct) BSSACBG X02730 g732568 Bacillus subtilis 1423 -11528545 219609 sacb levansucrase (db:genpept-bct1) (ec:2.4.1.10) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:135522) (re:136943) (di:direct) BSUB0018 Z99121 g2635958 Bacillus subtilis 1423 -11528545 408643 sacb levansucrase (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:44728) (re:46149) (di:complement) BSZ94043 Z94043 g1945682 Bacillus subtilis 1423 -11528545 1500685536 sacb levansucrase (db:genpept-syn) (de:cloning vector pex18t, complete sequence.) (le:209) (re:1630) (di:complement) AF004910 AF004910 g2218143 Cloning vector pEX18T 61449 -11528545 4000707320 sacb levansucrase precursor (db:genpept-syn) (de:cloning vector pex18gm, complete sequence.) (le:209) (re:1630) (di:complement) AF047518 AF047518 g2961141 Cloning vector pEX18Gm 73159 -11528545 7000686544 sacb levansucrase precursor (db:genpept-syn) (de:cloning vector pex18tc, complete sequence.) (le:209) (re:1630) (di:complement) AF047519 AF047519 g2961145 Cloning vector pEX18Tc 73160 -11528545 7000686545 sacb levansucrase (db:genpept-syn) (de:site-specific excision vector pflp2, complete sequence.) (le:2338) (re:3759) (di:complement) AF048702 AF048702 g2961154 site-specific excision vector pFLP2 73560 -11528545 7000686546 sacb levansucrase (db:genpept-syn) (de:cloning vector pex100t, complete sequence.) (le:209) (re:1630) (di:complement) XXU17500 U17500 g603178 Cloning vector pEX100T 37970 -11528545 97838 sacb (ec:2.4.1.10) (de:transferase) (sucrose 6-fructosyl transferase)) (db:swissprot) SACB_BACSU P05655 BACILLUS SUBTILIS 1423 -11528545 7000686543 sacb levansucrase:sacb precursor:sucrose 6-fructosyl-transferase (ec:2.4.1.10) (db:pir) A25040 A25040 Bacillus subtilis 1423 -11528545

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728632	235	22391	288	95

Description

6500724688 ipa-50d:saca sucrase-6-phosphate hydrolase:sucrose-6-phosphate hydrolase:sucrase:invertase (gtcfc:1.4:1.6:7.2) (ec:3.2.1.26) (keggfc:1.6:7.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) sacA sacA Bacillus subtilis 1423 -11528546 219287 saca:ipa-50d (ec:3.2.1.26) (de:sucrose-6-phosphate hydrolase, (sucrase) (invertase)) (db:swissprot) SCRB_BACSU P07819 BACILLUS SUBTILIS 1423 -11528546 169885 saca beta-fructofuranosidase:saca:sucrase:sucrose-6-phosphate hydrolase (ec:3.2.1.26) (db:pir2.dat) A25562 A25562 Bacillus subtilis 1423 -11528546 216659 (sr:b.subtilis (strain marburg 168) dna, clone pbsg8-1) (db:genpept-bct1) (de:b.subtilis saca gene encoding sucrase-6-phosphate hydrolase(sucrase), complete cds and sacp gene, partial cds.) (nt:sucrase (ec 3.2.1.26)) (le:139) (re:1581) (di:direct) BACSACA M15662 g143482 Bacillus subtilis 1423 -11528546 5000688517 ipa-50d::saca (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:53914) (re:55356) (di:direct) BSGENR X73124 g413974 Bacillus subtilis 1423 -11528546 7500891400 saca sucrase-6-phosphate hydrolase (db:genpept-bct1) (ec:3.2.1.26) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-50d) (le:102606) (re:104048) (di:complement) BSUB0020 Z99123 g2636339 Bacillus subtilis 1423 -11528546 98136 saca:ipa-50d (ec:3.2.1.26) (de:sucrose-6-phosphate hydrolase, (sucrase) (invertase)) (db:swissprot) SCRB_BACSU P07819 BACILLUS SUBTILIS 1423 -11528546 7000686573 saca sucrase-6-phosphate hydrolase saca (db:pir) G69702 G69702 Bacillus subtilis 1423 -11528546

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728658	236	22392	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728680	237	22393	429	142

Description

GTC ORF with score 125 to: (de:(yal051w) (pn:putative 118:peroxisome proliferating transcription factor) (gn:fun43:oaf1) (gtcfc:10.1:10.2) (ec:) (yaf1_yeast) (keggfc:11.2) (sgdfc:1.6.4:4.8.2:9.5.0) (db:gtc-saccharomyces cerevisiae))

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728701	238	22394	732	243

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728706	239	22395	513	170

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728759	240	22396	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728760	241	22397	327	108

Description

6500724689 celd:celf:lich 6-phospho-beta-glucosidase:probable 6-phospho-beta-glucosidase (gtcfc:1.4) (ec:3.2.1.86) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) licH licH Bacillus subtilis 1423 -11528547 7500878517 celf:celd:lich (ec:3.2.1.86) (de:probable 6-phospho-beta-glucosidase,) (db:swissprot) CELF_BACSU P46320 BACILLUS SUBTILIS 1423 -11528547 7000684790 lich 6-phospho-beta-glucosidase lich (db:pir2.dat) S57762 S57762 Bacillus subtilis 1423 -11528547 5000689433 celd putative 6-phospho-beta-glucosidase (db:genpept-bct1) (de:b.subtilis cela, celb, celc, celd and ywaa genes.) (le:4270) (re:5598) (di:direct) BSCELABCD Z49992 g895751 Bacillus subtilis 1423 -11528547 219052 lich 6-phospho-beta-glucosidase (fn:lichenan degradation products utilization) (db:genpept-bct1) (ec:3.2.1.86) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: celd, celf) (le:158910) (re:160238) (di:complement) BSUB0020 Z99123 g2636391 Bacillus subtilis 1423 -11528547 63805 celf:celd:lich (ec:3.2.1.86) (de:probable 6-phospho-beta-glucosidase,) (db:swissprot) CELF_BACSU P46320 BACILLUS SUBTILIS 1423 -11528547 170448 lich 6-phospho-beta-glucosidase lich (db:pir) S57762 S57762 Bacillus subtilis 1423 -11528547

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728761	242	22398	264	87

Description

5000688479 bgl:lics:n15b:bgls beta-glucanase precursor:endo-beta-1:3-1:4 glucanase:1:3-1:4-beta-d-glucan 4-glucanohydrolase:lichenase (gtcfc:1.4) (ec:3.2.1.73) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) bglS bglS Bacillus subtilis 1423 -11528548 219039 bgls:bgl:lics:n15b (ec:3.2.1.73) (de:(1,3-1,4-beta-d-glucan 4-glucanohydrolase) (lichenase)) (db:swissprot) GUB_BACSU P04957 BACILLUS SUBTILIS 1423 -11528548 7000685474 bgls licheninase:precursor:1:3-1:4-beta-d-glucan 4-gluconohydrolase:beta-glucanase:lichenase (cl:licheninase) (ec:3.2.1.73) (db:pir1.dat) LXBS I40370 Bacillus subtilis 1423 -11528548 6500724690 bgls beta-1:3-1:4-glucanase (fn:beta-glucan hydrolysing enzyme) (db:genpept-bct1) (ec:3.2.1.73) (de:b.subtilis bgls gene for beta-1,3-1,4-glucanase.) (le:184) (re:912) (di:direct) BSBGLS Z46862 g599674 Bacillus subtilis 1423 -11528548 222846 bgls endo-beta-1:3-1:4 glucanase (fn:lichenan degradation) (db:genpept-bct1) (ec:3.2.1.73) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: bgl, lics) (le:11351) (re:12079) (di:complement) BSUB0021 Z99124 g2636453 Bacillus subtilis 1423 -11528548 301513 lics beta-glucanase precursor (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (le:11506) (re:12234) (di:direct) D83026 D83026 g665993 Bacillus subtilis 1423 -11528548 75009 bgls:bgl:lics:n15b (ec:3.2.1.73) (de:(1,3-1,4-beta-d-glucan 4-glucanohydrolase) (lichenase)) (db:swissprot) GUB_BACSU P04957 BACILLUS SUBTILIS 1423 -11528548 170320 bgls licheninase:precursor:1:3-1:4-beta-d-glucan 4-gluconohydrolase:beta-glucanase:lichenase (cl:licheninase) (ec:3.2.1.73) (db:pir) LXBS B69594 Bacillus subtilis 1423 -11528548

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728804	243	22399	336	112

Description

6500724691 beta-glucosidase (gtcfc:1.4:1.6:5.13:6.5:7.2) (ec:3.2.1.21) (keggfc:1.6:5.13:6.5:7.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) bglH bglH Bacillus subtilis 1423 -11528549 7000692262 bglh 6-phospho-beta-glucosidase:bglh (cl:agrobacterium beta-glucosidase) (ec:3.2.1.86) (db:pir2.dat) H69593 H69593 Bacillus subtilis 1423 -11528549 215873 n17d hypothetical protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (nt:homologous to 6-phospho-beta-glucosidase) (le:15535) (re:16980) (di:direct) BACHUTWAPA D31856 g603779 Bacillus subtilis 1423 -11528549 215888 hypothetical 54.6-kda protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (nt:homologous to 6-phospho-beta-glucosidase) (le:3639) (re:5084) (di:direct) BACHYPTP D29985 g849026 Bacillus subtilis 1423 -11528549 7500954268 bglh beta-glucosidase (fn:cellulose degradation) (db:genpept-bct1) (ec:3.2.1.21) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:31855) (re:33300) (di:complement) BSUB0021 Z99124 g2636472 Bacillus subtilis 1423 -11528549

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728834	244	22400	390	130

Description

GTC ORF with score 322 to: (fn:involved in transcriptional activation) (sr:saccharomyces cerevisiae (strain ybp1) dna) (db:genpept-pln1) (de:yeast putative transcriptional activator (ada2) gene, complete cds.) (le:308) (re:1612) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728839	245	22401	615	205

Description

5000688747 gluconate permease (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) gntP gntP Bacillus subtilis 1423 -11528550 74252 gntp (de:gluconate permease) (db:swissprot) GNTP_BACSU P12012 BACILLUS SUBTILIS 1423 -11528550 7000685436 gntp gluconate permease gntp (cl:d-serine permease) (db:pir2.dat) A26190 A26190 Bacillus subtilis 1423 -11528550 7500882619 gntp gluconate permease (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:homologs are found in e. coli and h. influenzae;) (le:1607) (re:2953) (di:complement) AB005554 AB005554 g563931 Bacillus subtilis 1423 -11528550 215719 permease (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:b.subtilis (gluconate operon) gntr, gntk and gntp genes encodinggnt repressor, gluconate kinase and permease, and gntz gene.) (le:2530) (re:3876) (di:direct) BACGNT J02584 g143016 Bacillus subtilis 1423 -11528550 215727 gntp gluconate permease (fn:gluconate utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:115639) (re:116985) (di:direct) BSUB0021 Z99124 g2636554 Bacillus subtilis 1423 -11528550 170015 gntp gluconate permease gntp (db:pir) A26190 A26190 Bacillus subtilis 1423 -11528550 6500724692 gluconate permease (gtcfc:1.4) (keggfc:14.2) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) gntP gntP Bacillus subtilis 1423 -11528550

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728843	246	22402	549	182

Description

6500724693 6-phospho-beta-glucosidase (gtcfc:1.4) (ec:3.2.1.86) (keggfc:14.1) (bsorffc:2.1.1) (db:gtc-bacillus subtilis) bglA bglA Bacillus subtilis 1423 -11528551 61652 bgla (ec:3.2.1.86) (de:6-phospho-beta-glucosidase,) (db:swissprot) BGLA_BACSU P42973 BACILLUS SUBTILIS 1423 -11528551 7000684700 bgla 6-phospho-beta-glucosidase:bgla (cl:agrobacterium beta-glucosidase) (ec:3.2.1.86) (db:pir2.dat) I39953 I39953 Bacillus subtilis 1423 -11528551 302059 bgla phospho-bete-glucosidase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:2712) (re:4151) (di:complement) BACGNTZA D78193 g1064784 Bacillus subtilis 1423 -11528551 215763 bgla phospho-beta-glucosidase (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis phospho-beta-glucosidase (bgla) gene, completecds.) (le:76) (re:1515) (di:direct) BACPHOBGLU L19710 g506381 Bacillus subtilis 1423 -11528551 216469 bgla 6-phospho-beta-glucosidase (db:genpept-bct1) (ec:3.2.1.86) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:121094) (re:122533) (di:complement) BSUB0021 Z99124 g2636558 Bacillus subtilis 1423 -11528551 170437 bgla 6-phospho-beta-glucosidase:bgla (cl:agrobacterium beta-glucosidase) (ec:3.2.1.86) (db:pir) I39953 I39953 Bacillus subtilis 1423 -11528551 5000688478 (de:(bgla) (pn:6-phospho-beta-glucosidase) (gtcfc:7.01) (ec:3.2.1.86) (bgla_bacsu) (keggfc:11.1) (bsorffc:2.1.0) (db:gtc-bacillus subtilis)) bglA bglA Bacillus subtilis 1423 10004361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728847	247	22403	201	66

Description

6500724694 mtlb:mtld mannitol-1-phosphate dehydrogenase:mannitol-1-phosphate 5-dehydrogenase (gtcfc:1.5) (ec:1.1.1.17) (keggfc:1.5) (bsorffc:2.4.2) (db:gtc-bacillus subtilis) mtlD mtlD Bacillus subtilis 1423 -11528552 84552 mtld:mtlb (ec:1.1.1.17) (de:mannitol-1-phosphate 5-dehydrogenase,) (db:swissprot) MTLD_BACSU P42957 BACILLUS SUBTILIS 1423 -11528552 7000685877 mtld mannitol-1-phosphate 5-dehydrogenase:mtld (ec:1.1.1.17) (db:pir2.dat) I39888 I39888 Bacillus subtilis 1423 -11528552 7500886035 mtlb mannitol-1-phosphate dehydrogenase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:2134) (re:3234) (di:direct) BAC39R D38161 g1032473 Bacillus subtilis 1423 -11528552 215092 mtld mannitol-1-phosphate dehydrogenase (db:genpept-bct1) (ec:1.1.1.17) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: mtlb) (le:48439) (re:49539) (di:direct) BSUB0003 Z99106 g2632700 Bacillus subtilis 1423 -11528552 222662 mltd homologue of mannitol-1-phosphate dehydrogenase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:130842) (re:131942) (di:direct) D50453 D50453 g1805468 Bacillus subtilis 1423 -11528552 170333 mtld mannitol-1-phosphate dehydrogenase mtld (db:pir) I39888 I39888 Bacillus subtilis 1423 -11528552

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728869	248	22404	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728887	249	22405	669	223

Description

6500724695 hypothetical protein:similar to glucose-1-phosphate cytidylyltransferase (gtcfc:1.5:7.2:14.1) (ec:2.7.7.33) (keggfc:1.5:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnH yfnH Bacillus subtilis 1423 -11528553 7000693039 yfnh glucose-1-phosphate cytidylyltransferase:yfnh (cl:glucose-1-phosphate cytidylyltransferase) (ec:2.7.7.33) (db:pir2.dat) C69815 C69815 Bacillus subtilis 1423 -11528553 1500696650 yfnh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to glucose-1-phosphate) (le:197277) (re:198041) (di:direct) BSUB0004 Z99107 g2633040 Bacillus subtilis 1423 -11528553 7500964019 yfnh (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:15150) (re:15914) (di:complement) D86418 D86418 g2116766 Bacillus subtilis 1423 -11528553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728894	250	22406	531	176

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728917	251	22407	879	293

Description

6500724696 hypothetical protein:similar to phosphomannomutase (gtcfc:1.5:14.1) (ec:5.4.2.8) (keggfc:1.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhxB yhxB Bacillus subtilis 1423 -11528554 7500937202 yhxb (ec:5.4.2.8) (de:probable phosphomannomutase, (pmm)) (db:swissprot) YHXB_BACSU P18159 BACILLUS SUBTILIS 1423 -11528554 7000694416 yhxb phosphomannomutase homolog yhxb:hypothetical protein glpd 3 region (db:pir2.dat) C69835 C69835 Bacillus subtilis 1423 -11528554 6000690451 yhxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to phosphomannomutase) (le:203459) (re:205156) (di:direct) BSUB0005 Z99108 g2633254 Bacillus subtilis 1423 -11528554 7500937204 yhxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to phosphomannomutase) (le:6779) (re:8476) (di:direct) BSUB0006 Z99109 g2633266 Bacillus subtilis 1423 -11528554 4000714554 yhxb hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:see embl m34393 and swiss prot p18159.; this could) (le:6427) (re:8124) (di:direct) BSY14079 Y14079 g2226139 Bacillus subtilis 1423 -11528554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728921	252	22408	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728945	253	22409	942	314

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728962	254	22410	780	260

Description

6500724697 hypothetical protein:similar to mannose-6-phosphate isomerase (gtcfc:1.5:14.1) (ec:5.3.1.8) (keggfc:1.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdE yjdE Bacillus subtilis 1423 -11528555 7000694198 yjde mannose-6-phosphate isomerase homolog yjde (db:pir2.dat) H69848 H69848 Bacillus subtilis 1423 -11528555 7500964925 yjde (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to mannose-6-phosphate isomerase) (le:79774) (re:80721) (di:direct) BSUB0007 Z99110 g2633556 Bacillus subtilis 1423 -11528555

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728966	255	22411	465	154

Description

6500724698 fructose-1-phosphate kinase (gtcfc:1.5:1.6) (ec:2.7.1.56) (keggfc:1.5:1.6) (bsorffc:2.4.2) (db:gtc-bacillus subtilis) fruB fruB Bacillus subtilis 1423 -11528556 7000693010 frub fructose 1-phosphate kinase frub (cl:6-phosphofructokinase 2) (db:pir2.dat) A69627 A69627 Bacillus subtilis 1423 -11528556 7500963998 frub fructose-1-phosphate kinase (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to l. lactis tagatose-6-phosphate kinase,) (le:13433) (re:14344) (di:direct) AF012285 AF012285 g3282124 Bacillus subtilis 1423 -11528556 7500963997 frub fructose-1-phosphate kinase (db:genpept-bct1) (ec:2.7.1.56) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:112945) (re:113856) (di:direct) BSUB0008 Z99111 g2633810 Bacillus subtilis 1423 -11528556

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728967	256	22412	1137	379

Description

6500724699 hypothetical protein:similar to ndp-sugar epimerase (gtcfc:1.5:4.3:14.1) (ec:4.2.1.46) (keggfc:1.5:4.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytcB ytcB Bacillus subtilis 1423 -11528557 7000694314 ytcb ndp-sugar epimerase homolog ytcb (cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology) (db:pir2.dat) H69988 H69988 Bacillus subtilis 1423 -11528557 4000714119 ytcb ytcb (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to with dtdp glucose 4,6-dehydratase of) (le:21161) (re:22111) (di:complement) AF008220 AF008220 g2293288 Bacillus subtilis 1423 -11528557 7500965015 ytcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to ndp-sugar epimerase) (le:158316) (re:159266) (di:direct) BSUB0016 Z99119 g2635571 Bacillus subtilis 1423 -11528557

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728968	257	22413	618	205

Description

6500724700 hypothetical protein:similar to l-rhamnose isomerase (gtcfc:1.5:14.1) (ec:5.3.1.14) (keggfc:1.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yulE yulE Bacillus subtilis 1423 -11528558 7000694153 yule l-rhamnose isomerase homolog yule (db:pir2.dat) G70014 G70014 Bacillus subtilis 1423 -11528558 1500693712 yule (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to l-rhamnose isomerase) (le:199233) (re:200507) (di:complement) BSUB0016 Z99119 g2635602 Bacillus subtilis 1423 -11528558 6000691370 yule (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to l-rhamnose isomerase) (le:3) (re:1277) (di:complement) BSUB0017 Z99120 g2635614 Bacillus subtilis 1423 -11528558 7500964886 yule l-rhamnose isomerase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yula to yulf.) (nt:putative) (le:4952) (re:6226) (di:direct) BSZ93938 Z93938 g1934825 Bacillus subtilis 1423 -11528558

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501728998	258	22414	609	203

Description

6500724701 hypothetical protein:similar to rhamnulokinase (gtcfc:1.5:14.1) (ec:2.7.1.5) (keggfc:1.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yulC yulC Bacillus subtilis 1423 -11528559 7000694509 yulc rhamnulokinase homolog yulc (cl:rhamnulokinase) (db:pir2.dat) E70014 E70014 Bacillus subtilis 1423 -11528559 1500693710 yulc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to rhamnulokinase) (le:200865) (re:202322) (di:complement) BSUB0016 Z99119 g2635604 Bacillus subtilis 1423 -11528559 6000691374 yulc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to rhamnulokinase) (le:1635) (re:3092) (di:complement) BSUB0017 Z99120 g2635616 Bacillus subtilis 1423 -11528559 7500954062 yulc rhamnulose kinase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yula to yulf.) (nt:putative) (le:3137) (re:4594) (di:direct) BSZ93938 Z93938 g1934823 Bacillus subtilis 1423 -11528559

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729027	259	22415	459	153

Description

6500724702 yvyi:pmi mannose-6-phosphate isomerase:possible mannose-6-phosphate isomerase:phosphomannose isomerase:pmi:phosphohexomutase (gtcfc:1.5) (ec:5.3.1.8) (keggfc:1.5) (bsorffc:2.4.2) (db:gtc-bacillus subtilis) pmi pmi Bacillus subtilis 1423 -11528560 82930 pmi (ec:5.3.1.8) (de:(pmi) (phosphohexomutase)) (db:swissprot) MANA_BACSU P39841 BACILLUS SUBTILIS 1423 -11528560 7000685786 pmi mannose-6-phosphate isomerase:pmi (ec:5.3.1.8) (db:pir2.dat) A69680 A69680 Bacillus subtilis 1423 -11528560 7500885297 orfx unknown (sr:bacillus subtilis (strain ac327) dna, clones peh4 and pwcev4) (db:genpept-bct1) (de:bacillus subtilis gene for beta-n-acetylglucosaminidase, completecds.) (le:217) (re:1167) (di:direct) BACORFX D45048 g1129073 Bacillus subtilis 1423 -11528560 216422 unknown (db:genpept-bct1) (de:bacillus subtilis n-acetylglucosaminidase (lytd) gene, completecds.) (nt:orfx) (le:186) (re:1136) (di:direct) BSU02562 U02562 g476092 Bacillus subtilis 1423 -11528560 219759 pmi mannose-6-phosphate isomerase (db:genpept-bct1) (ec:5.3.1.8) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvyi) (le:89567) (re:90517) (di:complement) BSUB0019 Z99122 g2636105 Bacillus subtilis 1423 -11528560 170264 pmi mannose-6-phosphate isomerase:pmi (ec:5.3.1.8) (db:pir) A69680 A69680 Bacillus subtilis 1423 -11528560

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729035	260	22416	975	325

Description

5000688382 fbab:yxdi:b65c:iolj fructose-1:6-bisphosphate aldolase:probable fructose-bisphosphate aldolase 2 (gtcfc:1.5) (ec:4.1.2.13) (keggfc:14.1) (bsorffc:2.4.2) (db:gtc-bacillus subtilis) iolJ iolJ Bacillus subtilis 1423 -11528561 59125 fbab:iolj:b65c (ec:4.1.2.13) (de:probable fructose-bisphosphate aldolase 2,) (db:swissprot) ALF2_BACSU P42420 BACILLUS SUBTILIS 1423 -11528561 7000684555 iolj fructose-1:6-bisphosphate aldolase iolj (cl:fructose-bisphosphate aldolase ii) (db:pir2.dat) B69646 B69646 Bacillus subtilis 1423 -11528561 215919 b65c hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (nt:homologous to fructose bisphosphate aldolases) (le:10226) (re:11098) (di:direct) BACIOLO D14399 g709990 Bacillus subtilis 1423 -11528561 303051 iolj fructose-1:6-bisphosphate aldolase (fn:myo-inositol catabolism) (db:genpept-bct1) (ec:4.1.2.13) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: fbab, yxdi) (le:72591) (re:73463) (di:complement) BSUB0021 Z99124 g2636513 Bacillus subtilis 1423 -11528561 6500724703 fbab:yxdi:b65c fructose-1:6-bisphosphate aldolase:probable fructose-bisphosphate aldolase 2 (gtcfc:1.5) (ec:4.1.2.13) (keggfc:14.1) (bsorffc:2.4.2) (db:gtc-bacillus subtilis) iolJ iolJ Bacillus subtilis 1423 -11528561

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729078	261	22417	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729083	262	22418	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729088	263	22419	414	137

Description

6500724704 yyde:fbp fructose-1:6-bisphosphatase (gtcfc:1.5) (ec:3.1.3.11) (keggfc:14.1) (bsorffc:2.4.2) (db:gtc-bacillus subtilis) fbp fbp Bacillus subtilis 1423 -11528562 7000693012 fbp:yyde fructose-bisphosphatase (cl:bacillus subtilis fructose-bisphosphatase:phosphoesterase core homology) (ec:3.1.3.11) (db:pir1.dat) C69621 C69621 Bacillus subtilis 1423 -11528562 215770 yyde (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:9575) (re:11590) (di:direct) BACGNTZA D78193 g1064791 Bacillus subtilis 1423 -11528562 302066 fbp fructose-1:6-bisphosphatase (fn:gluconeogenesis) (db:genpept-bct1) (ec:3.1.3.11) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yyde) (le:127957) (re:129972) (di:direct) BSUB0021 Z99124 g2636566 Bacillus subtilis 1423 -11528562

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729110	264	22420	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729125	265	22421	672	224

Description

6500724705 yzba:ybbd hypothetical protein:hypothetical 70.6 kd protein in feua 5region precursor:orf1 (gtcfc:1.6:5.13:6.5:7.2:14.1) (ec:3.2.1.21) (keggfc:1.6:5.13:6.5:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbD ybbD Bacillus subtilis 1423 -11528563 110204 ybbd (de:hypothetical 70.6 kd protein in feua 5'region precursor (orf1)) (db:swissprot) YBBD_BACSU P40406 BACILLUS SUBTILIS 1423 -11528563 7000687283 ybbd beta-hexosaminidase homolog ybbd (db:pir2.dat) I39839 I39839 Bacillus subtilis 1423 -11528563 7500896566 ybbd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:5106) (re:7034) (di:complement) AB002150 AB002150 g1944006 Bacillus subtilis 1423 -11528563 215585 (sr:bacillus subtilis (individual_isolate ms94, strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis feua, b, and c genes, 3 orfs, 2 complete cds'sand 5'end.) (nt:possible n-terminal signal sequence; mature protein) (le:155) (re:2083) (di:direct) BACFEUABC L19954 g438455 Bacillus subtilis 1423 -11528563 1500685648 ybbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yzba; similar to) (le:186450) (re:188378) (di:complement) BSUB0001 Z99104 g2632433 Bacillus subtilis 1423 -11528563 169887 ybbd beta-hexosaminidase homolog ybbd (db:pir) I39839 I39839 Bacillus subtilis 1423 -11528563 5000689151 (de:(ybbd) (pn:hypothetical 70) (gtcfc:13.07) (ec:) (ybbd_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) ybbD ybbD Bacillus subtilis 1423 10051936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729128	266	22422	678	226

Description

6500724706 hypothetical protein:similar to oligo-1:6-glucosidase (gtcfc:1.6:7.2:14.1) (ec:3.2.1.20) (keggfc:1.6:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdG ycdG Bacillus subtilis 1423 -11528564 7000694332 ycdg oligo-1:6-glucosidase homolog ycdg (cl:alpha-glucosidase:alpha-amylase core homology) (db:pir2.dat) H69755 H69755 Bacillus subtilis 1423 -11528564 5500687022 ycdg ycdg (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:glca gene; probable alpha-glucosidase) (le:19548) (re:21233) (di:direct) AB000617 AB000617 g2415735 Bacillus subtilis 1423 -11528564 7500965027 ycdg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to oligo-1,6-glucosidase) (le:111363) (re:113048) (di:direct) BSUB0002 Z99105 g2632570 Bacillus subtilis 1423 -11528564

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729159	267	22423	987	329

Description

6500724707 hypothetical protein:probable beta-glucosidase:gentiobiase:cellobiase:beta-d-glucoside glucohydrolase:amygdalase (gtcfc:1.6:5.13:6.5:7.2:14.1) (ec:3.2.1.21) (keggfc:1.6:5.13:6.5:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckE yckE Bacillus subtilis 1423 -11528565 61645 ycke (ec:3.2.1.21) (de:(beta-d-glucoside glucohydrolase) (amygdalase)) (db:swissprot) BGL2_BACSU P42403 BACILLUS SUBTILIS 1423 -11528565 7000684699 ycke beta-glucosidase homolog ycke (cl:agrobacterium beta-glucosidase) (db:pir2.dat) G69760 G69760 Bacillus subtilis 1423 -11528565 217138 ycke beta-glucosidase (sr:bacillus subtilis (strain:168trpc2) dna, clone_lib:lambda dashi) (db:genpept-bct1) (de:bacillus subtilis dna around 28 degrees region of chromosomecontaining ycka-h genes.) (le:3104) (re:4537) (di:direct) BACYCK D30762 g710632 Bacillus subtilis 1423 -11528565 222607 ycke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to beta-glucosidase) (le:175180) (re:176613) (di:direct) BSUB0002 Z99105 g2632627 Bacillus subtilis 1423 -11528565 7500877781 ycke homologue of beta-glucosidase of b. circulans (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:49484) (re:50917) (di:direct) D50453 D50453 g1805413 Bacillus subtilis 1423 -11528565 5000688520 (de:(ycke) (pn:probable beta-glucosidase:probable beta-glucosidase :gentiobiase:cellobiase:beta-d-glucoside glucohydrolase:amygdalase) (gtcfc:7.02) (ec:3.2.1.21) (bgl2_bacsu) (keggfc:1.6:6.5:7.1) (bsorffc:2.1.0) (db:gtc-bacillu) yckE yckE Bacillus subtilis 1423 10004354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729174	268	22424	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729175	269	22425	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729178	270	22426	552	183

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729180	271	22427	621	207

Description

6500724708 alpha-d-galactoside galactohydrolase (gtcfc:1.6:8.1:8.5) (ec:3.2.1.22) (keggfc:1.6:8.1:8.5) (bsorffc:2.4.3) (db:gtc-bacillus subtilis) melA melA Bacillus subtilis 1423 -11528566 7502851502 mela (ec:3.2.1.22) (de:alpha-galactosidase, (melibiase)) (db:swissprot) AGAL_BACSU O34645 BACILLUS SUBTILIS 1423 -11528566 7000692180 mela alpha-d-galactoside galactohydrolase mela (cl:melibiose-specific alpha-galactosidase) (db:pir2.dat) E69656 E69656 Bacillus subtilis 1423 -11528566 4000714172 mela alpha-galactosidase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to alpha-galactosidase of e. coli) (le:76937) (re:78235) (di:complement) AF008220 AF008220 g2293305 Bacillus subtilis 1423 -11528566 7500954269 mela alpha-d-galactoside galactohydrolase (db:genpept-bct1) (ec:3.2.1.22) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:102192) (re:103490) (di:direct) BSUB0016 Z99119 g2635514 Bacillus subtilis 1423 -11528566

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729198	272	22428	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729228	273	22429	429	142

Description

6500724709 ipa-36d:galt galactose-1-phosphate uridyltransferase:galactose-1-phosphate uridylyltransferase (gtcfc:1.6:4.3) (ec:2.7.7.10) (keggfc:1.6:4.3) (bsorffc:2.4.3) (db:gtc-bacillus subtilis) galT galT Bacillus subtilis 1423 -11528567 7500882076 galt:ipa-36d (ec:2.7.7.10) (de:galactose-1-phosphate uridylyltransferase,) (db:swissprot) GAL7_BACSU P39575 BACILLUS SUBTILIS 1423 -11528567 7000685356 galt utp--hexose-1-phosphate uridylyltransferase::galactose-1-phosphate uridyltransferase galt:protein ipa-36d (cl:galactose-1-phosphate uridyl transferase) (ec:2.7.7.10) (db:pir2.dat) S39691 S39691 Bacillus subtilis 1423 -11528567 219273 ipa-36d::galt (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:36929) (re:38470) (di:direct) BSGENR X73124 g413960 Bacillus subtilis 1423 -11528567 7502851503 galt galactose-1-phosphate uridyltransferase (fn:galactose metabolism) (db:genpept-bct1) (ec:2.7.7.10) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-36d) (le:119489) (re:121030) (di:complement) BSUB0020 Z99123 g2636354 Bacillus subtilis 1423 -11528567 73038 galt:ipa-36d (ec:2.7.7.10) (de:galactose-1-phosphate uridylyltransferase,) (db:swissprot) GAL7_BACSU P39575 BACILLUS SUBTILIS 1423 -11528567 170124 galt galactose-1-phosphate uridyltransferase galt (db:pir) S39691 S39691 Bacillus subtilis 1423 -11528567

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729230	274	22430	606	201

Description

6500724710 ipa-35d:galk galactokinase (gtcfc:1.6) (ec:2.7.1.6) (keggfc:1.6) (bsorffc:2.4.3) (db:gtc-bacillus subtilis) galK galK Bacillus subtilis 1423 -11528568 7500882073 galk:ipa-35d (ec:2.7.1.6) (de:galactokinase,) (db:swissprot) GAL1_BACSU P39574 BACILLUS SUBTILIS 1423 -11528568 7000685354 galk galactokinase galk (cl:galactokinase galk) (db:pir2.dat) S39690 S39690 Bacillus subtilis 1423 -11528568 219272 ipa-35d::galk (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:35753) (re:36925) (di:direct) BSGENR X73124 g413959 Bacillus subtilis 1423 -11528568 7502851504 galk galactokinase (fn:galactose metabolism) (db:genpept-bct1) (ec:2.7.1.6) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-35d) (le:121034) (re:122206) (di:complement) BSUB0020 Z99123 g2636355 Bacillus subtilis 1423 -11528568 73025 galk:ipa-35d (ec:2.7.1.6) (de:galactokinase,) (db:swissprot) GAL1_BACSU P39574 BACILLUS SUBTILIS 1423 -11528568 170457 galk galactokinase galk (db:pir) S39690 S39690 Bacillus subtilis 1423 -11528568

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729320	275	22431	717	239

Description

6500724711 udp-glucose 4-epimerase:galactowaldenase:udp-galactose 4-epimerase (gtcfc:1.6:4.3:11.4) (ec:5.1.3.2) (keggfc:1.6:4.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) galE galE Bacillus subtilis 1423 -11528569 73068 gale (ec:5.1.3.2) (de:galactose 4-epimerase)) (db:swissprot) GALE_BACSU P55180 BACILLUS SUBTILIS 1423 -11528569 7000685360 gale udpglucose 4-epimerase::udpgalactose 4-epimerase (cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology) (ec:5.1.3.2) (db:pir2.dat) D69628 D69628 Bacillus subtilis 1423 -11528569 303670 gale udp-glucose 4-epimerase (db:genpept-bct1) (ec:5.1.3.2) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (le:140) (re:1159) (di:complement) BSGALE X99339 g1429254 Bacillus subtilis 1423 -11528569 222867 gale udp-glucose 4-epimerase (fn:galactose metabolism) (db:genpept-bct1) (ec:5.1.3.2) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:190340) (re:191359) (di:complement) BSUB0020 Z99123 g2636421 Bacillus subtilis 1423 -11528569 301534 gale (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:highly homologous to udp-glucose 4-epimerases) (le:33106) (re:34125) (di:direct) D83026 D83026 g1783241 Bacillus subtilis 1423 -11528569 219218 gale udp-glucose 4-epimerase (db:genpept-bct1) (ec:5.1.3.2) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (le:140) (re:1159) (di:complement) BSGALE X99339 g1429254 Bacillus subtilis 1423 -11528569

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729328	276	22432	600	200

Description

6500724712 hypothetical protein:probable 5-dehydro-4-deoxyglucarate dehydratase:5-keto-4-deoxy-glucarate dehydratase:kdgdh (gtcfc:1.7:14.1) (ec:4.2.1.41) (keggfc:1.7) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbC ycbC Bacillus subtilis 1423 -11528570 80567 ycbc (ec:4.2.1.41) (de:(5-keto-4-deoxy-glucarate dehydratase) (kdgdh)) (db:swissprot) KDGD_BACSU P42235 BACILLUS SUBTILIS 1423 -11528570 7000685668 ycbc 5-dehydro-4-deoxyglucarate dehydratase homolog ycbc (cl:dihydrodipicolinate synthase) (db:pir2.dat) F69752 F69752 Bacillus subtilis 1423 -11528570 217115 ycbc homologue of 5-keto-4-deoxyglucarate (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:1418) (re:2344) (di:direct) BACYCB20 D30808 g709997 Bacillus subtilis 1423 -11528570 7500884543 ycbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to 5-dehydro-4-deoxyglucarate dehydratase) (le:73232) (re:74158) (di:direct) BSUB0002 Z99105 g2632532 Bacillus subtilis 1423 -11528570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729329	277	22433	264	87

Description

6500724713 hypothetical protein:probable glucarate dehydratase:gdh (gtcfc:1.7:14.1) (ec:4.2.1.40) (keggfc:1.7) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbF ycbF Bacillus subtilis 1423 -11528571 75014 ycbf (ec:4.2.1.40) (de:probable glucarate dehydratase, (gdh)) (db:swissprot) GUDH_BACSU P42238 BACILLUS SUBTILIS 1423 -11528571 7000685477 ycbf glucarate dehydratase (cl:glucarate dehydratase) (ec:4.2.1.40) (db:pir2.dat) A69753 A69753 Bacillus subtilis 1423 -11528571 217118 ycbf glucarate dehydratase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:5328) (re:6695) (di:direct) BACYCB20 D30808 g710000 Bacillus subtilis 1423 -11528571 7500882848 ycbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glucarate dehydratase) (le:77142) (re:78509) (di:direct) BSUB0002 Z99105 g2632535 Bacillus subtilis 1423 -11528571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729331	278	22434	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729343	279	22435	735	245

Description

6500724714 hypothetical protein:probable malate oxidoreductase:nad:malic enzyme:me (gtcfc:1.8:14.1) (ec:1.1.1.38) (keggfc:1.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkJ yqkJ Bacillus subtilis 1423 -11528572 82952 yqkj (ec:1.1.1.38) (de:(me)) (db:swissprot) MAO1_BACSU P54572 BACILLUS SUBTILIS 1423 -11528572 7000685787 yqkj malate dehydrogenase homolog yqkj (cl:malate dehydrogenase (oxaloacetate-decarboxylating)) (db:pir2.dat) C69967 C69967 Bacillus subtilis 1423 -11528572 216234 yqkj (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:266869) (re:268188) (di:direct) BACJH642 D84432 g1303990 Bacillus subtilis 1423 -11528572 7500885313 yqkj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to malate dehydrogenase) (le:55431) (re:56750) (di:complement) BSUB0013 Z99116 g2634790 Bacillus subtilis 1423 -11528572

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729347	280	22436	765	254

Description

6500724715 2-isopropylmalate synthase:alpha-isopropylmalate synthase:alpha-ipm synthetase (gtcfc:1.8:5.2:5.7) (ec:4.1.3.12) (keggfc:1.8:5.7) (bsorffc:2.6.2:3.1.5) (db:gtc-bacillus subtilis) leuA leuA Bacillus subtilis 1423 -11528573 4000707544 leua (ec:4.1.3.12) (de:synthase) (alpha-ipm synthetase)) (db:swissprot) LEU1_BACSU P94565 BACILLUS SUBTILIS 1423 -11528573 7000685732 leua 2-isopropylmalate synthase::alpha-isopropylmalate synthase (cl:2-isopropylmalate synthase leua) (ec:4.1.3.12) (db:pir2.dat) H69649 H69649 Bacillus subtilis 1423 -11528573 220345 leua 2-isopropylmalate synthase (fn:leucine biosynthesis) (db:genpept-bct1) (ec:4.1.3.12) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:96108) (re:97664) (di:complement) BSUB0015 Z99118 g2635293 Bacillus subtilis 1423 -11528573 304218 leua 2-isopropylmalate synthase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:leucine biosynthesis; 2-isopropylmalate synthase;) (le:72243) (re:73799) (di:direct) BSZ75208 Z75208 g1770069 Bacillus subtilis 1423 -11528573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729348	281	22437	636	211

Description

6500724716 malate dehydrogenase:decarboxylating (gtcfc:1.8:2.4:12.2) (keggfc:1.8:2.3) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) malS malS Bacillus subtilis 1423 -11528574 7000694186 mals malate dehydrogenase mals (cl:malate dehydrogenase (oxaloacetate-decarboxylating)) (db:pir2.dat) D69655 D69655 Bacillus subtilis 1423 -11528574 4000714205 mals putative malolactic enzyme (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:120565) (re:122265) (di:direct) AF008220 AF008220 g2293209 Bacillus subtilis 1423 -11528574 7500964913 mals malate dehydrogenase decarboxylating (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:58161) (re:59861) (di:complement) BSUB0016 Z99119 g2635472 Bacillus subtilis 1423 -11528574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729369	282	22438	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729372	283	22439	969	322

Description

6500724717 hypothetical protein:probable malate oxidoreductase:nad:malic enzyme:me (gtcfc:1.8:14.1) (ec:1.1.1.38) (keggfc:1.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywkA ywkA Bacillus subtilis 1423 -11528575 304121 ywka (ec:1.1.1.38) (de:(me)) (db:swissprot) MAO2_BACSU P45868 BACILLUS SUBTILIS 1423 -11528575 7000685788 ywka malate dehydrogenase homolog ywka:malolactic enzyme (cl:malate dehydrogenase (oxaloacetate-decarboxylating)) (db:pir2.dat) S55433 S55433 Bacillus subtilis 1423 -11528575 6000684882 ywka malolactic enzyme (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:19612) (re:21360) (di:direct) BSDNA320D Z49782 g853772 Bacillus subtilis 1423 -11528575 7500885314 ywka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to malate dehydrogenase) (le:202383) (re:204131) (di:complement) BSUB0019 Z99122 g2636230 Bacillus subtilis 1423 -11528575 219149 ywka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to malate dehydrogenase) (le:1073) (re:2821) (di:complement) BSUB0020 Z99123 g2636242 Bacillus subtilis 1423 -11528575 82953 ywka (ec:1.1.1.38) (de:(me)) (db:swissprot) MAO2_BACSU P45868 BACILLUS SUBTILIS 1423 -11528575 170332 ywka malate dehydrogenase homolog ywka:malolactic enzyme (db:pir) S55433 S55433 Bacillus subtilis 1423 -11528575

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729395	284	22440	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729398	285	22441	732	243

Description

6500724718 ipa-88d:ywfj:pta probable phosphate acetyltransferase:phosphotransacetylase (gtcfc:1.8:13.10) (ec:2.3.1.8) (keggfc:1.8) (bsorffc:2.3.1:2.6.2) (db:gtc-bacillus subtilis) pta pta Bacillus subtilis 1423 -11528576 7000686206 pta phosphotransacetylase pta (cl:phosphate acetyltransferase) (db:pir2.dat) S39743 S39743 Bacillus subtilis 1423 -11528576 219325 ipa-88d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:91234) (re:92205) (di:direct) BSGENR X73124 g580883 Bacillus subtilis 1423 -11528576 7500965079 pta phosphotransacetylase (db:genpept-bct1) (ec:2.3.1.8) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-88d, ywfj) (le:65754) (re:66725) (di:complement) BSUB0020 Z99123 g2636302 Bacillus subtilis 1423 -11528576 92120 pta_bacsu (de:probable phosphate acetyltransferase (ec 2.3.1.8) (phosphotransacetylase).) P39646 P39646 Bacillus subtilis 1423 10034154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729468	286	22442	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729474	287	22443	339	112

Description

6500724719 yqip:mmge hypothetical protein:mmge protein (gtcfc:1.8:2.2) (keggfc:14.2) (bsorffc:2.6.1:2.6.2) (db:gtc-bacillus subtilis) mmgE mmgE Bacillus subtilis 1423 -11528577 83911 mmge (de:mmge protein) (db:swissprot) MMGE_BACSU P45859 BACILLUS SUBTILIS 1423 -11528577 7000685855 mmge hypothetical protein mmge (db:pir2.dat) F69658 F69658 Bacillus subtilis 1423 -11528577 216179 yqip (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:210004) (re:211422) (di:direct) BACJH642 D84432 g1303935 Bacillus subtilis 1423 -11528577 7500885692 mmge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqip) (le:112197) (re:113615) (di:complement) BSUB0013 Z99116 g2634847 Bacillus subtilis 1423 -11528577

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729493	288	22444	669	222

Description

6500724720 yqin:mmgc acyl-coa dehydrogenase (gtcfc:1.8:2.2) (ec:1.3.99.-) (keggfc:14.1) (bsorffc:2.6.1:2.6.2) (db:gtc-bacillus subtilis) mmgC mmgC Bacillus subtilis 1423 -11528578 7000692150 mmgc acyl-coa dehydrogenase mmgc (cl:acyl-coa dehydrogenase) (db:pir2.dat) D69658 D69658 Bacillus subtilis 1423 -11528578 216177 yqin (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:207701) (re:208837) (di:direct) BACJH642 D84432 g1303933 Bacillus subtilis 1423 -11528578 7500953846 mmgc acyl-coa dehydrogenase (db:genpept-bct1) (ec:1.3.99.-) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqin) (le:114782) (re:115918) (di:complement) BSUB0013 Z99116 g2634849 Bacillus subtilis 1423 -11528578

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729534	289	22445	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729553	290	22446	411	136

Description

6500724721 3-isopropylmalate dehydratase:small subunit:3-isopropylmalate dehydratase small subunit:isopropylmalate isomerase:alpha-ipm isomerase (gtcfc:1.8:5.2:5.7) (ec:4.2.1.33) (keggfc:5.7) (bsorffc:2.6.2:3.1.5) (db:gtc-bacillus subtilis) leuD leuD Bacillus subtilis 1423 -11528579 4000709083 leud (ec:4.2.1.33) (de:(isopropylmalate isomerase) (alpha-ipm isomerase)) (db:swissprot) LEUD_BACSU P94568 BACILLUS SUBTILIS 1423 -11528579 7000685736 leud 3-isopropylmalate dehydratase small subunit leud (cl:3-isopropylmalate dehydratase small chain) (db:pir2.dat) C69650 C69650 Bacillus subtilis 1423 -11528579 220348 leud 3-isopropylmalate dehydratase small subunit (fn:leucine biosynthesis) (db:genpept-bct1) (ec:4.2.1.33) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:92910) (re:93509) (di:complement) BSUB0015 Z99118 g2635290 Bacillus subtilis 1423 -11528579 304221 leud 3-isopropylmalate dehydratase:small subunit (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:3-isopropylmalate dehydratase, small subunit;) (le:76398) (re:76997) (di:direct) BSZ75208 Z75208 g1770072 Bacillus subtilis 1423 -11528579

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729555	291	22447	840	280

Description

6500724722 3-isopropylmalate dehydratase:large subunit (gtcfc:1.8:5.2:5.7) (ec:4.2.1.33) (keggfc:5.7) (bsorffc:2.6.2:3.1.5) (db:gtc-bacillus subtilis) leuC leuC Bacillus subtilis 1423 -11528580 1500685812 leuc (ec:4.2.1.33) (de:(superoxide-inducible protein 10) (soi10)) (db:swissprot) LEU2_BACSU P80858 BACILLUS SUBTILIS 1423 -11528580 7000685733 leuc 3-isopropylmalate dehydratase:large chain (ec:4.2.1.33) (db:pir2.dat) B69650 B69650 Bacillus subtilis 1423 -11528580 220347 leuc 3-isopropylmalate dehydratase large subunit (fn:leucine biosynthesis) (db:genpept-bct1) (ec:4.2.1.33) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:93522) (re:94940) (di:complement) BSUB0015 Z99118 g2635291 Bacillus subtilis 1423 -11528580 304220 leuc 3-isopropylmalate dehydratase:large subunit (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:3-isopropylmalate dehydratase large subunit;) (le:74967) (re:76385) (di:direct) BSZ75208 Z75208 g1770071 Bacillus subtilis 1423 -11528580

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729597	292	22448	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729601	293	22449	600	200

Description

6500724723 long chain acyl-coa synthetase:long-chain-fatty-acid--coa ligase:long-chain acyl-coa synthetase (gtcfc:1.8:3.2) (ec:6.2.1.3) (keggfc:3.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) lcfA lcfA Bacillus subtilis 1423 -11528581 5500685495 lcfa (ec:6.2.1.3) (de:synthetase)) (db:swissprot) LCFA_BACSU P94547 BACILLUS SUBTILIS 1423 -11528581 7000685713 lcfa long chain acyl-coa synthetase lcfa (cl:acetate--coa ligase homology) (db:pir2.dat) D69649 D69649 Bacillus subtilis 1423 -11528581 220314 lcfa long chain acyl-coa synthetase (fn:fatty acid metabolism) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:122618) (re:124300) (di:complement) BSUB0015 Z99118 g2635321 Bacillus subtilis 1423 -11528581 304187 lcfa long chain acyl-coenzyme synthetase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:shows homology with lcfa of escherichia coli;) (le:45607) (re:47289) (di:direct) BSZ75208 Z75208 g1770038 Bacillus subtilis 1423 -11528581

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729610	294	22450	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729645	295	22451	429	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729656	296	22452	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729674	297	22453	366	122

Description

5000688475 acetoin dehydrogenase:acetoin utilization acua protein (gtcfc:1.8) (keggfc:14.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acuA acuA Bacillus subtilis 1423 -11528582 58557 acua (de:acetoin utilization acua protein) (db:swissprot) ACUA_BACSU P39065 BACILLUS SUBTILIS 1423 -11528582 7000684517 acua acetoin utilization protein acua (db:pir2.dat) S39645 S39645 Bacillus subtilis 1423 -11528582 7500876530 acua acetoin catabolism protein acua (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:138398) (re:139030) (di:complement) AF008220 AF008220 g2293318 Bacillus subtilis 1423 -11528582 215124 acua acetoin utilization protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis homologues of mota and motb genes acetoinutilization operon genes acua, acub and acuc, and acetyl-coasynthase (acsa) genes, complete cds.) (nt:putative) (le:3409) (re:4041... BACACUCBA L17309 g348052 Bacillus subtilis 1423 -11528582 4000706891 acua acetoin dehydrogenase (fn:acetoin utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:41397) (re:42029) (di:direct) BSUB0016 Z99119 g2635453 Bacillus subtilis 1423 -11528582 169846 acua acetoin utilization protein acua (db:pir) S39645 S39645 Bacillus subtilis 1423 -11528582 6500724724 acetoin dehydrogenase:acetoin utilization acua protein (gtcfc:1.8) (keggfc:14.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acuA acuA Bacillus subtilis 1423 -11528582

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729680	298	22454	246	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729712	299	22455	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729760	300	22456	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729762	301	22457	261	86

Description

5000688476 acetoin dehydrogenase:acetoin utilization acub protein (gtcfc:1.8) (keggfc:14.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acuB acuB Bacillus subtilis 1423 -11528583 58558 acub (de:acetoin utilization acub protein) (db:swissprot) ACUB_BACSU P39066 BACILLUS SUBTILIS 1423 -11528583 7000684518 acub acetoin utilization protein acub (db:pir2.dat) S39644 S39644 Bacillus subtilis 1423 -11528583 7500876531 acub acetoin catabolism protein acub (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:137727) (re:138371) (di:complement) AF008220 AF008220 g2293317 Bacillus subtilis 1423 -11528583 215123 acub acetoin utilization protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis homologues of mota and motb genes acetoinutilization operon genes acua, acub and acuc, and acetyl-coasynthase (acsa) genes, complete cds.) (nt:putative) (le:2738) (re:3382... BACACUCBA L17309 g348051 Bacillus subtilis 1423 -11528583 4000706892 acub acetoin dehydrogenase (fn:acetoin utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:42056) (re:42700) (di:direct) BSUB0016 Z99119 g2635454 Bacillus subtilis 1423 -11528583 169847 acub acetoin utilization protein acub (db:pir) S39644 S39644 Bacillus subtilis 1423 -11528583 6500724725 acetoin dehydrogenase:acetoin utilization acub protein (gtcfc:1.8) (keggfc:14.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acuB acuB Bacillus subtilis 1423 -11528583

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729815	302	22458	426	141

Description

5000688477 acetoin dehydrogenase:acetoin utilization acuc protein (gtcfc:1.8) (keggfc:14.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acuC acuC Bacillus subtilis 1423 -11528584 58559 acuc (de:acetoin utilization acuc protein) (db:swissprot) ACUC_BACSU P39067 BACILLUS SUBTILIS 1423 -11528584 7000684519 acuc acetate / acetoin utilization protein acuc (cl:acetate utilization protein acuc:rpd3/acuc homology) (db:pir2.dat) S39643 S39643 Bacillus subtilis 1423 -11528584 7500876532 acuc acetoin catabolism protein acuc (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:136567) (re:137730) (di:complement) AF008220 AF008220 g2293316 Bacillus subtilis 1423 -11528584 215122 acuc acetoin utilization protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis homologues of mota and motb genes acetoinutilization operon genes acua, acub and acuc, and acetyl-coasynthase (acsa) genes, complete cds.) (nt:putative) (le:1578) (re:2741... BACACUCBA L17309 g348050 Bacillus subtilis 1423 -11528584 4000706893 acuc acetoin dehydrogenase (fn:acetoin utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:42697) (re:43860) (di:direct) BSUB0016 Z99119 g2635455 Bacillus subtilis 1423 -11528584 154908 acuc acetate / acetoin utilization protein acuc (cl:acetate utilization protein acuc:rpd3/acuc homology) (db:pir) S39643 S39643 Bacillus subtilis 1423 -11528584 6500724726 acetoin dehydrogenase:acetoin utilization acuc protein (gtcfc:1.8) (keggfc:14.2) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acuC acuC Bacillus subtilis 1423 -11528584

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729817	303	22459	843	281

Description

6500724727 acd:acda acyl-coa dehydrogenase (gtcfc:1.8) (ec:1.3.99.-) (keggfc:14.1) (bsorffc:2.6.2) (db:gtc-bacillus subtilis) acdA acdA Bacillus subtilis 1423 -11528585 304109 acda:acd (ec:1.3.99.-) (de:acyl-coa dehydrogenase,) (db:swissprot) ACDA_BACSU P45867 BACILLUS SUBTILIS 1423 -11528585 7000684491 acda acyl-coa dehydrogenase:acda (cl:acyl-coa dehydrogenase) (ec:1.3.99.3) (db:pir2.dat) S55421 S55421 Bacillus subtilis 1423 -11528585 7500876301 acd acyl-coa dehydrogenase (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:7395) (re:8534) (di:direct) BSDNA320D Z49782 g853760 Bacillus subtilis 1423 -11528585 7502851505 acda acyl-coa dehydrogenase (db:genpept-bct1) (ec:1.3.99.-) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:13899) (re:15038) (di:complement) BSUB0020 Z99123 g2636254 Bacillus subtilis 1423 -11528585 58025 acda:acd (ec:1.3.99.-) (de:acyl-coa dehydrogenase,) (db:swissprot) ACDA_BACSU P45867 BACILLUS SUBTILIS 1423 -11528585 169848 acda acyl-coa dehydrogenase:acda (cl:acyl-coa dehydrogenase) (ec:1.3.99.3) (db:pir) S55421 S55421 Bacillus subtilis 1423 -11528585 219137 acd acyl-coa dehydrogenase (db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:7395) (re:8534) (di:direct) BSDNA320D Z49782 g853760 Bacillus subtilis 1423 -11528585

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729838	304	22460	204	67

Description

6500724728 hypothetical protein:similar to ribulose-bisphosphate carboxylase (gtcfc:1.9:2.4:14.1) (ec:4.1.1.39) (keggfc:1.9:2.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrW ykrW Bacillus subtilis 1423 -11528586 7000694548 ykrw ribulose-bisphosphate carboxylase homolog ykrw (cl:ribulose-bisphosphate carboxylase large chain) (db:pir2.dat) G69863 G69863 Bacillus subtilis 1423 -11528586 7500965162 ykrw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to ribulose-bisphosphate carboxylase) (le:31710) (re:32954) (di:direct) BSUB0008 Z99111 g2633730 Bacillus subtilis 1423 -11528586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729839	305	22461	1038	345

Description

6500724729 hypothetical protein:similar to formylmethionine deformylase (gtcfc:1.9:5.4:10.6:14.1) (ec:3.5.1.31) (keggfc:1.9:5.4:10.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrB ykrB Bacillus subtilis 1423 -11528587 7000693004 ykrb formylmethionine deformylase homolog ykrb (cl:polypeptide deformylase) (db:pir2.dat) D69862 D69862 Bacillus subtilis 1423 -11528587 7500955891 ykrb unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to polypeptide deformylase from mycoplasma) (le:31298) (re:31852) (di:complement) AF012285 AF012285 g3282140 Bacillus subtilis 1423 -11528587 220079 ykrb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to formylmethionine deformylase) (le:130810) (re:131364) (di:complement) BSUB0008 Z99111 g2633827 Bacillus subtilis 1423 -11528587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729865	306	22462	234	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729871	307	22463	756	252

Description

6500724730 ylok:def polypeptide deformylase:pdf:formylmethionine deformylase (gtcfc:1.9:5.4:10.6:10.7) (ec:3.5.1.31) (keggfc:1.9:5.4:10.1) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) def def Bacillus subtilis 1423 -11528588 5500685085 def (ec:3.5.1.31) (de:deformylase)) (db:swissprot) DEF_BACSU P94462 BACILLUS SUBTILIS 1423 -11528588 7000685001 def polypeptide deformylase def (cl:polypeptide deformylase) (db:pir2.dat) F69613 F69613 Bacillus subtilis 1423 -11528588 219546 def polypeptide deformylase (db:genpept-bct1) (de:b.subtilis pria, def, fmt, sun genes.) (le:1762) (re:2244) (di:direct) BSPRIADFS Y10304 g1772499 Bacillus subtilis 1423 -11528588 306307 def polypeptide deformylase (db:genpept-bct1) (ec:3.5.1.31) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylok) (le:47491) (re:47973) (di:direct) BSUB0009 Z99112 g2633944 Bacillus subtilis 1423 -11528588 7502851506 ylok putative def protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:9263) (re:9745) (di:direct) BSY13937 Y13937 g2337801 Bacillus subtilis 1423 -11528588 4000709503 def (ec:3.5.1.31) (de:deformylase)) (db:swissprot) DEF_BACSU P94462 BACILLUS SUBTILIS 1423 -11528588

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729875	308	22464	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729877	309	22465	426	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729878	310	22466	408	136

Description

6500724731 hypothetical protein:similar to phosphoglycolate phosphatase (gtcfc:1.9:14.1) (ec:3.1.3.18) (keggfc:1.9) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvoE yvoE Bacillus subtilis 1423 -11528589 7000694415 yvoe phosphoglycolate phosphatase homolog yvoe (db:pir2.dat) G70044 G70044 Bacillus subtilis 1423 -11528589 5500701766 yvoe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to phosphoglycolate phosphatase) (le:191320) (re:191970) (di:complement) BSUB0018 Z99121 g2636010 Bacillus subtilis 1423 -11528589 7500965073 ptsl hpr ser-p phosphatase (fn:central role in the catabolite repression) (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:similar to ralstonia eutropha phosphoglycolate) (le:35863) (re:36513) (di:direct) AF017113 AF017113 g2618860 Bacillus subtilis 1423 -11528589

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729905	311	22467	543	180

Description

6500724732 ybxe:ndhf nadh dehydrogenase:subunit 5:nadh dehydrogenase subunit 5:nadh-ubiquinone oxidoreductase chain 5 (gtcfc:9.12:2.1:2.6:2.8) (ec:1.6.5.3) (keggfc:2.1:9.13) (bsorffc:2.5.1:2.5.2) (db:gtc-bacillus subtilis) ndhF ndhF Bacillus subtilis 1423 -11528590 85462 ndhf (ec:1.6.5.3) (de:oxidoreductase chain 5)) (db:swissprot) NDHF_BACSU P39755 BACILLUS SUBTILIS 1423 -11528590 7000685950 ndhf nadh dehydrogenase subunit 5 ndhf (db:pir2.dat) C69666 C69666 Bacillus subtilis 1423 -11528590 219901 ndhf nadh dehydrogenase subunit 5 (db:genpept-bct1) (de:bacillus subtilis nadh dehydrogenase subunit 5 (ndhf) gene,complete cds.) (le:519) (re:2036) (di:direct) BSU28323 U28323 g903587 Bacillus subtilis 1423 -11528590 6000684935 ndhf nadh dehydrogenase subunit 5 (db:genpept-bct1) (ec:1.6.5.3) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybxe) (le:205395) (re:206912) (di:direct) BSUB0001 Z99104 g2632450 Bacillus subtilis 1423 -11528590 7500886365 ndhf nadh dehydrogenase subunit 5 (db:genpept-bct1) (ec:1.6.5.3) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ybxe) (le:10745) (re:12262) (di:direct) BSUB0002 Z99105 g2632468 Bacillus subtilis 1423 -11528590 7500886366 ndhf nadh dehydrogenase subunit 5 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:8378) (re:9895) (di:direct) AB006424 AB006424 g3599601 Bacillus subtilis 1423 -11528590 5000688562 (de:(ndhf) (pn:nadh dehydrogenase subunit 5:nadh dehydrogenase subunit 5 :nadh-ubiquinone oxidoreductase chain 5) (gtcfc:9.12) (ec:1.6.5.3) (ndhf_bacsu) (keggfc:2.1:9.13) (bsorffc:2.5.0) (db:gtc-bacillus subtilis)) ndhF ndhF Bacillus subtilis 1423 10027639

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729906	312	22468	468	155

Description

6500724733 cytochrome caa3 oxidase:subunit ii:cytochrome c oxidase polypeptide ii precursor:cytochrome aa3 subunit 2:caa-3605 subunit 2:oxidase aa:3 subunit 2 (gtcfc:2.1:2.8) (ec:1.9.3.1) (keggfc:2.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) ctaC ctaC Bacillus subtilis 1423 -11528591 5500687749 ctac cytochrome c oxidase subunit ii:aa3 type (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:5598) (re:6668) (di:direct) BS16823KB Z98682 g2339992 Bacillus subtilis 1423 -11528591 7500953910 ctac cytochrome caa3 oxidase subunit ii (db:genpept-bct1) (ec:1.9.3.1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:165081) (re:166151) (di:direct) BSUB0008 Z99111 g2633860 Bacillus subtilis 1423 -11528591 7000692896 ctac cytochrome caa3 oxidase subunit ii ctac (cl:cytochrome-c oxidase chain ii:cytochrome-c oxidase chain ii homology) (db:pir) D69609 D69609 Bacillus subtilis 1423 -11528591

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729908	313	22469	657	218

Description

6500724734 cytochrome caa3 oxidase:subunit i:cytochrome c oxidase polypeptide i:cytochrome aa3 subunit 1:caa-3605 subunit 1 (gtcfc:2.1:2.8) (ec:1.9.3.1) (keggfc:2.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) ctaD ctaD Bacillus subtilis 1423 -11528592 7000692895 ctad cytochrome-c oxidase:chain i:caa3-605 cytochtrome-c oxidase chain i:cytochrome-aa3 chain i (cl:cytochrome-c oxidase chain i:cytochrome-c oxidase chain i homology) (ec:1.9.3.1) (db:pir2.dat) E69609 E69609 Bacillus subtilis 1423 -11528592 5500687750 ctad cytochrome c oxidase subunit i:aa3 type (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:6701) (re:8569) (di:direct) BS16823KB Z98682 g2339993 Bacillus subtilis 1423 -11528592 7500953905 ctad cytochrome caa3 oxidase subunit i (db:genpept-bct1) (ec:1.9.3.1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:166184) (re:168052) (di:direct) BSUB0008 Z99111 g2633861 Bacillus subtilis 1423 -11528592

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729909	314	22470	351	116

Description

6500724735 cytochrome caa3 oxidase:subunit iii:cytochrome c oxidase polypeptide iii:cytochrome aa3 subunit 3:caa-3605 subunit 3 (gtcfc:2.1:2.8) (ec:1.9.3.1) (keggfc:2.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) ctaE ctaE Bacillus subtilis 1423 -11528593 7000692897 ctae cytochrome-c oxidase:chain iii:cytochrome caa3 oxidase subunit iii ctae (cl:cytochrome-c oxidase chain iii) (ec:1.9.3.1) (db:pir2.dat) F69609 F69609 Bacillus subtilis 1423 -11528593 5500687751 ctae cytochrome c oxidase subunit iii:aa3 type (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:8569) (re:9192) (di:direct) BS16823KB Z98682 g2339994 Bacillus subtilis 1423 -11528593 7500953915 ctae cytochrome caa3 oxidase subunit iii (db:genpept-bct1) (ec:1.9.3.1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:168052) (re:168675) (di:direct) BSUB0008 Z99111 g2633862 Bacillus subtilis 1423 -11528593

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729910	315	22471	528	175

Description

6500724736 cytochrome caa3 oxidase:subunit iv:cytochrome c oxidase polypeptide ivb:cytochrome aa3 subunit 4b:caa-3605 subunit 4b (gtcfc:2.1:2.8) (ec:1.9.3.1) (keggfc:2.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) ctaF ctaF Bacillus subtilis 1423 -11528594 304095 ctaf (ec:1.9.3.1) (de:subunit 4b) (caa-3605 subunit 4b)) (db:swissprot) COX4_BACSU P24013 BACILLUS SUBTILIS 1423 -11528594 169947 ctaf cytochrome-c oxidase:chain ivb:cytochrome caa3 oxidase subunit iv ctaf (cl:cytochrome-c oxidase chain ivb) (ec:1.9.3.1) (db:pir2.dat) G69609 G69609 Bacillus subtilis 1423 -11528594 219112 ctaf cytochrome c oxidase subunit iv:aa3 type (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:9195) (re:9527) (di:direct) BS16823KB Z98682 g2339995 Bacillus subtilis 1423 -11528594 5500684516 ctaf cytochrome-c oxidase subunit ivb (db:genpept-bct1) (ec:1.9.3.1) (de:b. subtilis ctab-f genes for cytochrome a assembly factor andcytochrome-c oxidase (ec 1.9.3.1) subunits ii, i, ii, and ivb.) (le:5159) (re:5491) (di:direct) BSCTABF X54140 g39872 Bacillus subtilis 1423 -11528594 7502851507 ctaf cytochrome caa3 oxidase subunit iv (db:genpept-bct1) (ec:1.9.3.1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:168678) (re:169010) (di:direct) BSUB0008 Z99111 g2633863 Bacillus subtilis 1423 -11528594 65856 ctaf (ec:1.9.3.1) (de:subunit 4b) (caa-3605 subunit 4b)) (db:swissprot) COX4_BACSU P24013 BACILLUS SUBTILIS 1423 -11528594 7000684887 ctaf cytochrome-c oxidase:chain ivb (ec:1.9.3.1) (db:pir) S14399 S14399 Bacillus subtilis 1423 -11528594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729944	316	22472	666	222

Description

6500724737 flagellar-specific atp synthase:flagellum-specific atp synthase (gtcfc:2.1:12.9) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliI fliI Bacillus subtilis 1423 -11528595 215596 flii (ec:3.6.1.34) (de:flagellum-specific atp synthase,) (db:swissprot) FLII_BACSU P23445 BACILLUS SUBTILIS 1423 -11528595 125135 flii h+-transporting atp synthase:alpha chain flii:flagellar-specific::flii protein homolog (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir1.dat) PWBSAS D42365 Bacillus subtilis 1423 -11528595 7500881596 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 4) (le:2311) (re:3633) (di:direct) BACFLAAOA M72718 g142899 Bacillus subtilis 1423 -11528595 219197 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 4) (le:2311) (re:3633) (di:direct) BSFLAAO X56049 g580859 Bacillus subtilis 1423 -11528595 7502851508 flii flagellar-specific atp synthase (fn:flagellar synthesis) (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:96845) (re:98167) (di:direct) BSUB0009 Z99112 g2633996 Bacillus subtilis 1423 -11528595 7502851509 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 4) (le:2311) (re:3633) (di:direct) BSFLAAO X56049 g580859 Bacillus subtilis 1423 -11528595 71994 flii (ec:3.6.1.34) (de:flagellum-specific atp synthase,) (db:swissprot) FLII_BACSU P23445 BACILLUS SUBTILIS 1423 -11528595 7000685289 flii h+-transporting atp synthase:alpha chain flii:flagellar-specific::flii protein homolog (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir) PWBSAS E69624 Bacillus subtilis 1423 -11528595

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729949	317	22473	507	168

Description

6500724738 bfca:petc:qcra menaquinol:cytochrome c oxidoreductase:iron-sulfur subunit:menaquinol-cytochrome c reductase iron-sulfur subunit:rieske iron-sulfur protein (gtcfc:2.1:9.12) (ec:1.10.2.2) (keggfc:2.1) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) qcrA qcrA Bacillus subtilis 1423 -11528596 92701 qcra:bfca (de:sulfur protein)) (db:swissprot) QCRA_BACSU P46911 BACILLUS SUBTILIS 1423 -11528596 7000686256 qcra menaquinol:cytochrome c oxidoreductase iron-sulfur subunit qcra (db:pir2.dat) B69687 B69687 Bacillus subtilis 1423 -11528596 217149 qcra rieske iron-sulfur protein (fn:menaquinone oxidase) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:... BACYPIA L47709 g1146227 Bacillus subtilis 1423 -11528596 219875 qcra rieske iron-sulfur protein (db:genpept-bct1) (de:bacillus subtilis menaquinol:cytochrome c reductase complex (qcr),rieske iron-sulfur protein (qcra), cytochrome b (qcrb), cytochromec (qcrc) genes, complete cds.) (nt:qcra) (le:394) (re:897) (di:direct) BSU25535 U25535 g942581 Bacillus subtilis 1423 -11528596 7500889201 qcra menaquinol:cytochrome c oxidoreductase (fn:menaquinone oxidase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: bfca, petc) (le:168290) (re:168793) (di:complement) BSUB0012 Z99115 g2634674 Bacillus subtilis 1423 -11528596 5000689099 (de:(qcra) (pn:menaquinol-cytochrome c reductase iron-sulfur subunit:rieske iron-sulfur protein) (gn:bfca) (gtcfc:13.07) (ec:) (qcra_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) qcrA qcrA Bacillus subtilis 1423 10034729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729982	318	22474	798	265

Description

6500724739 hypothetical protein:similar to formate dehydrogenase (gtcfc:2.1:9.12:14.1) (ec:1.6.5.3) (keggfc:2.1:9.13) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrhE yrhE Bacillus subtilis 1423 -11528597 7000693002 yrhe formate dehydrogenase homolog yrhe (db:pir2.dat) D69974 D69974 Bacillus subtilis 1423 -11528597 7500963993 yrhe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to formate dehydrogenase) (le:181029) (re:183971) (di:direct) BSUB0014 Z99117 g2635168 Bacillus subtilis 1423 -11528597

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501729999	319	22475	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730009	320	22476	255	84

Description

6500724740 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:2.1:9.12:14.1) (ec:1.6.5.3) (keggfc:2.1:9.13) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yteU yteU Bacillus subtilis 1423 -11528598 7000692749 yteu conserved hypothetical protein yteu (cl:bacillus subtilis conserved hypothetical protein yusy) (db:pir2.dat) D69991 D69991 Bacillus subtilis 1423 -11528598 4000714190 yteu yteu (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to nadh dehydrogenases) (le:99805) (re:100473) (di:direct) AF008220 AF008220 g2293197 Bacillus subtilis 1423 -11528598 7500963824 yteu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to hypothetical proteins from b. subtilis) (le:79953) (re:80621) (di:complement) BSUB0016 Z99119 g2635493 Bacillus subtilis 1423 -11528598

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730036	321	22477	192	63

Description

6500724741 hypothetical protein:similar to nadh dehydrogenase (gtcfc:2.1:9.12:14.1) (ec:1.6.5.3) (keggfc:2.1:9.13) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yufT yufT Bacillus subtilis 1423 -11528599 7000694305 yuft nadh dehydrogenase homolog yuft (db:pir2.dat) A70010 A70010 Bacillus subtilis 1423 -11528599 1500693705 yuft (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to nadh dehydrogenase) (le:48758) (re:51082) (di:direct) BSUB0017 Z99120 g2635656 Bacillus subtilis 1423 -11528599 7500965011 yuft unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufk to yufv.) (nt:potential na/h antiporter/phaa homologue/nadh) (le:10546) (re:12870) (di:direct) BSZ93937 Z93937 g1934817 Bacillus subtilis 1423 -11528599

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730040	322	22478	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730061	323	22479	954	318

Description

6500724742 atp synthase:subunit epsilon:atp synthase epsilon chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpC atpC Bacillus subtilis 1423 -11528600 7500877521 atpc (ec:3.6.1.34) (de:atp synthase epsilon chain,) (db:swissprot) ATPE_BACSU P37812 BACILLUS SUBTILIS 1423 -11528600 7000684674 atpc h+-transporting atp synthase:epsilon chain atpc (cl:h+-transporting atp synthase epsilon chain) (ec:3.6.1.34) (db:pir2.dat) I40369 I40369 Bacillus subtilis 1423 -11528600 219022 atpc atp synthase subunit epsilon (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:6965) (re:7363) (di:direct) BSATPASE Z28592 g433992 Bacillus subtilis 1423 -11528600 7502851510 atpc atp synthase subunit epsilon (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:183034) (re:183432) (di:complement) BSUB0019 Z99122 g2636205 Bacillus subtilis 1423 -11528600 60968 atpc (ec:3.6.1.34) (de:atp synthase epsilon chain,) (db:swissprot) ATPE_BACSU P37812 BACILLUS SUBTILIS 1423 -11528600 141146 atpc h+-transporting atp synthase:epsilon chain atpc (cl:h+-transporting atp synthase epsilon chain) (ec:3.6.1.34) (db:pir) I40369 I40369 Bacillus subtilis 1423 -11528600

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730062	324	22480	540	179

Description

GTC ORF with score 133 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid c04a11, complete sequence.) (nt:predicted using genefinder; similarity to protein) (le:20207:20332:20820:21149) (re:20281:20577:21091:21782) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730089	325	22481	777	258

Description

6500724743 atp synthase:subunit beta:atp synthase beta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpD atpD Bacillus subtilis 1423 -11528601 7500877476 atpd (ec:3.6.1.34) (de:(veg31)) (db:swissprot) ATPB_BACSU P37809 BACILLUS SUBTILIS 1423 -11528601 7000684669 atpd h+-transporting atp synthase:beta chain atpd (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir2.dat) I40368 I40368 Bacillus subtilis 1423 -11528601 219021 atpd atp synthase subunit beta (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:5520) (re:6941) (di:direct) BSATPASE Z28592 g433991 Bacillus subtilis 1423 -11528601 7502851511 atpd atp synthase subunit beta (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:183456) (re:184877) (di:complement) BSUB0019 Z99122 g2636206 Bacillus subtilis 1423 -11528601 60852 atpd (ec:3.6.1.34) (de:(veg31)) (db:swissprot) ATPB_BACSU P37809 BACILLUS SUBTILIS 1423 -11528601 141075 atpd h+-transporting atp synthase:beta chain atpd (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir) I40368 I40368 Bacillus subtilis 1423 -11528601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730104	326	22482	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730135	327	22483	531	177

Description

6500724744 atp synthase:subunit gamma:atp synthase gamma chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpG atpG Bacillus subtilis 1423 -11528602 7000692244 atpg h+-transporting atp synthase:gamma chain:atp synthase subunit gamma (cl:h+-transporting atp synthase gamma chain) (ec:3.6.1.34) (db:pir2.dat) C69592 C69592 Bacillus subtilis 1423 -11528602 7500954338 atpg atp synthase subunit gamma (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:184903) (re:185766) (di:complement) BSUB0019 Z99122 g2636207 Bacillus subtilis 1423 -11528602

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730137	328	22484	291	96

Description

6500724745 atp synthase:subunit alpha:atp synthase alpha chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpA atpA Bacillus subtilis 1423 -11528603 7000684666 atpa h+-transporting atp synthase:alpha chain (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir2.dat) I40366 I40366 Bacillus subtilis 1423 -11528603 219019 atpa atp synthase subunit alpha (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:3046) (re:4554) (di:direct) BSATPASE Z28592 g580831 Bacillus subtilis 1423 -11528603 7500954332 atpa atp synthase subunit alpha (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:185843) (re:187351) (di:complement) BSUB0019 Z99122 g2636208 Bacillus subtilis 1423 -11528603 60794 atpa_bacsu (de:atp synthase alpha chain (ec 3.6.1.34).) P37808 P37808 Bacillus subtilis 1423 10003514

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730145	329	22485	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730146	330	22486	534	177

Description

6500724746 atp synthase:subunit delta:atp synthase delta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpH atpH Bacillus subtilis 1423 -11528604 7500877513 atph (ec:3.6.1.34) (de:atp synthase delta chain,) (db:swissprot) ATPD_BACSU P37811 BACILLUS SUBTILIS 1423 -11528604 7000684671 atph h+-transporting atp synthase:delta chain atph (cl:h+-transporting atp synthase delta chain) (ec:3.6.1.34) (db:pir2.dat) I40365 I40365 Bacillus subtilis 1423 -11528604 219018 atph atp synthase subunit delta (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:2484) (re:3029) (di:direct) BSATPASE Z28592 g433988 Bacillus subtilis 1423 -11528604 7502851512 atph atp synthase subunit delta (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:187368) (re:187913) (di:complement) BSUB0019 Z99122 g2636209 Bacillus subtilis 1423 -11528604 60929 atph (ec:3.6.1.34) (de:atp synthase delta chain,) (db:swissprot) ATPD_BACSU P37811 BACILLUS SUBTILIS 1423 -11528604 170031 atph h+-transporting atp synthase:delta chain atph (ec:3.6.1.34) (db:pir) I40365 I40365 Bacillus subtilis 1423 -11528604

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730178	331	22487	432	143

Description

6500724747 atp synthase:subunit b:atp synthase b chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpF atpF Bacillus subtilis 1423 -11528605 7500877538 atpf (ec:3.6.1.34) (de:atp synthase b chain,) (db:swissprot) ATPF_BACSU P37814 BACILLUS SUBTILIS 1423 -11528605 7000684676 atpf h+-transporting atp synthase:chain b atpf (cl:h+-transporting atp synthase chain i) (ec:3.6.1.34) (db:pir2.dat) I40364 I40364 Bacillus subtilis 1423 -11528605 219017 atpf atp synthase subunit b (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:1975) (re:2487) (di:direct) BSATPASE Z28592 g433987 Bacillus subtilis 1423 -11528605 7502851513 atpf atp synthase subunit b (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:187910) (re:188422) (di:complement) BSUB0019 Z99122 g2636210 Bacillus subtilis 1423 -11528605 61020 atpf (ec:3.6.1.34) (de:atp synthase b chain,) (db:swissprot) ATPF_BACSU P37814 BACILLUS SUBTILIS 1423 -11528605 141301 atpf h+-transporting atp synthase:chain b atpf (cl:h+-transporting atp synthase chain i) (ec:3.6.1.34) (db:pir) I40364 I40364 Bacillus subtilis 1423 -11528605

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730179	332	22488	255	84

Description

6500724748 atp synthase:subunit c:atp synthase c chain:lipid-binding protein (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpE atpE Bacillus subtilis 1423 -11528606 7500877573 atpe (ec:3.6.1.34) (de:atp synthase c chain, (lipid-binding protein)) (db:swissprot) ATPL_BACSU P37815 BACILLUS SUBTILIS 1423 -11528606 7000684681 atpe h+-transporting atp synthase:chain c atpe (cl:h+-transporting atp synthase lipid-binding protein) (ec:3.6.1.34) (db:pir2.dat) I40363 I40363 Bacillus subtilis 1423 -11528606 219016 atpe atp synthase subunit c (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:1600) (re:1812) (di:direct) BSATPASE Z28592 g433986 Bacillus subtilis 1423 -11528606 7502851514 atpe atp synthase subunit c (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:188585) (re:188797) (di:complement) BSUB0019 Z99122 g2636211 Bacillus subtilis 1423 -11528606 61126 atpe (ec:3.6.1.34) (de:atp synthase c chain, (lipid-binding protein)) (db:swissprot) ATPL_BACSU P37815 BACILLUS SUBTILIS 1423 -11528606 141200 atpe h+-transporting atp synthase:chain c atpe (cl:h+-transporting atp synthase lipid-binding protein) (ec:3.6.1.34) (db:pir) I40363 I40363 Bacillus subtilis 1423 -11528606

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730185	333	22489	606	202

Description

6500724749 atp synthase:subunit a:atp synthase a chain:protein 6 (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpB atpB Bacillus subtilis 1423 -11528607 7500877351 atpb (ec:3.6.1.34) (de:atp synthase a chain, (protein 6)) (db:swissprot) ATP6_BACSU P37813 BACILLUS SUBTILIS 1423 -11528607 7000684663 atpb h+-transporting atp synthase:chain a atpb (cl:h+-transporting atp synthase protein 6) (ec:3.6.1.34) (db:pir2.dat) I40362 I40362 Bacillus subtilis 1423 -11528607 219015 atpb atp synthase subunit a (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:820) (re:1554) (di:direct) BSATPASE Z28592 g580830 Bacillus subtilis 1423 -11528607 7502851515 atpb atp synthase subunit a (db:genpept-bct1) (ec:3.6.1.34) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:188843) (re:189577) (di:complement) BSUB0019 Z99122 g2636212 Bacillus subtilis 1423 -11528607 60653 atpb (ec:3.6.1.34) (de:atp synthase a chain, (protein 6)) (db:swissprot) ATP6_BACSU P37813 BACILLUS SUBTILIS 1423 -11528607 141261 atpb h+-transporting atp synthase:chain a atpb (cl:h+-transporting atp synthase protein 6) (ec:3.6.1.34) (db:pir) I40362 I40362 Bacillus subtilis 1423 -11528607

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730213	334	22490	627	208

Description

6500724750 glycerol-3-phosphate dehydrogenase:aerobic glycerol-3-phosphate dehydrogenase (gtcfc:2.1:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) glpD glpD Bacillus subtilis 1423 -11528608 74018 glpd (ec:1.1.99.5) (de:aerobic glycerol-3-phosphate dehydrogenase,) (db:swissprot) GLPD_BACSU P18158 BACILLUS SUBTILIS 1423 -11528608 7000685414 glpd glycerol-3-phosphate dehydrogenase:glpd (ec:1.1.99.5) (db:pir2.dat) C45868 C45868 Bacillus subtilis 1423 -11528608 7500882491 (sr:b.subtilis (strain w168) dna) (db:genpept-bct1) (de:b.subtilis glycerol kinase (glpk) and glycerol-3-phosphatedehydrogenase (glpd) genes, complete cds.) (nt:glycerol-3-phosphate dehydrogenase (glpd) (ec) (le:2329) (re:3996) (di:direct) BACGLPKD M34393 g142993 Bacillus subtilis 1423 -11528608 215684 glpd glycerol-3-phosphate dehydrogenase (fn:glycerol utilization) (db:genpept-bct1) (ec:1.1.99.5) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:201660) (re:203327) (di:direct) BSUB0005 Z99108 g2633253 Bacillus subtilis 1423 -11528608 4000707098 glpd glycerol-3-phosphate dehydrogenase (fn:glycerol utilization) (db:genpept-bct1) (ec:1.1.99.5) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:4980) (re:6647) (di:direct) BSUB0006 Z99109 g2633265 Bacillus subtilis 1423 -11528608 6000684757 glpd glycerol-3-phosphate dehydrogenase (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:see embl m34393 and swiss prot p18158.) (le:4628) (re:6295) (di:direct) BSY14079 Y14079 g2226138 Bacillus subtilis 1423 -11528608 170022 glpd glycerol-3-phosphate dehydrogenase:glpd (ec:1.1.99.5) (db:pir) C45868 C45868 Bacillus subtilis 1423 -11528608

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730238	335	22491	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730243	336	22492	708	236

Description

6500724751 cytochrome caa3 oxydase assembly factor:probable cytochrome c oxidase assembly factor (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) ctaB ctaB Bacillus subtilis 1423 -11528609 304091 ctab (de:probable cytochrome c oxidase assembly factor) (db:swissprot) COXX_BACSU P24009 BACILLUS SUBTILIS 1423 -11528609 7000684901 ctab cytochrome caa3 oxidase assembly factor ctab (cl:heme o synthase) (db:pir2.dat) C69609 C69609 Bacillus subtilis 1423 -11528609 219108 ctab ctab protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:4441) (re:5358) (di:direct) BS16823KB Z98682 g2339991 Bacillus subtilis 1423 -11528609 5500684518 ctab cytochrome a assembly facto (db:genpept-bct1) (ec:1.9.3.1) (de:b. subtilis ctab-f genes for cytochrome a assembly factor andcytochrome-c oxidase (ec 1.9.3.1) subunits ii, i, ii, and ivb.) (nt:putative) (le:408) (re:1325) (di:direct) BSCTABF X54140 g994794 Bacillus subtilis 1423 -11528609 7502851516 ctab cytochrome caa3 oxydase assembly factor (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:163924) (re:164841) (di:direct) BSUB0008 Z99111 g2633859 Bacillus subtilis 1423 -11528609 65941 ctab (de:probable cytochrome c oxidase assembly factor) (db:swissprot) COXX_BACSU P24009 BACILLUS SUBTILIS 1423 -11528609

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730244	337	22493	366	121

Description

6500724752 ypxc:resc essential protein similar to cytochrome c biogenesis protein:resc protein (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) resC resC Bacillus subtilis 1423 -11528610 93986 resc (de:resc protein) (db:swissprot) RESC_BACSU P35162 BACILLUS SUBTILIS 1423 -11528610 7000686300 resc essential protein similar to cytochrome c biogenesis protein resc (db:pir2.dat) S45558 S45558 Bacillus subtilis 1423 -11528610 7500889643 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx16) (le:20567) (re:21625) (di:direct) BACDIA L09228 g410140 Bacillus subtilis 1423 -11528610 215519 resc essential protein similar to cytochrome c (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypxc) (le:21958) (re:23016) (di:complement) BSUB0013 Z99116 g2634748 Bacillus subtilis 1423 -11528610 170271 resc essential protein similar to cytochrome c biogenesis protein resc (db:pir) S45558 S45558 Bacillus subtilis 1423 -11528610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730281	338	22494	696	231

Description

6500724753 ypxb:resb essential protein similar to cytochrome c biogenesis protein:resb protein (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) resB resB Bacillus subtilis 1423 -11528611 93985 resb (de:resb protein) (db:swissprot) RESB_BACSU P35161 BACILLUS SUBTILIS 1423 -11528611 7000686299 resb essential protein similar to cytochrome c biogenesis protein resb (db:pir2.dat) S45557 S45557 Bacillus subtilis 1423 -11528611 7500889642 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx15) (le:18803) (re:20431) (di:direct) BACDIA L09228 g410139 Bacillus subtilis 1423 -11528611 215518 resb essential protein similar to cytochrome c (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypxb) (le:23152) (re:24780) (di:complement) BSUB0013 Z99116 g2634749 Bacillus subtilis 1423 -11528611 170270 resb essential protein similar to cytochrome c biogenesis protein resb (db:pir) S45557 S45557 Bacillus subtilis 1423 -11528611

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730309	339	22495	615	204

Description

6500724754 ypxa:resa essential protein similar to cytochrome c biogenesis protein:resa protein (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) resA resA Bacillus subtilis 1423 -11528612 93982 resa (de:resa protein) (db:swissprot) RESA_BACSU P35160 BACILLUS SUBTILIS 1423 -11528612 7000686298 resa essential protein similar to cytochrome c biogenesis protein resa (cl:bacillus subtilis thioredoxin related protein ykvv) (db:pir2.dat) S45556 S45556 Bacillus subtilis 1423 -11528612 7500889641 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx14) (le:18261) (re:18806) (di:direct) BACDIA L09228 g410138 Bacillus subtilis 1423 -11528612 215517 resa essential protein similar to cytochrome c (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypxa) (le:24777) (re:25322) (di:complement) BSUB0013 Z99116 g2634750 Bacillus subtilis 1423 -11528612 170269 resa essential protein similar to cytochrome c biogenesis protein resa (db:pir) S45556 S45556 Bacillus subtilis 1423 -11528612

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730312	340	22496	852	283

Description

6500724755 cytochrome c550:cytochrome c-550 (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) cccA cccA Bacillus subtilis 1423 -11528613 62205 ccca (de:cytochrome c-550) (db:swissprot) C550_BACSU P24469 BACILLUS SUBTILIS 1423 -11528613 7000684736 ccca cytochrome c550 ccca (cl:bacillus cytochrome c550 ccca) (db:pir2.dat) A37129 A37129 Bacillus subtilis 1423 -11528613 7500878019 (sr:b.subtilis (strain w168) dna) (db:genpept-bct1) (de:b.subtilis 13 kd cytochrome c-550 (ccca) gene, complete cds.) (nt:cytochrome c-550 (ccca)) (le:542) (re:904) (di:direct) BACCCCA J05569 g142652 Bacillus subtilis 1423 -11528613 215326 ccca (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:119719) (re:120081) (di:direct) BACJH642 D84432 g1303834 Bacillus subtilis 1423 -11528613 216078 ccca cytochrome c550 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:203539) (re:203901) (di:complement) BSUB0013 Z99116 g2634952 Bacillus subtilis 1423 -11528613 169946 ccca cytochrome c550 ccca (cl:bacillus cytochrome c550 ccca) (db:pir) A37129 A37129 Bacillus subtilis 1423 -11528613

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730351	341	22497	738	246

Description

6500724756 yrde:cypa cytochrome p450-like enzyme:cytochrome p450 (gtcfc:2.1:2.8) (ec:1.14.-.-) (keggfc:14.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) cypA cypA Bacillus subtilis 1423 -11528614 5500685023 cypa (ec:1.14.-.-) (de:cytochrome p450,) (db:swissprot) CPXY_BACSU O08469 BACILLUS SUBTILIS 1423 -11528614 7000684904 cypa cytochrome p450-like enzyme cypa (cl:cytochrome p450) (db:pir2.dat) E69611 E69611 Bacillus subtilis 1423 -11528614 500685412 cypa cytochrome p450-like enzyme (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (le:1192) (re:2424) (di:direct) BSCYPAZL Y11043 g1926278 Bacillus subtilis 1423 -11528614 1500689772 yrde hypothetical cytochrome p450 protein yrde (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934647 Bacillus subtilis 1423 -11528614 7500879353 cypa cytochrome p450-like enzyme (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrde) (le:130926) (re:132158) (di:complement) BSUB0014 Z99117 g2635119 Bacillus subtilis 1423 -11528614

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730358	342	22498	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730397	343	22499	747	248

Description

GTC ORF with score 157 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730398	344	22500	468	155

Description

GTC ORF with score 167 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730425	345	22501	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730432	346	22502	1080	359

Description

6500724757 cytochrome p450-like enzyme (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) cypX cypX Bacillus subtilis 1423 -11528615 7000692901 cypx cytochrome p450-like enzyme cypx (db:pir2.dat) F69611 F69611 Bacillus subtilis 1423 -11528615 5500701757 cypx cytochrome p450-like enzyme (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:202098) (re:203315) (di:complement) BSUB0018 Z99121 g2636019 Bacillus subtilis 1423 -11528615 6000689217 cypx cytochrome p450-like enzyme (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:4558) (re:5775) (di:complement) BSUB0019 Z99122 g2636032 Bacillus subtilis 1423 -11528615 7500963925 cypb cypb (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:belongs to the family of p450 heme-thiolate) (le:24518) (re:25735) (di:direct) AF017113 AF017113 g2618851 Bacillus subtilis 1423 -11528615

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730478	347	22503	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730482	348	22504	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730485	349	22505	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730515	350	22506	1275	425

Description

6500724758 cytochrome c551 (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) cccB cccB Bacillus subtilis 1423 -11528616 7000692894 cccb cytochrome c551 cccb (db:pir2.dat) C69597 C69597 Bacillus subtilis 1423 -11528616 5500701740 cccb cytochrome c551 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:27711) (re:28049) (di:complement) BSUB0019 Z99122 g2636053 Bacillus subtilis 1423 -11528616 7500963923 cccb cytochrome c-551 (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:putative lipoprotein) (le:2244) (re:2582) (di:direct) AF017113 AF017113 g2618832 Bacillus subtilis 1423 -11528616

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730527	351	22507	465	154

Description

6500724759 narab:nara hypothetical protein:nara protein (gtcfc:2.1:2.8) (keggfc:14.2) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) narA narA Bacillus subtilis 1423 -11528617 219402 nara:narab (de:nara protein) (db:swissprot) NARA_BACSU P39757 BACILLUS SUBTILIS 1423 -11528617 7000685921 nara molybdopterin precursor biosynthesis nara (cl:haemophilus influenzae molybdenum cofactor biosynthesis protein a) (db:pir2.dat) D69664 D69664 Bacillus subtilis 1423 -11528617 219033 nara moaa-like protein (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:7852) (re:8877) (di:direct) BSATPC Z81356 g1648856 Bacillus subtilis 1423 -11528617 304086 narab unknown (db:genpept-bct1) (de:b.subtilis (168) nara gene.) (le:1294) (re:2319) (di:direct) BSNARAAB Z35277 g516272 Bacillus subtilis 1423 -11528617 7502851517 nara (fn:essential for nitrate assimilation and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: narab) (le:174290) (re:175315) (di:complement) BSUB0019 Z99122 g2636195 Bacillus subtilis 1423 -11528617 85234 nara:narab (de:nara protein) (db:swissprot) NARA_BACSU P39757 BACILLUS SUBTILIS 1423 -11528617

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730563	352	22508	198	65

Description

GTC ORF with score 95 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1412.) (nt:similar to saccharomyces cerevisiae metal) (le:<1) (re:1313) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730654	353	22509	285	94

Description

6500724760 ipa-40d:qoxd cytochrome aa3 quinol oxidase:subunit iv:quinol oxidase polypeptide iv:quinol oxidase aa3-600:subunit qoxd (gtcfc:2.1:2.8) (ec:1.9.3.-) (keggfc:14.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) qoxD qoxD Bacillus subtilis 1423 -11528618 216573 qoxd:ipa-40d (ec:1.9.3.-) (de:subunit qoxd)) (db:swissprot) QOX4_BACSU P34959 BACILLUS SUBTILIS 1423 -11528618 7000686261 qoxd quinol oxidase aa3-600 chain iv qoxd:cytochrome aa3 quinol oxidase subunit iv qoxd (db:pir2.dat) D38129 D38129 Bacillus subtilis 1423 -11528618 7500889210 qoxd quinol oxidase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis aa3-600 quinol oxidase (qoxa, qoxb, qoxc, qoxd)genes, complete cds.) (le:4425) (re:4799) (di:direct) BACQOXA M86548 g143399 Bacillus subtilis 1423 -11528618 219277 ipa-40d::qoxd (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:42877) (re:43251) (di:direct) BSGENR X73124 g413964 Bacillus subtilis 1423 -11528618 7502851518 qoxd cytochrome aa3 quinol oxidase subunit iv (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-40d) (le:114711) (re:115085) (di:complement) BSUB0020 Z99123 g2636349 Bacillus subtilis 1423 -11528618 92720 qoxd:ipa-40d (ec:1.9.3.-) (de:subunit qoxd)) (db:swissprot) QOX4_BACSU P34959 BACILLUS SUBTILIS 1423 -11528618 170475 qoxd quinol oxidase aa3-600 chain iv qoxd:cytochrome aa3 quinol oxidase subunit iv qoxd (db:pir) D38129 D38129 Bacillus subtilis 1423 -11528618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730655	354	22510	480	159

Description

6500724761 ipa-39d:qoxc cytochrome aa3 quinol oxidase:subunit iii:quinol oxidase polypeptide iii:quinol oxidase aa3-600:subunit qoxc (gtcfc:2.1:2.8) (ec:1.9.3.-) (keggfc:14.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) qoxC qoxC Bacillus subtilis 1423 -11528619 216572 qoxc:ipa-39d (ec:1.9.3.-) (de:subunit qoxc)) (db:swissprot) QOX3_BACSU P34958 BACILLUS SUBTILIS 1423 -11528619 7000686260 qoxc bo-type ubiquinol oxidase:chain iii qoxc:cytochrome aa3 quinol oxidase subunit iii qoxc (cl:cytochrome-c oxidase chain iii) (ec:1.10.3.-) (db:pir2.dat) C38129 C38129 Bacillus subtilis 1423 -11528619 7500889209 qoxc quinol oxidase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis aa3-600 quinol oxidase (qoxa, qoxb, qoxc, qoxd)genes, complete cds.) (le:3809) (re:4423) (di:direct) BACQOXA M86548 g143398 Bacillus subtilis 1423 -11528619 219276 ipa-39d::qoxc (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:42261) (re:42875) (di:direct) BSGENR X73124 g413963 Bacillus subtilis 1423 -11528619 7502851519 qoxc cytochrome aa3 quinol oxidase subunit iii (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-39d) (le:115087) (re:115701) (di:complement) BSUB0020 Z99123 g2636350 Bacillus subtilis 1423 -11528619 92719 qoxc:ipa-39d (ec:1.9.3.-) (de:subunit qoxc)) (db:swissprot) QOX3_BACSU P34958 BACILLUS SUBTILIS 1423 -11528619 137196 qoxc quinol oxidase aa3-600 chain iii qoxc:cytochrome aa3 quinol oxidase subunit iii qoxc (cl:cytochrome-c oxidase chain iii) (db:pir) C38129 C38129 Bacillus subtilis 1423 -11528619

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730656	355	22511	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730658	356	22512	483	160

Description

6500724762 ipa-38d:qoxb cytochrome aa3 quinol oxidase:subunit i:quinol oxidase polypeptide i:quinol oxidase aa3-600:subunit qoxb:oxidase aa:3 subunit 1 (gtcfc:2.1:2.8) (ec:1.9.3.-) (keggfc:14.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) qoxB qoxB Bacillus subtilis 1423 -11528620 216571 qoxb:ipa-38d (ec:1.9.3.-) (de:subunit qoxb) (oxidase aa(3) subunit 1)) (db:swissprot) QOX1_BACSU P34956 BACILLUS SUBTILIS 1423 -11528620 7000686259 qoxb bo-type ubiquinol oxidase:chain i:cytochrome aa3 quinol oxidase chain i:quinol oxidase aa3-600 (cl:cytochrome-c oxidase chain i:cytochrome-c oxidase chain i homology) (ec:1.10.3.-) (db:pir2.dat) B38129 B38129 Bacillus subtilis 1423 -11528620 7500889208 qoxb quinol oxidase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis aa3-600 quinol oxidase (qoxa, qoxb, qoxc, qoxd)genes, complete cds.) (le:1846) (re:3795) (di:direct) BACQOXA M86548 g143397 Bacillus subtilis 1423 -11528620 219275 ipa-38d::qoxb (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:40298) (re:42247) (di:direct) BSGENR X73124 g413962 Bacillus subtilis 1423 -11528620 7502851520 qoxb cytochrome aa3 quinol oxidase subunit i (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-38d) (le:115715) (re:117664) (di:complement) BSUB0020 Z99123 g2636351 Bacillus subtilis 1423 -11528620 92714 qoxb:ipa-38d (ec:1.9.3.-) (de:subunit qoxb) (oxidase aa(3) subunit 1)) (db:swissprot) QOX1_BACSU P34956 BACILLUS SUBTILIS 1423 -11528620 137083 qoxb quinol oxidase aa3-600 chain i qoxb:cytochrome aa3 quinol oxidase subunit i qoxb (cl:cytochrome-c oxidase chain i:cytochrome-c oxidase chain i homology) (db:pir) B38129 B38129 Bacillus subtilis 1423 -11528620

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730676	357	22513	282	93

Description

6500724763 ipa-37d:qoxa cytochrome aa3 quinol oxidase:subunit ii:quinol oxidase polypeptide ii precursor:quinol oxidase aa3-600:subunit qoxa:oxidase aa:3 subunit 2 (gtcfc:2.1:2.8) (ec:1.9.3.-) (keggfc:14.1) (bsorffc:2.5.1) (db:gtc-bacillus subtilis) qoxA qoxA Bacillus subtilis 1423 -11528621 7000692890 qoxa cytochrome aa3 quinol oxidase subunit ii qoxa:quinol oxidase aa3-600 chain qoxa (cl:bo-type ubiquinol oxidase chain ii precursor) (db:pir2.dat) E69687 E69687 Bacillus subtilis 1423 -11528621 7500963919 qoxa cytochrome aa3 quinol oxidase subunit ii (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-37d) (le:117692) (re:118657) (di:complement) BSUB0020 Z99123 g2636352 Bacillus subtilis 1423 -11528621

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730716	358	22514	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730743	359	22515	849	282

Description

6500724764 kat-19:kat:kata vegetative catalase 1:vegetative catalase (gtcfc:2.2:5.14:12.12) (ec:1.11.1.6) (keggfc:2.2:5.14) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) katA katA Bacillus subtilis 1423 -11528622 220387 kata vegetative catalase 1 (db:genpept-bct1) (ec:1.11.1.6) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: kat-19) (le:156223) (re:157674) (di:complement) BSUB0005 Z99108 g2633205 Bacillus subtilis 1423 -11528622 7500953923 kata catalase (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:23073) (re:24524) (di:complement) BSZ82044 Z82044 g1673404 Bacillus subtilis 1423 -11528622 7000694900 kata vegetative catalase 1 kata (cl:catalase) (db:pir) C69647 C69647 Bacillus subtilis 1423 -11528622

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730744	360	22516	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730755	361	22517	741	247

Description

5000688536 glyc:ipc-34d:glya serine hydroxymethyltransferase:serine methylase:shmt (gtcfc:2.2:5.3:5.9:6.5:9.3:9.6) (ec:2.1.2.1) (keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) (gtcfc:energy metabolism-methane metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:l-amino acid metabolis... glyA glyA Bacillus subtilis 1423 -11528623 7500882594 glya:glyc:ipc-34d (ec:2.1.2.1) (de:(shmt)) (db:swissprot) GLYA_BACSU P39148 BACILLUS SUBTILIS 1423 -11528623 7000685432 glya:glyc glycine hydroxymethyltransferase:glya:serine hydroxymethyltransferase (cl:glycine hydroxymethyltransferase) (ec:2.1.2.1) (db:pir2.dat) I40483 I40483 Bacillus subtilis 1423 -11528623 219667 glyc serine hydroxymethyltransferase (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:5499) (re:6746) (di:direct) BSSPORUPP Z38002 g556886 Bacillus subtilis 1423 -11528623 6500724765 glya serine hydroxymethyltransferase (fn:glycine/serine/threonine metabolism) (db:genpept-bct1) (ec:2.1.2.1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: glyc, ipc-34d) (le:191155) (re:192402) (di:complement) BSUB0019 Z99122 g2636215 Bacillus subtilis 1423 -11528623 74191 glya:glyc:ipc-34d (ec:2.1.2.1) (de:(shmt)) (db:swissprot) GLYA_BACSU P39148 BACILLUS SUBTILIS 1423 -11528623 137817 glya:glyc glycine hydroxymethyltransferase:glya:serine hydroxymethyltransferase (cl:glycine hydroxymethyltransferase) (ec:2.1.2.1) (db:pir) I40483 I40483 Bacillus subtilis 1423 -11528623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730785	362	22518	456	151

Description

5000688436 kate:n15d:katb catalase 2 (gtcfc:2.2:5.14:12.12) (ec:1.11.1.6) (keggfc:2.2:5.14) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) katB katB Bacillus subtilis 1423 -11528624 62963 katb:kate:n15d (ec:1.11.1.6) (de:catalase 2,) (db:swissprot) CATB_BACSU P42234 BACILLUS SUBTILIS 1423 -11528624 7000684757 katb:kate catalase:katb (cl:catalase) (ec:1.11.1.6) (db:pir2.dat) D69647 D69647 Bacillus subtilis 1423 -11528624 6000684555 katb catalase 2 (db:genpept-bct1) (ec:1.11.1.6) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: kate) (le:208532) (re:210592) (di:complement) BSUB0020 Z99123 g2636440 Bacillus subtilis 1423 -11528624 7500878205 katb catalase 2 (db:genpept-bct1) (ec:1.11.1.6) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: kate) (le:7652) (re:9712) (di:complement) BSUB0021 Z99124 g2636451 Bacillus subtilis 1423 -11528624 6500724766 kate:n15d catalase 2 (gtcfc:2.2:5.14:12.12) (ec:1.11.1.6) (keggfc:2.2:5.14) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) katB katB Bacillus subtilis 1423 -11528624

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730786	363	22519	261	86

Description

6500724767 hypothetical protein:similar to aspartate aminotransferase (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5:14.1) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrV ykrV Bacillus subtilis 1423 -11528625 7000692237 ykrv aspartate aminotransferase homolog ykrv (cl:aspartate transaminase) (db:pir2.dat) F69863 F69863 Bacillus subtilis 1423 -11528625 7500963435 ykrv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to aspartate aminotransferase) (le:30317) (re:31513) (di:direct) BSUB0008 Z99111 g2633729 Bacillus subtilis 1423 -11528625

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730788	364	22520	735	244

Description

6500724768 uat:pata aminotransferase (gtcfc:2.4:5.1:5.10:5.11:5.15:5.2:5.5) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (bsorffc:3.1.6) (db:gtc-bacillus subtilis) patA patA Bacillus subtilis 1423 -11528626 7000692207 pata probable aspartate transaminase (cl:aspartate transaminase) (ec:2.6.1.-) (db:pir2.dat) C69672 C69672 Bacillus subtilis 1423 -11528626 7500963414 pata aminotransferase (db:genpept-bct1) (ec:2.6.1.-) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: uat) (le:76469) (re:77647) (di:complement) BSUB0008 Z99111 g2633771 Bacillus subtilis 1423 -11528626

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730797	365	22521	624	208

Description

6500724769 aspartate aminotransferase:transaminase a:aspat (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) aspB aspB Bacillus subtilis 1423 -11528627 57862 aspb (ec:2.6.1.1) (de:aspartate aminotransferase, (transaminase a) (aspat)) (db:swissprot) AAT1_BACSU P53001 BACILLUS SUBTILIS 1423 -11528627 7000684479 aspb aspartate aminotransferase aspb (cl:aspartate transaminase) (db:pir2.dat) C69591 C69591 Bacillus subtilis 1423 -11528627 217168 aspb aspartate aminotransferase (db:genpept-bct1) (ec:2.6.1.1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (le:19124) (re:2... BACYPIA L47709 g1146246 Bacillus subtilis 1423 -11528627 7500876243 aspb aspartate aminotransferase (db:genpept-bct1) (ec:2.6.1.1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:151362) (re:152543) (di:complement) BSUB0012 Z99115 g2634655 Bacillus subtilis 1423 -11528627 5000688379 (de:(aspb) (pn:aspartate aminotransferase:transaminase a:aspat) (gtcfc:2.04:5.10) (ec:2.6.1.1) (aat1_bacsu) (keggfc:2.3:5.1:5.2:5.5:5.10) (db:gtc-bacillus subtilis)) aspB aspB Bacillus subtilis 1423 10000642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730822	366	22522	546	181

Description

6500724770 hypothetical protein:similar to aspartate aminotransferase (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5:14.1) (ec:2.6.1.1) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yugH yugH Bacillus subtilis 1423 -11528628 7000692238 yugh aspartate aminotransferase homolog yugh (cl:aspartate transaminase) (db:pir2.dat) G70010 G70010 Bacillus subtilis 1423 -11528628 1500693682 yugh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to aspartate aminotransferase) (le:27936) (re:29009) (di:complement) BSUB0017 Z99120 g2635636 Bacillus subtilis 1423 -11528628 7500963436 yugh unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (le:3131) (re:4204) (di:direct) BSZ93934 Z93934 g1934791 Bacillus subtilis 1423 -11528628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730835	367	22523	765	254

Description

6500724771 ipa-85d:ywfg hypothetical protein:probable aspartate aminotransferase:transaminase a:aspat (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) ywfG ywfG Bacillus subtilis 1423 -11528629 7500876244 ywfg:ipa-85d (ec:2.6.1.1) (de:(aspat)) (db:swissprot) AAT2_BACSU P39643 BACILLUS SUBTILIS 1423 -11528629 7000684480 ywfg aspartate aminotransferase homolog ywfg:protein ipa-85d (cl:aspartate transaminase) (db:pir2.dat) S39740 S39740 Bacillus subtilis 1423 -11528629 5000688387 ipa-85d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:88074) (re:89273) (di:direct) BSGENR X73124 g414009 Bacillus subtilis 1423 -11528629 219322 ywfg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-85d; similar to aspartate) (le:68686) (re:69885) (di:complement) BSUB0020 Z99123 g2636305 Bacillus subtilis 1423 -11528629 57865 ywfg:ipa-85d (ec:2.6.1.1) (de:(aspat)) (db:swissprot) AAT2_BACSU P39643 BACILLUS SUBTILIS 1423 -11528629 170163 ywfg aspartate aminotransferase homolog ywfg (db:pir) S39740 S39740 Bacillus subtilis 1423 -11528629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730862	368	22524	189	62

Description

6500724772 spovn:ald l-alanine dehydrogenase:alanine dehydrogenase:stage v sporulation protein n (gtcfc:2.5:5.2) (ec:1.4.1.1) (keggfc:2.4) (bsorffc:2.2.1) (db:gtc-bacillus subtilis) (gtcfc:energy metabolism-reductive carboxylate cycle (co2 fixation):l-amino acid metabolism-alanine and aspartate metabolism) (keggfc:energy metabolism-reductive carbo... ald ald Bacillus subtilis 1423 -11528630 307783 ald:spovn (ec:1.4.1.1) (de:alanine dehydrogenase, (stage v sporulation protein n)) (db:swissprot) DHA_BACSU Q08352 BACILLUS SUBTILIS 1423 -11528630 7000685035 ald alanine dehydrogenase:ald (cl:alanine dehydrogenase:alanine dehydrogenase homology) (ec:1.4.1.1) (db:pir2.dat) A49337 A49337 Bacillus subtilis 1423 -11528630 7500880241 ald alanine dehydrogenase (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis alanine dehydrogenase (ald) gene, complete cds.) (le:230) (re:1366) (di:direct) BACALD L20916 g299163 Bacillus subtilis 1423 -11528630 215141 ald l-alanine dehydrogenase (db:genpept-bct1) (ec:1.4.1.1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: spovn) (le:80380) (re:81516) (di:direct) BSUB0017 Z99120 g2635688 Bacillus subtilis 1423 -11528630 5000688388 ald alanine dehydrogenase (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (nt:also known as spovn) (le:6611) (re:7747) (di:direct) BSZ82015 Z82015 g1665852 Bacillus subtilis 1423 -11528630 68434 ald:spovn (ec:1.4.1.1) (de:alanine dehydrogenase, (stage v sporulation protein n)) (db:swissprot) DHA_BACSU Q08352 BACILLUS SUBTILIS 1423 -11528630 136588 ald alanine dehydrogenase:ald (cl:alanine dehydrogenase:alanine dehydrogenase homology) (ec:1.4.1.1) (db:pir) A49337 A49337 Bacillus subtilis 1423 -11528630 220365 ald alanine dehydrogenase (db:genpept-bct1) (de:b.subtilis yuk(a,b,c,d,e,f), yuk(i,j,k,l,m) and ald genes.) (nt:also known as spovn) (le:6611) (re:7747) (di:direct) BSZ82015 Z82015 g1665852 Bacillus subtilis 1423 -11528630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730870	369	22525	690	229

Description

6500724773 hypothetical protein:similar to asparaginase (gtcfc:2.6:5.2:6.5:14.1) (ec:3.5.1.1) (keggfc:2.5:5.2:6.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yccC yccC Bacillus subtilis 1423 -11528631 7000692233 yccc asparaginase homolog yccc (cl:asparaginase) (db:pir2.dat) F69754 F69754 Bacillus subtilis 1423 -11528631 5500687009 yccc yccc (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable l-asparaginase precursor) (le:4008) (re:5135) (di:direct) AB000617 AB000617 g2415720 Bacillus subtilis 1423 -11528631 7500954313 yccc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to asparaginase) (le:95819) (re:96946) (di:direct) BSUB0002 Z99105 g2632555 Bacillus subtilis 1423 -11528631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730871	370	22526	210	69

Description

5000688404 nird:nasbd:nase subunit:assimilatory nitrite reductase:nad:ph small subunit (gtcfc:2.6) (ec:1.6.6.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nasE nasE Bacillus subtilis 1423 -11528632 85267 nase:nird:nasbd (ec:1.6.6.4) (de:assimilatory nitrite reductase (nad(p)h) small subunit,) (db:swissprot) NASE_BACSU P42436 BACILLUS SUBTILIS 1423 -11528632 7000685936 nase:nird nitrite reductase nadh:nase:assimilatory nitrite reductase nird (ec:1.6.6.4) (db:pir2.dat) I40030 I40030 Bacillus subtilis 1423 -11528632 216383 nasbd subunit of nitrite reductase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around narb region (nasb operon and nasagene).) (le:9295) (re:9615) (di:direct) BACNARB D30689 g710021 Bacillus subtilis 1423 -11528632 222595 nase assimilatory nitrite reductase subunit (db:genpept-bct1) (ec:1.6.6.4) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: nasbd, nird) (le:160334) (re:160654) (di:complement) BSUB0002 Z99105 g2632615 Bacillus subtilis 1423 -11528632 7500886317 nasbd subunit of nitrite reductase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:34637) (re:34957) (di:complement) D50453 D50453 g1805401 Bacillus subtilis 1423 -11528632 6500724774 nird:nasbd subunit:assimilatory nitrite reductase:nad:ph small subunit (gtcfc:2.6) (ec:1.6.6.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nasE nasE Bacillus subtilis 1423 -11528632

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730872	371	22527	192	63

Description

GTC ORF with score 199 to: (sr:human) (db:genpept-pri2) (de:human (c-myb) gene, complete primary cds, and five completealternatively spliced cds.) (nt:alternatively spliced product using exon 13a) (le:2226:6595:8528:10484) (re:2248:6712:8599:10576) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730874	372	22528	246	81

Description

6500724775 nasbc:nirb:nsbc:nasd assimilatory nitrite reductase:subunit:nitrite reductase:nad:ph (gtcfc:2.6) (ec:1.6.6.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nasD nasD Bacillus subtilis 1423 -11528633 85265 nasd:nirb:nasbc (ec:1.6.6.4) (de:nitrite reductase (nad(p)h),) (db:swissprot) NASD_BACSU P42435 BACILLUS SUBTILIS 1423 -11528633 7000685935 nasd:nirb nitrite reductase nadh:nasd:assimilatory nitrite reductase nirb (ec:1.6.6.4) (db:pir2.dat) I40029 I40029 Bacillus subtilis 1423 -11528633 216382 nasbc subunit of nitrite reductase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around narb region (nasb operon and nasagene).) (le:6846) (re:9263) (di:direct) BACNARB D30689 g710020 Bacillus subtilis 1423 -11528633 222596 nasd assimilatory nitrite reductase subunit (db:genpept-bct1) (ec:1.6.6.4) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: nasbc, nirb) (le:160686) (re:163103) (di:complement) BSUB0002 Z99105 g2632616 Bacillus subtilis 1423 -11528633 7500886314 nasbc subunit of nitrite reductase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:34989) (re:37406) (di:complement) D50453 D50453 g1805402 Bacillus subtilis 1423 -11528633 5000688403 (de:(nasd) (pn:nitrite reductase:nad:ph) (gn:nirb:nsbc) (gtcfc:2.06) (ec:1.6.6.4) (nasd_bacsu) (keggfc:2.5) (bsorffc:2.5.0) (db:gtc-bacillus subtilis)) nasD nasD Bacillus subtilis 1423 10027446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730876	373	22529	354	117

Description

6500724776 narb:nasbb:nasc assimilatory nitrate reductase:catalytic subunit (gtcfc:2.6) (ec:1.7.99.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nasC nasC Bacillus subtilis 1423 -11528634 85264 nasc:narb:nasbb (ec:1.7.99.4) (de:assimilatory nitrate reductase catalytic subunit,) (db:swissprot) NASC_BACSU P42434 BACILLUS SUBTILIS 1423 -11528634 7000685934 nasc nitrate reductase:nasc:assimilatory nitrate reductase:nitrate reductase narb (cl:formate dehydrogenase) (ec:1.7.99.4) (db:pir2.dat) E69665 E69665 Bacillus subtilis 1423 -11528634 222597 nasc assimilatory nitrate reductase catalytic (db:genpept-bct1) (ec:1.7.99.4) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: narb, nasbb) (le:163225) (re:165357) (di:complement) BSUB0002 Z99105 g2632617 Bacillus subtilis 1423 -11528634 7500886313 nasbb catalytic subunit of nitrate reductase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:37528) (re:39660) (di:complement) D50453 D50453 g1805403 Bacillus subtilis 1423 -11528634

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730900	374	22530	288	95

Description

6500724777 nasba:nasb assimilatory nitrate reductase:electron transfer subunit:assimilatory nitrate reductase electron transfer subunit (gtcfc:2.6) (ec:1.6.6.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nasB nasB Bacillus subtilis 1423 -11528635 85263 nasb:nasba (de:assimilatory nitrate reductase electron transfer subunit) (db:swissprot) NASB_BACSU P42433 BACILLUS SUBTILIS 1423 -11528635 7000685933 nasb nitrite reductase nadh:nasb:assimilatory nitrate reductase electron transfer chain (ec:1.6.6.4) (db:pir2.dat) I40027 I40027 Bacillus subtilis 1423 -11528635 216380 nasba electolon trasporter subunit of nitrate (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around narb region (nasb operon and nasagene).) (le:2273) (re:4585) (di:direct) BACNARB D30689 g710018 Bacillus subtilis 1423 -11528635 222598 nasb assimilatory nitrate reductase electron (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: nasba) (le:165364) (re:167676) (di:complement) BSUB0002 Z99105 g2632618 Bacillus subtilis 1423 -11528635 7500886312 nasba electron transfer subunit of nitrate reductase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:39667) (re:41979) (di:complement) D50453 D50453 g1805404 Bacillus subtilis 1423 -11528635

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730903	375	22531	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730906	376	22532	192	63

Description

6500724778 glutamine synthetase:glutamate--ammonia ligase (gtcfc:2.6:5.1:11.4) (ec:6.3.1.2) (keggfc:2.5:5.1:7.3) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) glnA glnA Bacillus subtilis 1423 -11528636 125992 glna glutamate--ammonia ligase::glutamine synthetase (cl:glutamate--ammonia ligase) (ec:6.3.1.2) (db:pir1.dat) AJBSQS JT0392 Bacillus subtilis 1423 -11528636 215676 glutamine synthetase (sr:bacillus subtilis (sub_strain jh642/168, strain marburg) dna) (db:genpept-bct1) (ec:6.3.1.2) (de:bacillus subtilis glutamine synthetase (glna) gene, complete cds.) (le:630) (re:1964) (di:direct) BACGLNAZ M22811 g142986 Bacillus subtilis 1423 -11528636 220165 glna glutamine synthetase (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750111 Bacillus subtilis 1423 -11528636 7500953380 glna glutamine synthetase (db:genpept-bct1) (ec:6.3.1.2) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:96469) (re:97803) (di:direct) BSUB0010 Z99113 g2634130 Bacillus subtilis 1423 -11528636

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730912	377	22533	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730922	378	22534	642	214

Description

6500724779 glutamate synthase:small subunit (gtcfc:2.6:5.1) (ec:1.4.1.13) (keggfc:2.5:5.1) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) gltB gltB Bacillus subtilis 1423 -11528637 7000693048 gltb glutamate synthase small subunit gltb (db:pir2.dat) H69634 H69634 Bacillus subtilis 1423 -11528637 6000690964 gltb glutamate synthase small subunit (fn:glutamate biosynthesis) (db:genpept-bct1) (ec:1.4.1.13) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:226628) (re:228109) (di:complement) BSUB0010 Z99113 g2634227 Bacillus subtilis 1423 -11528637 7500964025 gltb glutamate synthase small subunit (fn:glutamate biosynthesis) (db:genpept-bct1) (ec:1.4.1.13) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:7658) (re:9139) (di:complement) BSUB0011 Z99114 g2634238 Bacillus subtilis 1423 -11528637

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730953	379	22535	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730954	380	22536	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730991	381	22537	228	75

Description

6500724780 hypothetical protein:hypothetical 46.7 kd oxidoreductase in recq-cmk intergenic region (gtcfc:2.6:5.1:14.1) (keggfc:2.5:5.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypcA ypcA Bacillus subtilis 1423 -11528638 115527 ypca (ec:1.4.1.-) (de:(ec 1.4.1.-)) (db:swissprot) YPCA_BACSU P50735 BACILLUS SUBTILIS 1423 -11528638 7000688203 ypca glutamate dehydrogenase homolog ypca (cl:glutamate dehydrogenase (nad(p)+)) (db:pir2.dat) G69933 G69933 Bacillus subtilis 1423 -11528638 6000685524 ypca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to glutamate dehydrogenase) (le:205764) (re:207044) (di:complement) BSUB0012 Z99115 g2634714 Bacillus subtilis 1423 -11528638 7500952179 ypca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to glutamate dehydrogenase) (le:6044) (re:7324) (di:complement) BSUB0013 Z99116 g2634731 Bacillus subtilis 1423 -11528638 216712 ypca glutamate dehydrogenase (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146206 Bacillus subtilis 1423 -11528638 7502851521 ypca glutamate dehydrogenase (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146206 Bacillus subtilis 1423 -11528638

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501730994	382	22538	654	217

Description

GTC ORF with score 113 to: (fn:required for t-2 toxin biosynthesis) (db:genpept) (de:fusarium sporotrichioides t-2 toxin biosynthesis proteins (tri8),(tri7); and 15-decalonectrin 15-o-acetyltransferase (tri3) genes,complete cds.) (le:2216:3075) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731021	383	22539	363	120

Description

GTC ORF with score 108 to: (or:Bordetella pertussis) (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf1; similar to eubacterium baif) (le:10149) (re:10967) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731047	384	22540	855	285

Description

6500724781 l-aspartase:aspartate ammonia-lyase:aspartase (gtcfc:2.6:5.2) (ec:4.3.1.1) (keggfc:2.5:5.2) (bsorffc:2.2.1) (db:gtc-bacillus subtilis) ansB ansB Bacillus subtilis 1423 -11528639 60391 ansb (ec:4.3.1.1) (de:aspartate ammonia-lyase, (aspartase)) (db:swissprot) ASPA_BACSU P26899 BACILLUS SUBTILIS 1423 -11528639 125626 ansb:aspa aspartate ammonia-lyase::l-aspartase ansb (cl:fumarate hydratase) (ec:4.3.1.1) (db:pir1.dat) UFBSD B39440 Bacillus subtilis 1423 -11528639 215187 ansb l-aspartase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (ec:4.3.1.1) (de:bacillus subtilis l-asparaginase (ansa) gene, complete cds;l-aspartase (ansb) gene, complete cds.) (le:1379) (re:2806) (di:direct) BACANS M63264 g142518 Bacillus subtilis 1423 -11528639 216232 ansb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:263877) (re:265304) (di:direct) BACJH642 D84432 g1303988 Bacillus subtilis 1423 -11528639 7500877255 ansb l-aspartase (db:genpept-bct1) (ec:4.3.1.1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:58315) (re:59742) (di:complement) BSUB0013 Z99116 g2634792 Bacillus subtilis 1423 -11528639 5000688393 (de:(ansb) (pn:aspartate ammonia-lyase:aspartate ammonia-lyase :aspartase) (gtcfc:2.06) (ec:4.3.1.1) (aspa_bacsu) (keggfc:2.5:5.2) (bsorffc:2.2.0) (db:gtc-bacillus subtilis)) ansB ansB Bacillus subtilis 1423 10003117

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731054	385	22541	687	228

Description

6500724782 l-asparaginase:l-asparagine amidohydrolase (gtcfc:2.6:5.2:6.5) (ec:3.5.1.1) (keggfc:2.5:5.2:6.5) (bsorffc:2.2.1) (db:gtc-bacillus subtilis) ansA ansA Bacillus subtilis 1423 -11528640 60398 ansa (ec:3.5.1.1) (de:l-asparaginase, (l-asparagine amidohydrolase)) (db:swissprot) ASPG_BACSU P26900 BACILLUS SUBTILIS 1423 -11528640 7000684648 ansa asparaginase:ansa:l-asparaginase ansa (cl:asparaginase) (ec:3.5.1.1) (db:pir2.dat) A39440 A39440 Bacillus subtilis 1423 -11528640 7500877258 ansa l-asparaginase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (ec:3.5.1.1) (de:bacillus subtilis l-asparaginase (ansa) gene, complete cds;l-aspartase (ansb) gene, complete cds.) (le:345) (re:1334) (di:direct) BACANS M63264 g142517 Bacillus subtilis 1423 -11528640 215186 ansa (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:262843) (re:263832) (di:direct) BACJH642 D84432 g1303987 Bacillus subtilis 1423 -11528640 216231 ansa l-asparaginase (db:genpept-bct1) (ec:3.5.1.1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:59787) (re:60776) (di:complement) BSUB0013 Z99116 g2634793 Bacillus subtilis 1423 -11528640 140858 ansa asparaginase:ansa:l-asparaginase ansa (cl:asparaginase) (ec:3.5.1.1) (db:pir) A39440 A39440 Bacillus subtilis 1423 -11528640 5000688392 (de:(ansa) (pn:l-asparaginase:l-asparaginase :l-asparagine amidohydrolase) (gtcfc:2.06) (ec:3.5.1.1) (aspg_bacsu) (keggfc:2.5:5.2:6.5) (bsorffc:2.2.0) (db:gtc-bacillus subtilis)) ansA ansA Bacillus subtilis 1423 10003124

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731075	386	22542	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731089	387	22543	204	68

Description

5000688395 gcvt:yqhi hypothetical protein:probable aminomethyltransferase:glycine cleavage system t protein (gtcfc:2.6:5.3:9.6:14.1) (ec:2.1.2.10) (keggfc:2.5:5.3:9.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) (gtcfc:energy metabolism-nitrogen metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:metabolism of cofactors and vitamins-bi... yqhI yqhI Bacillus subtilis 1423 -11528641 73462 gcvt (ec:2.1.2.10) (de:t protein)) (db:swissprot) GCST_BACSU P54378 BACILLUS SUBTILIS 1423 -11528641 7000685379 yqhi aminomethyltransferase homolog yqhi (cl:aminomethyltransferase) (db:pir2.dat) H69958 H69958 Bacillus subtilis 1423 -11528641 216134 yqhi (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:170272) (re:171360) (di:direct) BACJH642 D84432 g1303890 Bacillus subtilis 1423 -11528641 217173 yqhi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to aminomethyltransferase) (le:152261) (re:153349) (di:complement) BSUB0013 Z99116 g2634891 Bacillus subtilis 1423 -11528641 6500724783 gcvt hypothetical protein:probable aminomethyltransferase:glycine cleavage system t protein (gtcfc:2.6:5.3:9.6:14.1) (ec:2.1.2.10) (keggfc:2.5:5.3:9.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhI yqhI Bacillus subtilis 1423 -11528641

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731091	388	22544	324	107

Description

6500724784 asn:asnb asparagine synthetase (gtcfc:2.6:5.2) (ec:6.3.5.4) (keggfc:2.5:5.2) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) asnB asnB Bacillus subtilis 1423 -11528642 7000692235 asnb asparagine synthetase asnb (db:pir2.dat) H69590 H69590 Bacillus subtilis 1423 -11528642 4000714150 asnb asparagine synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:51441) (re:53339) (di:direct) AF008220 AF008220 g2293165 Bacillus subtilis 1423 -11528642 7500963433 asnb asparagine synthetase (db:genpept-bct1) (ec:6.3.5.4) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: asn) (le:127088) (re:128986) (di:complement) BSUB0016 Z99119 g2635538 Bacillus subtilis 1423 -11528642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731092	389	22545	324	107

Description

6500724785 hypothetical protein:similar to opine catabolism (gtcfc:2.6:5.13:14.1) (ec:1.4.99.1) (keggfc:2.5:5.13) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yurR yurR Bacillus subtilis 1423 -11528643 7502851522 yurr (de:hypothetical 39.4 kd oxidoreductase in hom-mrga intergenic region) (db:swissprot) YURR_BACSU O32159 BACILLUS SUBTILIS 1423 -11528643 7000694345 yurr opine catabolism homolog yurr (db:pir2.dat) A70019 A70019 Bacillus subtilis 1423 -11528643 7500965035 yurr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to opine catabolism) (le:154848) (re:155966) (di:complement) BSUB0017 Z99120 g2635760 Bacillus subtilis 1423 -11528643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731113	390	22546	507	169

Description

6500724786 nitrate reductase:gamma subunit:nitrate reductase gamma chain (gtcfc:2.6) (ec:1.7.99.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) narI narI Bacillus subtilis 1423 -11528644 219419 nari (ec:1.7.99.4) (de:nitrate reductase gamma chain,) (db:swissprot) NARI_BACSU P42177 BACILLUS SUBTILIS 1423 -11528644 7000685925 nari nitrate reductase:gamma chain nari:respiratory nitrate reductase epsilon chain (ec:1.7.99.4) (db:pir2.dat) S60088 S60088 Bacillus subtilis 1423 -11528644 5000688400 nari nitrate reductase gamma subunit (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:9771) (re:10442) (di:direct) BSNARYWI Z49884 g971344 Bacillus subtilis 1423 -11528644 7500886303 nari nitrate reductase gamma subunit (db:genpept-bct1) (ec:1.7.99.4) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:24211) (re:24882) (di:complement) BSUB0020 Z99123 g2636262 Bacillus subtilis 1423 -11528644 85240 nari (ec:1.7.99.4) (de:nitrate reductase gamma chain,) (db:swissprot) NARI_BACSU P42177 BACILLUS SUBTILIS 1423 -11528644 170372 nari nitrate reductase:gamma chain nari:respiratory nitrate reductase epsilon chain (ec:1.7.99.4) (db:pir) S60088 S60088 Bacillus subtilis 1423 -11528644

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731116	391	22547	777	258

Description

6500724787 nitrate reductase:protein j:nitrate reductase delta chain (gtcfc:2.6) (ec:1.7.99.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) narJ narJ Bacillus subtilis 1423 -11528645 219418 narj (ec:1.7.99.4) (de:nitrate reductase delta chain,) (db:swissprot) NARJ_BACSU P42178 BACILLUS SUBTILIS 1423 -11528645 7000685926 narj nitrate reductase:protein j:nitrate reductase delta chain:respiratory nitrate reductase gamma chain (ec:1.7.99.4) (db:pir2.dat) I40428 I40428 Bacillus subtilis 1423 -11528645 7500886304 narj respiratory nitrate reductase (db:genpept-bct1) (de:b.subtilis narghji genes.) (nt:gamma subunit) (le:5186) (re:5740) (di:direct) BSNARGHIJ X91819 g1009368 Bacillus subtilis 1423 -11528645 219405 narj nitrate reductase delta subunit (db:genpept-bct1) (de:b.subtilis narg, narh, narj and nari genes.) (le:3468) (re:4022) (di:direct) BSNARGHJI X85014 g1001850 Bacillus subtilis 1423 -11528645 5000688401 narj nitrate reductase protein j (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:9220) (re:9774) (di:direct) BSNARYWI Z49884 g971343 Bacillus subtilis 1423 -11528645 219409 narj nitrate reductase protein j (db:genpept-bct1) (ec:1.7.99.4) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:24879) (re:25433) (di:complement) BSUB0020 Z99123 g2636263 Bacillus subtilis 1423 -11528645 85242 narj (ec:1.7.99.4) (de:nitrate reductase delta chain,) (db:swissprot) NARJ_BACSU P42178 BACILLUS SUBTILIS 1423 -11528645 170505 narj nitrate reductase protein j narj:nitrate reductase delta chain:respiratory nitrate reductase gamma chain (db:pir) I40428 I40428 Bacillus subtilis 1423 -11528645

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731167	392	22548	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731177	393	22549	222	73

Description

GTC ORF with score 140 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c31f10.) (nt:spac31f10.12, unknown; (splicing may be incorrectly) (le:18609:18889:19051:19315) (re:18811:18938:19255:19372) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731196	394	22550	318	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731202	395	22551	1032	344

Description

6500724788 nitrate reductase:beta subunit:nitrate reductase beta chain (gtcfc:2.6) (ec:1.7.99.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) narH narH Bacillus subtilis 1423 -11528646 219417 narh (ec:1.7.99.4) (de:nitrate reductase beta chain,) (db:swissprot) NARH_BACSU P42176 BACILLUS SUBTILIS 1423 -11528646 7000685923 narh nitrate reductase:beta chain narh:respiratory nitrate reductase beta chain (cl:nitrate reductase beta chain:ferredoxin 2(4fe-4s) homology) (ec:1.7.99.4) (db:pir2.dat) S60573 S60086 Bacillus subtilis 1423 -11528646 5000688399 narh nitrate reductase beta subunit (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:7731) (re:9194) (di:direct) BSNARYWI Z49884 g971342 Bacillus subtilis 1423 -11528646 7500886302 narh nitrate reductase beta subunit (db:genpept-bct1) (ec:1.7.99.4) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:25459) (re:26922) (di:complement) BSUB0020 Z99123 g2636264 Bacillus subtilis 1423 -11528646 85238 narh (ec:1.7.99.4) (de:nitrate reductase beta chain,) (db:swissprot) NARH_BACSU P42176 BACILLUS SUBTILIS 1423 -11528646 136995 narh nitrate reductase beta subunit narh (cl:nitrate reductase beta chain:ferredoxin 2(4fe-4s) homology) (db:pir) F69664 F69664 Bacillus subtilis 1423 -11528646

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731228	396	22552	444	147

Description

6500724789 nitrate reductase:alpha subunit:nitrate reductase alpha chain (gtcfc:2.6) (ec:1.7.99.4) (keggfc:2.5) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) narG narG Bacillus subtilis 1423 -11528647 219416 narg (ec:1.7.99.4) (de:nitrate reductase alpha chain,) (db:swissprot) NARG_BACSU P42175 BACILLUS SUBTILIS 1423 -11528647 7000685922 narg nitrate reductase:alpha chain narg:respiratory nitrate reductase alpha chain narg (cl:nitrate reductase alpha chain) (ec:1.7.99.4) (db:pir2.dat) S60085 S60085 Bacillus subtilis 1423 -11528647 5000688398 narg nitrate reductase alpha subunit (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:4055) (re:7741) (di:direct) BSNARYWI Z49884 g971341 Bacillus subtilis 1423 -11528647 7500886301 narg nitrate reductase alpha subunit (db:genpept-bct1) (ec:1.7.99.4) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:26912) (re:30598) (di:complement) BSUB0020 Z99123 g2636265 Bacillus subtilis 1423 -11528647 85236 narg (ec:1.7.99.4) (de:nitrate reductase alpha chain,) (db:swissprot) NARG_BACSU P42175 BACILLUS SUBTILIS 1423 -11528647 170369 narg nitrate reductase:alpha chain narg:respiratory nitrate reductase alpha chain narg (cl:nitrate reductase alpha chain) (ec:1.7.99.4) (db:pir) S60085 S60085 Bacillus subtilis 1423 -11528647

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731229	397	22553	378	125

Description

6500724790 ipa-75d:yweb hypothetical protein:hypothetical 46.7 kd oxidoreductase in ung-roca intergenic region (gtcfc:2.6:5.1:14.1) (keggfc:2.5:5.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yweB yweB Bacillus subtilis 1423 -11528648 7502851523 yweb:ipa-75d (ec:1.4.1.-) (de:(ec 1.4.1.-)) (db:swissprot) YWEB_BACSU P39633 BACILLUS SUBTILIS 1423 -11528648 7000693044 yweb glutamate dehydrogenase homolog yweb (cl:glutamate dehydrogenase (nad(p)+)) (db:pir2.dat) A70055 A70055 Bacillus subtilis 1423 -11528648 7500953850 yweb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-75d; similar to glutamate) (le:81139) (re:82413) (di:complement) BSUB0020 Z99123 g2636315 Bacillus subtilis 1423 -11528648

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731238	398	22554	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731277	399	22555	219	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731284	400	22556	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731291	401	22557	204	67

Description

6500724791 histidine ammonia-lyase:histidase (gtcfc:2.6:5.11:10.11) (ec:4.3.1.3) (keggfc:2.5:5.11) (bsorffc:3.1.6:4.3.4) (db:gtc-bacillus subtilis) hutH hutH Bacillus subtilis 1423 -11528649 78087 huth (ec:4.3.1.3) (de:histidine ammonia-lyase, (histidase)) (db:swissprot) HUTH_BACSU P10944 BACILLUS SUBTILIS 1423 -11528649 125697 huth histidine ammonia-lyase::histidase huth (cl:histidine ammonia-lyase) (ec:4.3.1.3) (db:pir1.dat) UFBSHS S18810 Bacillus subtilis 1423 -11528649 215859 (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis huth and hutp genes, encoding histidase and a positiveregulatory protein, complete cds.) (nt:histidase) (le:1689) (re:3215) (di:direct) BACHUT M20659 g143076 Bacillus subtilis 1423 -11528649 215864 huth histidase (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:5749) (re:7275) (di:complement) BACHUTWAPA D31856 g603770 Bacillus subtilis 1423 -11528649 7500883628 huth histidase (fn:histidine utilization) (db:genpept-bct1) (ec:4.3.1.3) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:41560) (re:43086) (di:direct) BSUB0021 Z99124 g2636481 Bacillus subtilis 1423 -11528649 5000688423 (de:(huth) (pn:histidine ammonia-lyase:histidine ammonia-lyase :histidase) (gtcfc:5.11) (ec:4.3.1.3) (huth_bacsu) (keggfc:5.11) (bsorffc:2.2.0) (db:gtc-bacillus subtilis)) hutH hutH Bacillus subtilis 1423 10020426

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731320	402	22558	474	158

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731323	403	22559	870	290

Description

6500724792 nasbe:nasf uroporphyrin-iii c-methyltransferase:urogen iii methylase:sumt:uroporphyrinogen iii methylase:urom (gtcfc:2.6:9.10) (ec:2.1.1.107) (keggfc:9.10) (bsorffc:2.5.2:3.4.7) (db:gtc-bacillus subtilis) nasF nasF Bacillus subtilis 1423 -11528650 85268 nasf:nasbe (ec:2.1.1.107) (de:methylase) (sumt) (uroporphyrinogen iii methylase) (urom)) (db:swissprot) NASF_BACSU P42437 BACILLUS SUBTILIS 1423 -11528650 7000685937 nasf uroporphyrin-iii c-methyltransferase nasf (cl:uroporphyrinogen-iii synthase) (db:pir2.dat) I40031 I40031 Bacillus subtilis 1423 -11528650 216384 nasbe s-adenosyl-l-methionine:uroporphyrinogen iii (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around narb region (nasb operon and nasagene).) (le:9676) (re:11127) (di:direct) BACNARB D30689 g710022 Bacillus subtilis 1423 -11528650 222594 nasf uroporphyrin-iii c-methyltransferase (fn:porphyrin biosynthesis) (db:genpept-bct1) (ec:2.1.1.107) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: nasbe) (le:158822) (re:160273) (di:complement) BSUB0002 Z99105 g2632614 Bacillus subtilis 1423 -11528650 7500886318 nasbe s-adenosyl-l-methionine:uroporphyrinogen iii (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:33125) (re:34576) (di:complement) D50453 D50453 g1805400 Bacillus subtilis 1423 -11528650 5000688551 (de:(nasf) (pn:uroporphyrin-iii c-methyltransferase:sumt:urom:uroporphyrin-iii c-methyltransferase :urogen iii methylase:sumt:uroporphyrinogen iii methylase:urom) (gn:nasbe) (gtcfc:9.10) (ec:2.1.1.107) (nasf_bacsu) (keggfc:9.10)) nasF nasF Bacillus subtilis 1423 10027449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731373	404	22560	372	124

Description

6500724793 nitrate transporter (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nasA nasA Bacillus subtilis 1423 -11528651 85261 nasa (de:nitrate transporter) (db:swissprot) NASA_BACSU P42432 BACILLUS SUBTILIS 1423 -11528651 7000685932 nasa nitrate transporter nasa (db:pir2.dat) C69665 C69665 Bacillus subtilis 1423 -11528651 7500886311 nasa nitrate transporter (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around narb region (nasb operon and nasagene).) (le:828) (re:2093) (di:complement) BACNARB D30689 g1437473 Bacillus subtilis 1423 -11528651 216379 nasa nitrate transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:167856) (re:169121) (di:direct) BSUB0002 Z99105 g2632619 Bacillus subtilis 1423 -11528651 222599 nasa nitrate transporter (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:42159) (re:43424) (di:direct) D50453 D50453 g1805405 Bacillus subtilis 1423 -11528651 170374 nasa nitrate transporter nasa (db:pir) C69665 C69665 Bacillus subtilis 1423 -11528651

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731379	405	22561	783	261

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731386	406	22562	255	85

Description

5000688525 hypothetical protein:nifs protein homolog (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nifS nifS Bacillus subtilis 1423 -11528652 85963 nifs (de:nifs protein homolog) (db:swissprot) NIFS_BACSU P38033 BACILLUS SUBTILIS 1423 -11528652 7000685966 nifs nad biosynthesis protein nifs (cl:nitrogen fixation protein nifs) (db:pir2.dat) B47071 B47071 Bacillus subtilis 1423 -11528652 7500886453 (fn:required for nad biosynthesis) (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis l-aspartate oxidase (nadb) and nifs genes,complete cds.) (nt:homologous to the nifs gene products of other) (le:543) (re:1730) (di:comple... BACNADB M98822 g143241 Bacillus subtilis 1423 -11528652 216377 nifs (fn:required for nad biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:53699) (re:54886) (di:direct) BSUB0015 Z99118 g2635253 Bacillus subtilis 1423 -11528652 170379 nifs nad biosynthesis protein nifs (db:pir) B47071 B47071 Bacillus subtilis 1423 -11528652 6500724794 hypothetical protein:nifs protein homolog (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nifS nifS Bacillus subtilis 1423 -11528652

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731398	407	22563	210	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731452	408	22564	624	207

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731461	409	22565	630	210

Description

GTC ORF with score 640 to: (fn:membrane protein mediating transport of) (db:genpept-pln1) (de:candida albicans oligopeptide transporter (opt1) gene, completecds.) (nt:oligopeptide transporter) (le:482:2166) (re:2107:2891) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731462	410	22566	522	173

Description

6500724795 nifs protein homolog (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nifZ nifZ Bacillus subtilis 1423 -11528653 7000694320 nifz nifs protein homolog nifz (cl:nitrogen fixation protein nifs) (db:pir2.dat) F69666 F69666 Bacillus subtilis 1423 -11528653 4000714221 nifs2 nifs2 (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similar to r.sphaeroides nitrogenase stabilizer) (le:151019) (re:152164) (di:direct) AF008220 AF008220 g2293229 Bacillus subtilis 1423 -11528653 7500965019 nifz nifs protein homolog (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:28263) (re:29408) (di:complement) BSUB0016 Z99119 g2635443 Bacillus subtilis 1423 -11528653

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731484	411	22567	693	231

Description

5000688906 nitrogen-regulated pii-like protein:nitrogen regulatory pii-like protein (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nrgB nrgB Bacillus subtilis 1423 -11528654 220389 nrgb (de:nitrogen regulatory pii-like protein) (db:swissprot) NRGB_BACSU Q07428 BACILLUS SUBTILIS 1423 -11528654 7000685985 nrgb nitrogen-regulated pii-like protein nrgb (cl:regulatory protein p-ii) (db:pir2.dat) B36865 B36865 Bacillus subtilis 1423 -11528654 7500886594 nrgb pii-like protein (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis operon membrane-associated protein (nrga), andpii-like protein (nrgb) genes, complete cds.) (nt:putative) (le:1352) (re:1702) (di:direct) BACNRGABO L03216 g143265 Bacillus subtilis 1423 -11528654 216402 nrgb nitrogen-regulated pii-like protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:159980) (re:160330) (di:direct) BSUB0019 Z99122 g2636177 Bacillus subtilis 1423 -11528654 7502851524 nrgb unknown:similar to bacillus licheniformis bcrc (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mb1 genes.) (le:973) (re:1323) (di:complement) BSZ82987 Z82987 g1684644 Bacillus subtilis 1423 -11528654 86513 nrgb (de:nitrogen regulatory pii-like protein) (db:swissprot) NRGB_BACSU Q07428 BACILLUS SUBTILIS 1423 -11528654 170382 nrgb nitrogen-regulated pii-like protein nrgb (db:pir) B36865 B36865 Bacillus subtilis 1423 -11528654 6500724796 nitrogen-regulated pii-like protein:nitrogen regulatory pii-like protein (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) nrgB nrgB Bacillus subtilis 1423 -11528654

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731490	412	22568	555	184

Description

6500724797 naraa:narq hypothetical protein:narq protein (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) narQ narQ Bacillus subtilis 1423 -11528655 219401 narq:naraa (de:narq protein) (db:swissprot) NARQ_BACSU P39756 BACILLUS SUBTILIS 1423 -11528655 7000685928 narq required for formate dehydrogenase activity narq (db:pir2.dat) B69665 B69665 Bacillus subtilis 1423 -11528655 219032 narq unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:7048) (re:7836) (di:direct) BSATPC Z81356 g1648855 Bacillus subtilis 1423 -11528655 304085 naraa unknown (db:genpept-bct1) (de:b.subtilis (168) nara gene.) (le:490) (re:1278) (di:direct) BSNARAAB Z35277 g580895 Bacillus subtilis 1423 -11528655 7502851525 narq (fn:required for formate dehydrogenase activity) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: naraa) (le:175331) (re:176119) (di:complement) BSUB0019 Z99122 g2636196 Bacillus subtilis 1423 -11528655 85249 narq:naraa (de:narq protein) (db:swissprot) NARQ_BACSU P39756 BACILLUS SUBTILIS 1423 -11528655

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731495	413	22569	720	240

Description

6500724798 nitrite extrusion protein:nitrite facilitator (gtcfc:2.6) (keggfc:14.2) (bsorffc:2.5.2) (db:gtc-bacillus subtilis) narK narK Bacillus subtilis 1423 -11528656 219412 nark (de:nitrite extrusion protein (nitrite facilitator)) (db:swissprot) NARK_BACSU P46907 BACILLUS SUBTILIS 1423 -11528656 7000685927 nark nitrite extrusion protein nark (db:pir2.dat) S60080 S60080 Bacillus subtilis 1423 -11528656 7500886305 nark nitrite extrusion protein (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:486) (re:1673) (di:direct) BSNARYWI Z49884 g971337 Bacillus subtilis 1423 -11528656 7502851526 nark nitrite extrusion protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:32980) (re:34167) (di:complement) BSUB0020 Z99123 g2636269 Bacillus subtilis 1423 -11528656 85244 nark (de:nitrite extrusion protein (nitrite facilitator)) (db:swissprot) NARK_BACSU P46907 BACILLUS SUBTILIS 1423 -11528656 170375 nark nitrite extrusion protein nark (db:pir) S60080 S60080 Bacillus subtilis 1423 -11528656

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731496	414	22570	309	102

Description

GTC ORF with score 138 to: (sr:homo sapiens adult male brain cdna to mrna, clone_lib:pbluescripti) (db:genpept-pri3) (de:homo sapiens mrna for kiaa0809 protein, partial cds.) (nt:hk05250 cdna clone for kiaa0809 has a 1-bp deletion) (le:<1) (re:3727) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731519	415	22571	609	202

Description

GTC ORF with score 351 to: (fn:involved in poly-3-hydroxybutyrate degradation) (db:genpept-bct2) (ec:6.2.1.16) (de:sinorhizobium meliloti acetoacetyl-coa synthetase (acsa) gene,complete cds.) (nt:acetoacetyl-coa ligase; acyl-activating enzyme) (le:548)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731524	416	22572	951	317

Description

GTC ORF with score 253 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731569	417	22573	750	249

Description

6500724799 cysteine synthetase a:cysteine synthase:o-acetylserine sulfhydrylase:o-acetylserine:thiol-lyase:csase (gtcfc:2.7:5.3:5.5:6.4) (ec:4.2.99.8) (keggfc:2.6:5.5:6.4) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) cysK cysK Bacillus subtilis 1423 -11528657 7000689192 cysk cysteine synthase:a cysk (cl:threonine dehydratase) (ec:4.2.99.8) (db:pir2.dat) S66103 S66103 Bacillus subtilis 1423 -11528657 7500954428 cysk cysteine synthetase a (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:145370) (re:146296) (di:direct) BAC180K D26185 g467462 Bacillus subtilis 1423 -11528657 215062 cysk cysteine synthetase a (fn:cysteine biosynthesis) (db:genpept-bct1) (ec:4.2.99.8) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:81768) (re:82694) (di:direct) BSUB0001 Z99104 g2632340 Bacillus subtilis 1423 -11528657 206165 cysk cysteine synthase:a cysk (cl:threonine dehydratase) (ec:4.2.99.8) (db:pir) S66103 S66103 Bacillus subtilis 1423 -11528657

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731601	418	22574	180	59

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731603	419	22575	798	265

Description

6500724800 cysa:cyse serine acetyltransferase:sat (gtcfc:2.7:5.3:5.5) (ec:2.3.1.30) (keggfc:2.6:5.5) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) cysE cysE Bacillus subtilis 1423 -11528658 67649 cyse:cysa (ec:2.3.1.30) (de:serine acetyltransferase, (sat)) (db:swissprot) CYSE_BACSU Q06750 BACILLUS SUBTILIS 1423 -11528658 7000684967 cyse:cysa serine o-acetyltransferase:cyse (cl:bacillus serine acetyltransferase:serine acetyltransferase homology) (ec:2.3.1.30) (db:pir2.dat) B53402 B53402 Bacillus subtilis 1423 -11528658 7500879904 cysa serine acetyltransferase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:176399) (re:177052) (di:direct) BAC180K D26185 g467481 Bacillus subtilis 1423 -11528658 215081 serine acetyltransferase (sr:bacillus subtilis (strain 168t) dna) (db:genpept-bct1) (de:bacillus subtilis glutamyl-trna transferase (gltx), serineacetyltransferase (cyse), and cysteinyl-trna synthetase (cyss)genes, complete cds's.) (le:3459) (re:4112) (di:direct) BACGLUSYN L14580 g289283 Bacillus subtilis 1423 -11528658 215700 cyse serine acetyltransferase (fn:cysteine biosynthesis) (db:genpept-bct1) (ec:2.3.1.30) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: cysa) (le:112797) (re:113450) (di:direct) BSUB0001 Z99104 g2632360 Bacillus subtilis 1423 -11528658 170524 cyse:cysa serine o-acetyltransferase:cyse (cl:galactoside acetyltransferase) (ec:2.3.1.30) (db:pir) B53402 B53402 Bacillus subtilis 1423 -11528658 5000688406 (de:(cyse) (pn:serine acetyltransferase:sat:serine acetyltransferase :sat) (gn:cysa) (gtcfc:2.07) (ec:2.3.1.30) (cyse_bacsu) (keggfc:2.6:5.5) (bsorffc:3.1.3) (db:gtc-bacillus subtilis)) cysE cysE Bacillus subtilis 1423 10010247

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731615	420	22576	717	238

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731655	421	22577	612	203

Description

6500724801 hypothetical protein:similar to adenylylsulfate kinase (gtcfc:2.7:4.1:6.4:14.1) (ec:2.7.1.25) (keggfc:2.6:4.1:6.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisZ yisZ Bacillus subtilis 1423 -11528659 7000692158 yisz adenylylsulfate kinase homolog yisz (cl:adenylylsulfate kinase:adenylylsulfate kinase homology) (db:pir2.dat) A69839 A69839 Bacillus subtilis 1423 -11528659 7500954075 yisz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to adenylylsulfate kinase) (le:169851) (re:170450) (di:complement) BSUB0006 Z99109 g2633427 Bacillus subtilis 1423 -11528659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731666	422	22578	621	206

Description

6500724802 hypothetical protein:similar to sulfate adenylyltransferase (gtcfc:2.7:4.1:6.4:14.1) (ec:2.7.7.4) (keggfc:2.6:4.1:6.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitA yitA Bacillus subtilis 1423 -11528660 7000694653 yita sulfate adenylyltransferase homolog yita (db:pir2.dat) B69839 B69839 Bacillus subtilis 1423 -11528660 3000694807 yita (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to sulfate adenylyltransferase) (le:170447) (re:171424) (di:complement) BSUB0006 Z99109 g2633428 Bacillus subtilis 1423 -11528660 7500965237 yita (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - probable sulfate adenylyl transferase) (le:27673) (re:28650) (di:complement) BSY09476 Y09476 g2145393 Bacillus subtilis 1423 -11528660

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731679	423	22579	207	68

Description

GTC ORF with score 218 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f7h19 (essaiiproject).) (nt:strong similarity to fizzy-related protein,) (le:25865:26901:27117:27634) (re:26284:27023:27221:27876) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731682	424	22580	312	103

Description

6500724803 hypothetical protein:similar to cystathionine gamma-synthase (gtcfc:2.7:5.3:5.4:5.5:6.4:14.1) (ec:4.2.99.9) (keggfc:2.6:5.3:5.4:5.5:6.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcI yjcI Bacillus subtilis 1423 -11528661 7000692885 yjci cystathionine gamma-synthase homolog yjci (cl:o-succinylhomoserine (thiol)-lyase) (db:pir2.dat) A69847 A69847 Bacillus subtilis 1423 -11528661 7500963915 yjci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to cystathionine gamma-synthase) (le:63573) (re:64694) (di:direct) BSUB0007 Z99110 g2633541 Bacillus subtilis 1423 -11528661

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731723	425	22581	213	70

Description

6500724804 homoserine o-succinyltransferase:probable homoserine o-succinyltransferase:homoserine o-transsuccinylase (gtcfc:2.7:5.16:5.4) (ec:2.3.1.46) (keggfc:2.6:5.4) (bsorffc:3.1.7) (db:gtc-bacillus subtilis) metB metB Bacillus subtilis 1423 -11528662 83532 metb (ec:2.3.1.46) (de:transsuccinylase)) (db:swissprot) META_BACSU P54167 BACILLUS SUBTILIS 1423 -11528662 7000685834 metb homoserine o-succinyltransferase metb (db:pir2.dat) B69657 B69657 Bacillus subtilis 1423 -11528662 217088 metb homoserine o-succinyltransferase (fn:methionine byosynthesis) (db:genpept-bct1) (ec:2.3.1.46) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:46.6% identity to the escherichia coli homoserine) (le:15399) (re:16073) (di:complement) BACYACA L77246 g1256631 Bacillus subtilis 1423 -11528662 7500885514 metb homoserine o-succinyltransferase (fn:methionine biosynthesis) (db:genpept-bct1) (ec:2.3.1.46) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:109079) (re:109753) (di:direct) BSUB0012 Z99115 g2634611 Bacillus subtilis 1423 -11528662 5000688408 (de:(metb) (pn:probable homoserine o-succinyltransferase:homoserine o-transsuccinylase) (gtcfc:2.07) (ec:2.3.1.46) (meta_bacsu) (keggfc:2.6:5.4) (db:gtc-bacillus subtilis)) metB metB Bacillus subtilis 1423 10025746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731762	426	22582	450	149

Description

6500724805 hypothetical protein:similar to cysteine synthase (gtcfc:2.7:5.5:6.4:14.1) (ec:4.2.99.8) (keggfc:2.6:5.5:6.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytkP ytkP Bacillus subtilis 1423 -11528663 7000692889 ytkp cysteine synthase homolog ytkp (cl:threonine dehydratase) (db:pir2.dat) H69994 H69994 Bacillus subtilis 1423 -11528663 4000714197 ytkp putative cysteine synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:111728) (re:112663) (di:complement) AF008220 AF008220 g2293314 Bacillus subtilis 1423 -11528663 7500954424 ytkp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to cysteine synthase) (le:67763) (re:68698) (di:direct) BSUB0016 Z99119 g2635481 Bacillus subtilis 1423 -11528663

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731768	427	22583	501	166

Description

6500724806 hypothetical protein:similar to sulfite reductase (gtcfc:2.7:6.4:14.1) (ec:1.8.1.2) (keggfc:2.6:6.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvgR yvgR Bacillus subtilis 1423 -11528664 7000694658 yvgr sulfite reductase homolog yvgr (cl:sulfite reductase (nadph):flavodoxin homology:nadph--ferrihemoprotein reductase homology) (db:pir2.dat) G70040 G70040 Bacillus subtilis 1423 -11528664 7500953860 yvgr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:similar to sulfite reductase) (le:31851) (re:33668) (di:complement) BSUB0018 Z99121 g2635857 Bacillus subtilis 1423 -11528664

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731813	428	22584	930	310

Description

6500724807 ykia:ane3:hmp flavohemoprotein:haemoglobin-like protein:flavohemoglobin (gtcfc:2.8) (keggfc:14.2) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) hmp hmp Bacillus subtilis 1423 -11528665 77372 hmp:ane3 (de:flavohemoprotein (haemoglobin-like protein) (flavohemoglobin)) (db:swissprot) HMPA_BACSU P49852 BACILLUS SUBTILIS 1423 -11528665 7000685544 hmp flavohemoglobin hmp (cl:flavohemoglobin:cytochrome-b5 reductase homology:globin homology) (db:pir2.dat) B69642 B69642 Bacillus subtilis 1423 -11528665 214920 (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis hmp dna for 7 orfs, complete cds.) (nt:high homology to flavohemoprotein (haemoglobin-like) (le:999) (re:2198) (di:direct) BAC168TRP2 D78189 g1063247 Bacillus subtilis 1423 -11528665 301703 ykia ykia (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:flavohemoprotein) (le:24916) (re:26115) (di:direct) BSAJ2571 AJ002571 g2632025 Bacillus subtilis 1423 -11528665 6000684807 hmp flavohemoglobin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykia) (le:177865) (re:179064) (di:direct) BSUB0007 Z99110 g2633658 Bacillus subtilis 1423 -11528665 5000689086 (de:(hmp) (pn:flavohemoprotein:haemoglobin-like protein:flavohemoglobin) (gn:ane3) (gtcfc:13.07) (ec:) (hmpa_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) hmp hmp Bacillus subtilis 1423 10019733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731814	429	22585	888	296

Description

6500724808 ylxd:pyrdb:pyrdii dihydroorotate dehydrogenase:electron transfer subunit:dihydroorotate dehydrogenase electron transfer subunit (gtcfc:2.8) (keggfc:14.2) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) pyrDII pyrDII Bacillus subtilis 1423 -11528666 92659 pyrdii:pyrdb (de:dihydroorotate dehydrogenase electron transfer subunit) (db:swissprot) PYRZ_BACSU P25983 BACILLUS SUBTILIS 1423 -11528666 7000686255 pyrdii dihydroorotate dehydrogenase electron transfer subunit pyrdii (db:pir2.dat) G39845 G39845 Bacillus subtilis 1423 -11528666 7500889195 (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (nt:orf2) (le:9331) (re:10101) (di:di... BACPYROP M59757 g143391 Bacillus subtilis 1423 -11528666 216563 pyrdii dihydroorotate dehydrogenase electron transfer (fn:pyrimidine biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylxd) (le:27927) (re:28697) (di:direct) BSUB0009 Z99112 g2633926 Bacillus subtilis 1423 -11528666 170196 pyrdii dihydroorotate dehydrogenase electron transfer subunit pyrdii (db:pir) G39845 G39845 Bacillus subtilis 1423 -11528666 5000689098 (de:(pyrdii) (pn:dihydroorotate dehydrogenase electron transfer subunit) (gn:pyrdb) (gtcfc:13.07) (ec:) (pyrz_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) pyrDII pyrDII Bacillus subtilis 1423 10034691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731816	430	22586	909	303

Description

6500724809 ypba:fer ferredoxin (gtcfc:2.8) (keggfc:14.2) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) fer fer Bacillus subtilis 1423 -11528667 7000692978 fer ferredoxin fer (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) D69621 D69621 Bacillus subtilis 1423 -11528667 6000689574 fer ferredoxin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: ypba) (le:213423) (re:213671) (di:direct) BSUB0012 Z99115 g2634722 Bacillus subtilis 1423 -11528667 7500953748 fer ferredoxin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypba) (le:13703) (re:13951) (di:direct) BSUB0013 Z99116 g2634739 Bacillus subtilis 1423 -11528667 216704 fer ferredoxin (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146198 Bacillus subtilis 1423 -11528667 7502851527 fer ferredoxin (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146198 Bacillus subtilis 1423 -11528667

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731817	431	22587	855	285

Description

6500724810 electron transfer flavoprotein:alpha subunit:electron transfer flavoprotein alpha-subunit:alpha-etf:electron transfer flavoprotein large subunit:etfls (gtcfc:2.8) (keggfc:14.2) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) etfA etfA Bacillus subtilis 1423 -11528668 4000707920 etfa (de:transfer flavoprotein large subunit) (etfls)) (db:swissprot) ETFA_BACSU P94551 BACILLUS SUBTILIS 1423 -11528668 7000685188 etfa electron transfer flavoprotein alpha subunit etfa (cl:electron transfer flavoprotein alpha chain) (db:pir2.dat) D69620 D69620 Bacillus subtilis 1423 -11528668 220318 etfa electron transfer flavoprotein alpha subunit (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:119337) (re:120314) (di:complement) BSUB0015 Z99118 g2635317 Bacillus subtilis 1423 -11528668 304191 etfa electron transfer flavoprotein:alpha subunit (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to the alpha subunit of an electron) (le:49593) (re:50570) (di:direct) BSZ75208 Z75208 g1770042 Bacillus subtilis 1423 -11528668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731819	432	22588	870	290

Description

6500724811 electron transfer flavoprotein:beta subunit:electron transfer flavoprotein beta-subunit:beta-etf:electron transfer flavoprotein small subunit:etfss (gtcfc:2.8) (keggfc:14.2) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) etfB etfB Bacillus subtilis 1423 -11528669 4000707922 etfb (de:transfer flavoprotein small subunit) (etfss)) (db:swissprot) ETFB_BACSU P94550 BACILLUS SUBTILIS 1423 -11528669 7000685189 etfb electron transfer flavoprotein beta subunit etfb (cl:electron transfer flavoprotein beta chain) (db:pir2.dat) E69620 E69620 Bacillus subtilis 1423 -11528669 220317 etfb electron transfer flavoprotein beta subunit (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:120350) (re:121123) (di:complement) BSUB0015 Z99118 g2635318 Bacillus subtilis 1423 -11528669 304190 etfb electron transfer flavoprotein:beta subunit (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to the beta subunit of an electron) (le:48784) (re:49557) (di:direct) BSZ75208 Z75208 g1770041 Bacillus subtilis 1423 -11528669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731820	433	22589	765	255

Description

5000688409 atp synthase:subunit i:atp synthase protein i (gtcfc:2.8) (keggfc:14.2) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpI atpI Bacillus subtilis 1423 -11528670 7500877596 atpi (de:atp synthase protein i) (db:swissprot) ATPZ_BACSU P37816 BACILLUS SUBTILIS 1423 -11528670 7000684683 atpi h+-transporting atp synthase:chain i atpi (cl:bacillus h+-transporting atp synthase chain i) (ec:3.6.1.34) (db:pir2.dat) I40360 I40360 Bacillus subtilis 1423 -11528670 219014 atpi atp synthase subunit i (db:genpept-bct1) (de:b.subtilis (168) atpase genes for atp synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.) (le:429) (re:812) (di:direct) BSATPASE Z28592 g433984 Bacillus subtilis 1423 -11528670 7502851528 atpi atp synthase subunit i (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:189585) (re:189968) (di:complement) BSUB0019 Z99122 g2636213 Bacillus subtilis 1423 -11528670 61192 atpi (de:atp synthase protein i) (db:swissprot) ATPZ_BACSU P37816 BACILLUS SUBTILIS 1423 -11528670 170030 atpi h+-transporting atp synthase:chain i atpi (ec:3.6.1.34) (db:pir) I40360 I40360 Bacillus subtilis 1423 -11528670 6500724812 atp synthase:subunit i:atp synthase protein i (gtcfc:2.8) (keggfc:14.2) (bsorffc:2.7.1) (db:gtc-bacillus subtilis) atpI atpI Bacillus subtilis 1423 -11528670

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731825	434	22590	1248	416

Description

6500724813 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein synthase (gtcfc:3.1:14.1) (ec:2.3.1.41) (keggfc:3.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfB yhfB Bacillus subtilis 1423 -11528671 7000692058 yhfb 3-oxoacyl-acyl-carrier protein synthase homolog yhfb (cl:3-oxoacyl-(acyl-carrier-protein) synthase iii) (db:pir2.dat) H69829 H69829 Bacillus subtilis 1423 -11528671 4000714633 yhfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to 3-oxoacyl- acyl-carrier protein) (le:92743) (re:93720) (di:complement) BSUB0006 Z99109 g2633353 Bacillus subtilis 1423 -11528671 7500963302 yhfb hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to beta-ketoacyl-acyl carrier protein) (le:12602) (re:13579) (di:complement) BSY14083 Y14083 g2226235 Bacillus subtilis 1423 -11528671

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731841	435	22591	318	105

Description

6500724814 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein synthase (gtcfc:3.1:14.1) (keggfc:3.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjaX yjaX Bacillus subtilis 1423 -11528672 7000692059 yjax 3-oxoacyl-acyl-carrier protein synthase homolog yjax (cl:3-oxoacyl-(acyl-carrier-protein) synthase iii) (db:pir2.dat) F69842 F69842 Bacillus subtilis 1423 -11528672 6000690631 yjax (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to 3-oxoacyl- acyl-carrier protein) (le:208189) (re:209127) (di:direct) BSUB0006 Z99109 g2633470 Bacillus subtilis 1423 -11528672 7500963303 yjax (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to 3-oxoacyl- acyl-carrier protein) (le:13299) (re:14237) (di:direct) BSUB0007 Z99110 g2633487 Bacillus subtilis 1423 -11528672

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731865	436	22592	570	189

Description

6500724815 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein synthase (gtcfc:3.1:14.1) (ec:2.3.1.41) (keggfc:3.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjaY yjaY Bacillus subtilis 1423 -11528673 7000692060 yjay 3-oxoacyl-acyl-carrier-protein synthase,) (cl:3-oxoacyl-(acyl-carrier-protein) synthase i:3-oxoacyl-(acyl-carrier-protein) synthase i homology) (ec:2.3.1.41) (db:pir2.dat) G69842 G69842 Bacillus subtilis 1423 -11528673 6000690633 yjay (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to 3-oxoacyl-acyl-carrier protein) (le:209150) (re:210391) (di:direct) BSUB0006 Z99109 g2633471 Bacillus subtilis 1423 -11528673 7500963304 yjay (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to 3-oxoacyl- acyl-carrier protein) (le:14260) (re:15501) (di:direct) BSUB0007 Z99110 g2633488 Bacillus subtilis 1423 -11528673

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731871	437	22593	198	65

Description

6500724816 hypothetical protein:similar to enoyl-acyl-carrier protein reductase (gtcfc:3.1:14.1) (ec:1.3.1.9) (keggfc:3.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbW yjbW Bacillus subtilis 1423 -11528674 7000692966 yjbw enoyl-acyl-carrier-protein reductase (nadh), yjbw) (cl:enoyl-(acyl-carrier-protein) reductase (nadh):short-chain alcohol dehydrogenase homology) (ec:1.3.1.9) (db:pir2.dat) G69845 G69845 Bacillus subtilis 1423 -11528674 7500953790 yjbw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to enoyl- acyl-carrier protein reductase) (le:52836) (re:53645) (di:direct) BSUB0007 Z99110 g2633526 Bacillus subtilis 1423 -11528674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731878	438	22594	891	296

Description

6500724817 ylpe:fabd malonyl coa-acyl carrier protein transacylase:mct (gtcfc:3.1:9.5) (ec:2.3.1.39) (keggfc:3.1) (bsorffc:3.4.9) (db:gtc-bacillus subtilis) fabD fabD Bacillus subtilis 1423 -11528675 7000694187 fabd malonyl coa-acyl carrier protein transacylase fabd (cl:(acyl-carrier-protein) s-malonyltransferase:(acyl-carrier-protein) s-malonyltransferase homology) (db:pir2.dat) H69620 H69620 Bacillus subtilis 1423 -11528675 5500687811 fabd malonyl coa-acyl carrier protein transacylase (fn:fatty acid biosynthesis) (db:genpept-bct1) (ec:2.3.1.39) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylpe) (le:64546) (re:65499) (di:direct) BSUB0009 Z99112 g2633962 Bacillus subtilis 1423 -11528675 7500964914 ylpe putative fabd protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:26318) (re:27271) (di:direct) BSY13937 Y13937 g2337819 Bacillus subtilis 1423 -11528675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731886	439	22595	309	102

Description

GTC ORF with score 241 to: (sr:acremonium cellulolyticus y-94 (isolate:y-94) dna) (db:genpept) (de:acremonium cellulolyticus y-94 acc2 gene for cellobiohydrolase ii,complete cds.) (le:241:390:517:870:1199) (re:319:458:799:1123:1597) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731887	440	22596	312	103

Description

GTC ORF with score 422 to: (sr:acremonium cellulolyticus y-94 (isolate:y-94) dna) (db:genpept) (de:acremonium cellulolyticus y-94 acc2 gene for cellobiohydrolase ii,complete cds.) (le:241:390:517:870:1199) (re:319:458:799:1123:1597) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731888	441	22597	342	113

Description

6500724818 ylpf:fabg 3-oxoacyl-acyl-carrier protein reductase:3-ketoacyl-acyl carrier protein reductase (gtcfc:3.1:9.5) (ec:1.1.1.100) (keggfc:3.1) (bsorffc:3.4.9) (db:gtc-bacillus subtilis) fabG fabG Bacillus subtilis 1423 -11528676 7502851529 fabg (ec:1.1.1.100) (de:acyl carrier protein reductase)) (db:swissprot) FABG_BACSU P51831 BACILLUS SUBTILIS 1423 -11528676 7000692051 fabg:srb 3-oxoacyl-acyl-carrier-protein reductase,:3-ketoacyl-acyl carrier protein reductase fabg:srb protein) (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.1.1.100) (db:pir2.dat) A69621 A69621 Bacillus subtilis 1423 -11528676 7500953783 fabg 3-ketoacyl-acyl carrier protein reductase (fn:fatty acid biosynthesis) (db:genpept-bct1) (ec:1.1.1.100) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylpf) (le:65492) (re:66232) (di:direct) BSUB0009 Z99112 g2633963 Bacillus subtilis 1423 -11528676

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731917	442	22598	510	169

Description

6500724819 hypothetical protein:similar to acetyl-coa c-acyltransferase (gtcfc:3.1:3.2:3.5:5.13:5.6:14.1) (ec:2.3.1.16) (keggfc:3.1:3.2:3.5:5.6:5.13) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yusK yusK Bacillus subtilis 1423 -11528677 7000692137 yusk acetyl-coa c-acyltransferase homolog yusk (cl:acetyl-coa acetyltransferase) (db:pir2.dat) D70021 D70021 Bacillus subtilis 1423 -11528677 7500963369 yusk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to acetyl-coa c-acyltransferase) (le:170898) (re:172073) (di:complement) BSUB0017 Z99120 g2635779 Bacillus subtilis 1423 -11528677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731918	443	22599	288	95

Description

6500724820 hypothetical protein:similar to long-chain fatty-acid-coa ligase (gtcfc:3.2:14.1) (ec:6.2.1.3) (keggfc:3.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfL yhfL Bacillus subtilis 1423 -11528678 7000694172 yhfl long-chain fatty-acid-coa ligase homolog yhfl (cl:acetate--coa ligase homology) (db:pir2.dat) A69831 A69831 Bacillus subtilis 1423 -11528678 4000714643 yhfl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to long-chain fatty-acid-coa ligase) (le:100952) (re:102493) (di:direct) BSUB0006 Z99109 g2633363 Bacillus subtilis 1423 -11528678 7500964902 yhfl hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to lcfa, long-chain fatty acid-coa) (le:20811) (re:22352) (di:direct) BSY14083 Y14083 g2226245 Bacillus subtilis 1423 -11528678

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731920	444	22600	219	72

Description

6500724821 hypothetical protein:similar to long-chain fatty-acid-coa ligase (gtcfc:3.2:14.1) (ec:6.2.1.3) (keggfc:3.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfT yhfT Bacillus subtilis 1423 -11528679 7000694173 yhft long-chain fatty-acid-coa ligase homolog yhft (db:pir2.dat) A69832 A69832 Bacillus subtilis 1423 -11528679 4000714653 yhft (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to long-chain fatty-acid-coa ligase) (le:110451) (re:111890) (di:complement) BSUB0006 Z99109 g2633372 Bacillus subtilis 1423 -11528679 7500964903 yhft hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to long-chain-acyl-coa synthetase from) (le:4879) (re:6318) (di:complement) BSY14084 Y14084 g2226256 Bacillus subtilis 1423 -11528679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731931	445	22601	957	319

Description

6500724822 pss:pssa cdp-diacylglycerol--serine o-phosphatidyltransferase:phosphatidylserine synthase (gtcfc:3.2:5.3:8.1) (ec:2.7.8.8) (keggfc:5.3:8.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) pssA pssA Bacillus subtilis 1423 -11528680 92031 pssa:pss (ec:2.7.8.8) (de:(phosphatidylserine synthase)) (db:swissprot) PSS_BACSU P39823 BACILLUS SUBTILIS 1423 -11528680 7000686201 pssa cdpdiacylglycerol--serine o-phosphatidyltransferase:pssa:phosphatidylserine synthase pssa (cl:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase homology) (ec:2.7.8.8) (db:pir2.dat) A55537 A55537 Bacillus subtilis 1423 -11528680 7500888870 pss phosphatidylserine synthase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis genes for phosphatidylserine decarboxylase andphosphatidylserine synthase, complete cds.) (le:582) (re:1115) (di:direct) BACPSSPSD D38022 g1065993 Bacillus subtilis 1423 -11528680 216521 pssa phosphatidylserine synthase (fn:phospholipid biosynthesis) (db:genpept-bct1) (ec:2.7.8.8) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: pss) (le:53083) (re:53616) (di:direct) BSUB0002 Z99105 g2632513 Bacillus subtilis 1423 -11528680 7500888871 pss phosphatidylserine synthase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (ec:2.7.8.8) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:50734) (re:51267) (di:direct) AB006424 AB006424 g3599649 Bacillus subtilis 1423 -11528680 139388 pssa cdpdiacylglycerol--serine o-phosphatidyltransferase:pssa:phosphatidylserine synthase pssa (cl:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase:bacillus subtilis cdpdiacylglycerol--serine o-phosphatidyltransferase homology) (ec:2.7.8.8) (db:pir) A55537 A55537 Bacillus subtilis 1423 -11528680

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731961	446	22602	615	204

Description

6500724823 phosphatidylserine decarboxylase:phosphatidylserine decarboxylase proenzyme (gtcfc:3.2:5.3:8.1) (ec:4.1.1.65) (keggfc:5.3:8.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) psd psd Bacillus subtilis 1423 -11528681 69245 psd (ec:4.1.1.65) (de:phosphatidylserine decarboxylase proenzyme,) (db:swissprot) DPSD_BACSU P39822 BACILLUS SUBTILIS 1423 -11528681 7000685092 psd phosphatidylserine decarboxylase psd (db:pir2.dat) B69683 B69683 Bacillus subtilis 1423 -11528681 216522 psd phosphatidylserine decarboxylase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis genes for phosphatidylserine decarboxylase andphosphatidylserine synthase, complete cds.) (le:1587) (re:2378) (di:direct) BACPSSPSD D38022 g532272 Bacillus subtilis 1423 -11528681 7500880606 psd phosphatidylserine decarboxylase (fn:phospholipid biosynthesis) (db:genpept-bct1) (ec:4.1.1.65) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:54088) (re:54879) (di:direct) BSUB0002 Z99105 g2632515 Bacillus subtilis 1423 -11528681 7500880607 psd phosphatidylserine decarboxylase proenzyme (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (ec:4.1.1.65) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:51739) (re:52530) (di:direct) AB006424 AB006424 g3599651 Bacillus subtilis 1423 -11528681

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501731996	447	22603	894	297

Description

6500724824 lip:lipa lipase:ase precursor:triacylglycerol ase (gtcfc:3.2:8.1) (ec:3.1.1.3) (keggfc:8.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) lipA lipA Bacillus subtilis 1423 -11528682 5500687010 lipa triacylglycerol lipase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (le:5298) (re:5936) (di:direct) AB000617 AB000617 g2415721 Bacillus subtilis 1423 -11528682 7500964896 lipa lipase (db:genpept-bct1) (ec:3.1.1.3) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:97109) (re:97747) (di:direct) BSUB0002 Z99105 g2632556 Bacillus subtilis 1423 -11528682 7000694164 lipa lipase lipa (db:pir) B69652 B69652 Bacillus subtilis 1423 -11528682

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732033	448	22604	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732059	449	22605	198	65

Description

6500724825 yfip:lipb lipase (gtcfc:3.2:8.1) (ec:3.1.1.3) (keggfc:8.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) lipB lipB Bacillus subtilis 1423 -11528683 7000694165 lipb lipase lipb (db:pir2.dat) C69652 C69652 Bacillus subtilis 1423 -11528683 222813 lipb lipase (db:genpept-bct1) (ec:3.1.1.3) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfip) (le:106705) (re:107337) (di:direct) BSUB0005 Z99108 g2633159 Bacillus subtilis 1423 -11528683 7500964897 yfip (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:8581) (re:9213) (di:direct) D78508 D78508 g1817540 Bacillus subtilis 1423 -11528683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732060	450	22606	798	266

Description

6500724826 hypothetical protein:similar to alcohol dehydrogenase (gtcfc:3.2:8.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) yhxC yhxC Bacillus subtilis 1423 -11528684 7500937206 yhxc (ec:1.-.-.-) (de:(ec 1.-.-.-) (orfx)) (db:swissprot) YHXC_BACSU P40397 BACILLUS SUBTILIS 1423 -11528684 7000692167 yhxc alcohol dehydrogenase homolog yhxc (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D69835 D69835 Bacillus subtilis 1423 -11528684 4000714658 yhxc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to alcohol dehydrogenase) (le:115670) (re:116527) (di:direct) BSUB0006 Z99109 g2633376 Bacillus subtilis 1423 -11528684 4000714657 yhxc hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:the c-terminal part of this protein has been) (le:10098) (re:10955) (di:direct) BSY14084 Y14084 g2226261 Bacillus subtilis 1423 -11528684 7500937209 yhxc hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:the c-terminal part of this protein has been) (le:10098) (re:10955) (di:direct) BSY14084 Y14084 g2226260 Bacillus subtilis 1423 -11528684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732100	451	22607	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732118	452	22608	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732143	453	22609	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732152	454	22610	1014	337

Description

6500724827 phosphatidate cytidylyltransferase:cdp-diglyceride synthase (gtcfc:3.2:8.1) (ec:2.7.7.41) (keggfc:8.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) cdsA cdsA Bacillus subtilis 1423 -11528685 7500878458 cdsa (ec:2.7.7.41) (de:synthase)) (db:swissprot) CDSA_BACSU O31752 BACILLUS SUBTILIS 1423 -11528685 7000694400 cdsa phosphatidate cytidylyltransferase cdsa (db:pir2.dat) G69597 G69597 Bacillus subtilis 1423 -11528685 7500878460 cdsa phosphatidate cytidylyltransferase (fn:phospholipid biosynthesis) (db:genpept-bct1) (ec:2.7.7.41) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:122972) (re:123781) (di:direct) BSUB0009 Z99112 g2634026 Bacillus subtilis 1423 -11528685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732180	455	22611	825	274

Description

6500724828 ymfn:pgsa cdp-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase:phosphatidylglycerophosphate synthase:pgp synthase (gtcfc:3.2:8.1) (ec:2.7.8.5) (keggfc:8.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) pgsA pgsA Bacillus subtilis 1423 -11528686 7000694401 pgsa cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase:pgsa (cl:cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase) (ec:2.7.8.5) (db:pir2.dat) E69675 E69675 Bacillus subtilis 1423 -11528686 7500965066 pgsa phosphatidylglycerophosphate synthase (fn:acidic phospholipid biosynthesis) (db:genpept-bct1) (ec:2.7.8.5) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymfn) (le:163573) (re:164154) (di:direct) BSUB0009 Z99112 g2634064 Bacillus subtilis 1423 -11528686

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732183	456	22612	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732187	457	22613	378	125

Description

6500724829 yqxf:dgk:dgka diacylglycerol kinase:dagk:diglyceride kinase:dgk (gtcfc:3.2:8.1) (ec:2.7.1.107) (keggfc:8.1) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) dgkA dgkA Bacillus subtilis 1423 -11528687 80579 dgka:dgk (ec:2.7.1.107) (de:(dgk)) (db:swissprot) KDGL_BACSU P19638 BACILLUS SUBTILIS 1423 -11528687 7000685671 dgka diacylglycerol kinase dgka:hypothetical protein cdd 5 region (db:pir2.dat) (mp:225 (degrees)) G69614 G69614 Bacillus subtilis 1423 -11528687 216068 dgka (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:107804) (re:108148) (di:direct) BACJH642 D84432 g1303824 Bacillus subtilis 1423 -11528687 6000684843 dgka diacylglycerol kinase (fn:phospholipid biosynthesis) (db:genpept-bct1) (ec:2.7.1.107) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqxf) (le:215472) (re:215816) (di:complement) BSUB0013 Z99116 g2634963 Bacillus subtilis 1423 -11528687 7500884546 dgka diacylglycerol kinase (fn:phospholipid biosynthesis) (db:genpept-bct1) (ec:2.7.1.107) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqxf) (le:11282) (re:11626) (di:complement) BSUB0014 Z99117 g2634977 Bacillus subtilis 1423 -11528687

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732200	458	22614	723	240

Description

6500724830 imidazoleglycerol-phosphate dehydratase (gtcfc:3.2:5.11:8.1) (ec:4.2.1.19) (keggfc:5.11) (bsorffc:3.5.1) (db:gtc-bacillus subtilis) hisB hisB Bacillus subtilis 1423 -11528688 7000694100 hisb imidazoleglycerol-phosphate dehydratase hisb (cl:imidazoleglycerol-phosphate dehydratase:imidazoleglycerol-phosphate dehydratase homology) (db:pir2.dat) G69640 G69640 Bacillus subtilis 1423 -11528688 5500701773 hisb imidazoleglycerol-phosphate dehydratase (fn:histidine biosynthesis) (db:genpept-bct1) (ec:4.2.1.19) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:185200) (re:185784) (di:complement) BSUB0018 Z99121 g2636003 Bacillus subtilis 1423 -11528688 7500964861 hisb imidazoleglycerol-phosphate dehydratase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:42049) (re:42633) (di:direct) AF017113 AF017113 g2618867 Bacillus subtilis 1423 -11528688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732234	459	22615	279	93

Description

6500724831 prolipoprotein diacylglyceryl transferase (gtcfc:3.2:8.1:8.2) (ec:2.4.99.-) (keggfc:14.1) (bsorffc:3.5.1:7.7.1) (db:gtc-bacillus subtilis) lgt lgt Bacillus subtilis 1423 -11528689 7500884979 lgt:gerf (ec:2.4.99.-) (de:germination protein gerf)) (db:swissprot) LGT_BACSU O34752 BACILLUS SUBTILIS 1423 -11528689 7000694451 lgt prolipoprotein diacylglyceryl transferase lgt (cl:prolipoprotein diacylglyceryl transferase) (db:pir2.dat) C69651 C69651 Bacillus subtilis 1423 -11528689 7500884981 lgt prolipoprotein diacylglyceryl transferase (fn:lipoprotein biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:192929) (re:193738) (di:complement) BSUB0018 Z99121 g2636012 Bacillus subtilis 1423 -11528689 5500701764 lgt prolipoprotein diacylglyceryl transferase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:34095) (re:34904) (di:direct) AF017113 AF017113 g2618858 Bacillus subtilis 1423 -11528689

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732235	460	22616	564	187

Description

5000689055 polyketide synthase of type i:putative polyketide synthase pksk:pks (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksK pksK Bacillus subtilis 1423 -11528690 89891 pksk (de:putative polyketide synthase pksk (pks)) (db:swissprot) PKSK_BACSU P40803 BACILLUS SUBTILIS 1423 -11528690 7000686151 pksk polyketide synthase pksk (cl:acetate--coa ligase homology:3-oxoacyl-(acyl-carrier-protein) synthase i homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology:short-chain alcohol dehydrogenase homology) (db:pir2.dat) A69679 A69679 Bacillus subtilis 1423 -11528690 219788 polyketide synthase (db:genpept-bct1) (de:bacillus subtilis w168 polyketide synthase (pksx and pksorfx6)genes, complete cds.) (nt:pksorfx6; putative polyketide synthase of type i) (le:6658) (re:20001) (di:direct) BSU11039 U11039 g528995 Bacillus subtilis 1423 -11528690 6000685013 pksk polyketide synthase of type i (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:195423) (re:208766) (di:direct) BSUB0009 Z99112 g2634089 Bacillus subtilis 1423 -11528690 7500888140 pksk polyketide synthase of type i (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:12643) (re:25986) (di:direct) BSUB0010 Z99113 g2634101 Bacillus subtilis 1423 -11528690 6500724832 polyketide synthase of type i:putative polyketide synthase pksk:pks (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksK pksK Bacillus subtilis 1423 -11528690

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732276	461	22617	606	201

Description

5000689056 pksx:pksa:outg:pksl polyketide synthase of type i:putative polyketide synthase pksl:pks (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksL pksL Bacillus subtilis 1423 -11528691 303523 pksl:pksx:pksa:outg (de:putative polyketide synthase pksl (pks)) (db:swissprot) PKSL_BACSU Q05470 BACILLUS SUBTILIS 1423 -11528691 170443 pksl:pksx polyketide synthase:pksl (cl:3-oxoacyl-(acyl-carrier-protein) synthase i homology:acyl carrier protein homology:short-chain alcohol dehydrogenase homology) (ec:2.3.1.-) (db:pir2.dat) PN0637 S25021 Bacillus subtilis 1423 -11528691 219789 hypothetical polyketide synthase (db:genpept-bct1) (de:b.subtilis gene encoding hypothetical polyketide synthase.) (le:316) (re:13599) (di:direct) BSPKSH Z14098 g40058 Bacillus subtilis 1423 -11528691 219536 pksx polyketide synthase (db:genpept-bct1) (de:bacillus subtilis w168 polyketide synthase (pksx and pksorfx6)genes, complete cds.) (nt:putative polyketide synthase of type i) (le:20317) (re:33600) (di:direct) BSU11039 U11039 g528996 Bacillus subtilis 1423 -11528691 6500724833 pksl polyketide synthase of type i (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: pksx, pksa, outg) (le:26302) (re:39585) (di:direct) BSUB0010 Z99113 g2634102 Bacillus subtilis 1423 -11528691 89892 pksl:pksx:pksa:outg (de:putative polyketide synthase pksl (pks)) (db:swissprot) PKSL_BACSU Q05470 BACILLUS SUBTILIS 1423 -11528691 7000686152 pksl:pksx polyketide synthase:pksl (cl:3-oxoacyl-(acyl-carrier-protein) synthase i homology:acyl carrier protein homology:short-chain alcohol dehydrogenase homology) (ec:2.3.1.-) (db:pir) PN0637 PN0637 Bacillus subtilis 1423 -11528691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732283	462	22618	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732285	463	22619	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732293	464	22620	687	229

Description

GTC ORF with score 120 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t01d1.) (nt:coded for by c. elegans cdna yk45f3.5; coded for by) (le:1973:2033:4085:4293) (re:1975:2158:4237:4410) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732336	465	22621	375	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732375	466	22622	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732382	467	22623	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732383	468	22624	225	74

Description

6500724834 polyketide synthase (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksM pksM Bacillus subtilis 1423 -11528692 7000694430 pksm polyketide synthase pksm (cl:short-chain alcohol dehydrogenase homology:3-oxoacyl-(acyl-carrier-protein) synthase i homology) (db:pir2.dat) C69679 C69679 Bacillus subtilis 1423 -11528692 7500965083 pksm polyketide synthase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:39601) (re:52422) (di:direct) BSUB0010 Z99113 g2634103 Bacillus subtilis 1423 -11528692

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732384	469	22625	795	264

Description

6500724835 polyketide synthase (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksN pksN Bacillus subtilis 1423 -11528693 7000694431 pksn polyketide synthase pksn (db:pir2.dat) D69679 D69679 Bacillus subtilis 1423 -11528693 7500965084 pksn polyketide synthase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:52455) (re:54092) (di:direct) BSUB0010 Z99113 g2634104 Bacillus subtilis 1423 -11528693

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732432	470	22626	693	231

Description

GTC ORF with score 781 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c31h12.) (nt:spcc31h12.07, len:759, similarity:homo sapiens,) (le:14184:14264:14495:14592) (re:14214:14435:14526:16636) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732434	471	22627	237	78

Description

GTC ORF with score 97 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c31h12.) (nt:spcc31h12.07, len:759, similarity:homo sapiens,) (le:14184:14264:14495:14592) (re:14214:14435:14526:16636) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732443	472	22628	417	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732492	473	22629	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732499	474	22630	498	166

Description

GTC ORF with score 102 to: (sr:african clawed frog) (db:genpept-vrt) (de:xenopus laevis middle molecular weight neurofilament proteinnf-m(1) mrna, complete cds.) (nt:neuronal intermediate filament protein; duplicated) (le:11) (re:2704) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732500	475	22631	732	243

Description

6500724836 polyketide synthase of type i (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksP pksP Bacillus subtilis 1423 -11528694 7000694432 pksp polyketide synthase pksp (cl:acetate--coa ligase homology:3-oxoacyl-(acyl-carrier-protein) synthase i homology:acyl carrier protein homology:short-chain alcohol dehydrogenase homology) (db:pir2.dat) E69679 E69679 Bacillus subtilis 1423 -11528694 7500965085 pksp polyketide synthase of type i (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:54125) (re:68917) (di:direct) BSUB0010 Z99113 g2634105 Bacillus subtilis 1423 -11528694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732503	476	22632	345	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732506	477	22633	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732528	478	22634	882	293

Description

6500724837 polyketide synthase (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksR pksR Bacillus subtilis 1423 -11528695 7000694433 pksr polyketide synthase pksr (cl:3-oxoacyl-(acyl-carrier-protein) synthase i homology) (db:pir2.dat) F69679 F69679 Bacillus subtilis 1423 -11528695 7500965086 pksr polyketide synthase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:68932) (re:76563) (di:direct) BSUB0010 Z99113 g2634106 Bacillus subtilis 1423 -11528695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732529	479	22635	408	135

Description

6500724838 hydroxylase of the polyketide produced by the pks cluster (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) pksS pksS Bacillus subtilis 1423 -11528696 7000693117 pkss hydroxylase of the polyketide produced by the pks cluster pkss (cl:cytochrome p450) (db:pir2.dat) G69679 G69679 Bacillus subtilis 1423 -11528696 7500964062 pkss hydroxylase of the polyketide produced by the (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:76702) (re:77832) (di:complement) BSUB0010 Z99113 g2634107 Bacillus subtilis 1423 -11528696

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732561	480	22636	237	78

Description

6500724839 alpha-ketoglutarate permease (gtcfc:3.3) (keggfc:14.2) (bsorffc:3.5.2) (db:gtc-bacillus subtilis) csbX csbX Bacillus subtilis 1423 -11528697 7000692181 csbx alpha-ketoglutarate permease csbx (db:pir2.dat) H69607 H69607 Bacillus subtilis 1423 -11528697 7500963395 csbx alpha-ketoglutarate permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:41600) (re:42907) (di:complement) BSUB0015 Z99118 g2635241 Bacillus subtilis 1423 -11528697

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732562	481	22637	186	61

Description

6500724840 hypothetical protein:geranyltranstransferase:farnesyl-diphosphate synthase:fpp synthase (gtcfc:3.4:9.13:14.1) (ec:2.5.1.10) (keggfc:3.4:9.11) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiD yqiD Bacillus subtilis 1423 -11528698 79991 yqid (ec:2.5.1.10) (de:(fpp synthase)) (db:swissprot) ISPA_BACSU P54383 BACILLUS SUBTILIS 1423 -11528698 7000685650 yqid geranyltranstransferase homolog yqid (cl:geranyltranstransferase) (db:pir2.dat) A69961 A69961 Bacillus subtilis 1423 -11528698 216163 yqid (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:192926) (re:193744) (di:direct) BACJH642 D84432 g1303919 Bacillus subtilis 1423 -11528698 7500884295 yqid (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to geranyltranstransferase) (le:129877) (re:130695) (di:complement) BSUB0013 Z99116 g2634862 Bacillus subtilis 1423 -11528698 5000688563 (de:(yqid) (pn:geranyltranstransferase:farnesyl-diphosphate synthase:fpp synthase) (gtcfc:9.13) (ec:2.5.1.10) (ispa_bacsu) (keggfc:3.4:9.11) (db:gtc-bacillus subtilis)) yqiD yqiD Bacillus subtilis 1423 10022241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732601	482	22638	237	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732641	483	22639	546	181

Description

6500724841 dnag:dnak:dnan dna polymerase iii:beta subunit:dna polymerase iii:beta chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaN dnaN Bacillus subtilis 1423 -11528699 219452 dnan:dnag (ec:2.7.7.7) (de:dna polymerase iii, beta chain,) (db:swissprot) DP3B_BACSU P05649 BACILLUS SUBTILIS 1423 -11528699 124042 dnan dna-directed dna polymerase:iii beta chain dnan:42k protein oric region (cl:dna-directed dna polymerase iii beta chain) (ec:2.7.7.7) (db:pir1.dat) (mp:0) B22930 B22930 Bacillus subtilis 1423 -11528699 214992 dnag beta subunit of dna polymerase iii (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:65541) (re:66677) (di:direct) BAC180K D26185 g467392 Bacillus subtilis 1423 -11528699 7500880546 (db:genpept-bct1) (de:bacillus subtilis oric region.) (nt:pot. orf 378 (aa 1-378)) (le:2715) (re:3851) (di:direct) BSORIC X02369 g40015 Bacillus subtilis 1423 -11528699 7502851530 dnan dna polymerase iii beta subunit (fn:dna synthesis) (db:genpept-bct1) (ec:2.7.7.7) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: dnag, dnak) (le:1939) (re:3075) (di:direct) BSUB0001 Z99104 g2632269 Bacillus subtilis 1423 -11528699 69052 dnan:dnag (ec:2.7.7.7) (de:dna polymerase iii, beta chain,) (db:swissprot) DP3B_BACSU P05649 BACILLUS SUBTILIS 1423 -11528699

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732646	484	22640	582	193

Description

6500724842 guaa:guab inositol-monophosphate dehydrogenase (gtcfc:4.1:8.2) (ec:1.1.1.205) (keggfc:4.1) (bsorffc:3.2.1:7.7.1) (db:gtc-bacillus subtilis) guaB guaB Bacillus subtilis 1423 -11528700 206262 guab imp dehydrogenase::inositol-monophosphate dehydrogenase guab (cl:imp dehydrogenase:cbs homology) (ec:1.1.1.205) (db:pir1.dat) DEBSMP S66039 Bacillus subtilis 1423 -11528700 214999 guab imp dehydrogenase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:79515) (re:80981) (di:direct) BAC180K D26185 g467399 Bacillus subtilis 1423 -11528700 7500953177 guab inositol-monophosphate dehydrogenase (fn:gmp biosynthesis) (db:genpept-bct1) (ec:1.1.1.205) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: guaa) (le:15913) (re:17379) (di:direct) BSUB0001 Z99104 g2632276 Bacillus subtilis 1423 -11528700

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732660	485	22641	285	94

Description

6500724843 dnah:dna-8132:dnax dna polymerase iii:gamma and tau subunits:dna polymerase iii subunits gamma and tau (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaX dnaX Bacillus subtilis 1423 -11528701 7000692940 dnax:dnazx dna-directed dna polymerase:iii chain dnax:dna polymerase iii gamma and tau subunits dnax (ec:2.7.7.7) (db:pir2.dat) S13786 S13786 Bacillus subtilis 1423 -11528701 7500963962 dnah dna polymerase iii subunit (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:90414) (re:92105) (di:direct) BAC180K D26185 g467409 Bacillus subtilis 1423 -11528701 304134 dnazx (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (le:261) (re:1952) (di:direct) BSRECM X17014 g580914 Bacillus subtilis 1423 -11528701 219567 dnax dna polymerase iii gamma and tau subunits (fn:dna synthesis) (db:genpept-bct1) (ec:2.7.7.7) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: dnah, dna-8132) (le:26812) (re:28503) (di:direct) BSUB0001 Z99104 g2632286 Bacillus subtilis 1423 -11528701 7502851531 dnazx (db:genpept) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (le:261) (re:1952) (di:direct) BSRECM X17014 g580914 Bacillus subtilis 1423 -11528701 169971 dnax:dnazx dna-directed dna polymerase:iii chain dnax:dna polymerase iii gamma and tau subunits dnax (ec:2.7.7.7) (db:pir) S13786 S13786 Bacillus subtilis 1423 -11528701 215009 dnazx (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (le:261) (re:1952) (di:direct) BSRECM X17014 g580914 Bacillus subtilis 1423 -11528701

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732661	486	22642	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732662	487	22643	315	104

Description

6500724844 hpt:hprt hypoxanthine-guanine phosphoribosyltransferase:hgprt:hgprtase (gtcfc:4.1:4.4) (ec:2.4.2.8) (keggfc:4.1) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) hprT hprT Bacillus subtilis 1423 -11528702 77555 hprt:hpt (ec:2.4.2.8) (de:(hgprtase)) (db:swissprot) HPRT_BACSU P37472 BACILLUS SUBTILIS 1423 -11528702 7000685556 hprt hypoxanthine phosphoribosyltransferase:hprt:hypoxanthine-guanine phosphoribosyltransferase hprt (cl:hypoxanthine phosphoribosyltransferase) (ec:2.4.2.8) (db:pir2.dat) S66098 S66098 Bacillus subtilis 1423 -11528702 7500883503 hprt hypoxanthine-guanine phosphoribosyltransferase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:139944) (re:140486) (di:direct) BAC180K D26185 g467457 Bacillus subtilis 1423 -11528702 215057 hprt hypoxanthine-guanine phosphoribosyltransferase (fn:purine salvage) (db:genpept-bct1) (ec:2.4.2.8) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:76342) (re:76884) (di:direct) BSUB0001 Z99104 g2632335 Bacillus subtilis 1423 -11528702 206261 hprt hypoxanthine phosphoribosyltransferase:hprt:hypoxanthine-guanine phosphoribosyltransferase hprt (cl:hypoxanthine phosphoribosyltransferase) (ec:2.4.2.8) (db:pir) S66098 S66098 Bacillus subtilis 1423 -11528702

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732665	488	22644	279	92

Description

6500724845 rfm:crse:rpob rna polymerase:beta subunit:dna-directed rna polymerase beta chain:transcriptase beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.3) (ec:2.7.7.6) (keggfc:4.1:4.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rpoB rpoB Bacillus subtilis 1423 -11528703 96188 rpob:rfm:crse (ec:2.7.7.6) (de:beta chain) (rna polymerase beta subunit)) (db:swissprot) RPOB_BACSU P37870 BACILLUS SUBTILIS 1423 -11528703 7000686460 rpob dna-directed rna polymerase:beta chain (cl:dna-directed rna polymerase beta chain) (ec:2.7.7.6) (db:pir2.dat) F69698 F69698 Bacillus subtilis 1423 -11528703 216612 rpob rna polymerase beta-subunit (db:genpept-bct1) (de:bacillus subtilis ribosomal protein l7/12 (rpll) gene, beta subunitof rna polymerase (rpobc) gene, 3' end, complete cds, 5' end.) (le:1089) (re:4670) (di:direct) BACRPLL L24376 g402363 Bacillus subtilis 1423 -11528703 7500890613 rpob rna polymerase beta subunit (db:genpept-bct1) (ec:2.7.7.6) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:121916) (re:125497) (di:direct) BSUB0001 Z99104 g2632374 Bacillus subtilis 1423 -11528703

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732693	489	22645	348	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732722	490	22646	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732723	491	22647	669	223

Description

6500724846 lpm:std:rpoc rna polymerase:beta subunit:dna-directed rna polymerase beta chain:transcriptase beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.3) (ec:2.7.7.6) (keggfc:4.1:4.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rpoC rpoC Bacillus subtilis 1423 -11528704 7000694553 rpoc rna polymerase beta subunit rpoc (db:pir2.dat) G69698 G69698 Bacillus subtilis 1423 -11528704 7500965165 rpoc rna polymerase beta subunit (db:genpept-bct1) (ec:2.7.7.6) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:125559) (re:129158) (di:direct) BSUB0001 Z99104 g2632375 Bacillus subtilis 1423 -11528704

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732782	492	22648	387	128

Description

6500724847 adenylate kinase:atp-amp transphosphorylase (gtcfc:4.1) (ec:2.7.4.3) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) adk adk Bacillus subtilis 1423 -11528705 80323 adk (ec:2.7.4.3) (de:(superoxide-inducible protein 16) (soi16)) (db:swissprot) KAD_BACSU P16304 BACILLUS SUBTILIS 1423 -11528705 7000685659 adk adenylate kinase::atp-amp transphosphorylase (cl:adenylate kinase) (ec:2.7.4.3) (db:pir2.dat) JS0492 JS0492 Bacillus subtilis 1423 -11528705 7500884457 adk adenylate kinase (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044985 Bacillus subtilis 1423 -11528705 216697 adk adenylate kinase (db:genpept-bct1) (ec:2.7.4.3) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:145875) (re:146528) (di:direct) BSUB0001 Z99104 g2632404 Bacillus subtilis 1423 -11528705 216628 adenylate kinase (sr:bacillus subtilis (strain:207-21) dna) (db:genpept-bct2) (de:bacillus subtilis genes for ribosomal proteins, secy, adenylatekinase and methionine amino peptidase, complete cds.) (le:2055) (re:2708) (di:direct) BACSECY D00619 g216340 Bacillus subtilis 1423 -11528705 139013 adk adenylate kinase:adk (cl:adenylate kinase) (ec:2.7.4.3) (db:pir) JS0492 JS0492 Bacillus subtilis 1423 -11528705

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732795	493	22649	441	146

Description

6500724848 rna polymerase:alpha subunit:dna-directed rna polymerase alpha chain:transcriptase alpha chain:rna polymerase alpha subunit (gtcfc:4.1:4.2:10.3) (ec:2.7.7.6) (keggfc:4.1:4.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rpoA rpoA Bacillus subtilis 1423 -11528706 96164 rpoa (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA_BACSU P20429 BACILLUS SUBTILIS 1423 -11528706 7000686458 rpoa dna-directed rna polymerase:alpha chain rpoa:transcriptase alpha chain (cl:dna-directed rna polymerase alpha chain) (ec:2.7.7.6) (db:pir2.dat) E32307 E32307 Bacillus subtilis 1423 -11528706 7500890595 rpoa rna polymerase alpha-core-subunit (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis initiation factor 1, ribosomal proteins b, s13, s11, l17and rna polymerase alpha core protein genes, complete cds.) (le:1581) (re:2525) (di:direct) BACALPHA M26414 g142463 Bacillus subtilis 1423 -11528706 215152 rpoa rna polymerase alpha-core-subunit (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044991 Bacillus subtilis 1423 -11528706 216634 rpoa rna polymerase alpha subunit (db:genpept-bct1) (ec:2.7.7.6) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:148929) (re:149873) (di:direct) BSUB0001 Z99104 g2632410 Bacillus subtilis 1423 -11528706 139072 rpoa dna-directed rna polymerase:alpha chain rpoa:transcriptase alpha chain (cl:dna-directed rna polymerase alpha chain) (ec:2.7.7.6) (db:pir) E32307 E32307 Bacillus subtilis 1423 -11528706

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732822	494	22650	765	255

Description

6500724849 guab:guaa gmp synthase:glutamine-hydrolyzing:glutamine amidotransferase:gmp synthetase (gtcfc:4.1:5.1:8.2) (ec:6.3.5.2) (keggfc:4.1:5.1) (bsorffc:3.2.1:7.7.1) (db:gtc-bacillus subtilis) guaA guaA Bacillus subtilis 1423 -11528707 7500882834 guaa (ec:6.3.5.2) (de:amidotransferase) (gmp synthetase)) (db:swissprot) GUAA_BACSU P29727 BACILLUS SUBTILIS 1423 -11528707 7000693073 guaa gmp synthase glutamine-hydrolyzing:guaa (cl:gmp synthase (glutamine-hydrolyzing):trpg homology) (ec:6.3.5.2) (db:pir2.dat) C69638 C69638 Bacillus subtilis 1423 -11528707 4000714505 guaa gmp synthetase (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (le:9970) (re:11511) (di:direct) BSU51115 U51115 g2239288 Bacillus subtilis 1423 -11528707 7500882837 guaa gmp synthetase (fn:gmp biosynthesis) (db:genpept-bct1) (ec:6.3.5.2) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: guab) (le:91559) (re:93100) (di:direct) BSUB0004 Z99107 g2632949 Bacillus subtilis 1423 -11528707

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732843	495	22651	270	89

Description

6500724850 phosphoribosylaminoimidazole carboxylase i:phosphoribosylaminoimidazole carboxylase catalytic subunit:air carboxylase:airc (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purE purE Bacillus subtilis 1423 -11528708 92412 pure (ec:4.1.1.21) (de:(ec 4.1.1.21) (air carboxylase) (airc)) (db:swissprot) PUR6_BACSU P12044 BACILLUS SUBTILIS 1423 -11528708 125307 pure phosphoribosylaminoimidazole carboxylase:catalytic chain:phosphoribosylaminoimidazole carboxylase chain i (cl:phosphoribosylaminoimidazole carboxylase catalytic chain:phosphoribosylaminoimidazole carboxylase catalytic chain homology) (ec:4.1.1.21) (db:pir1.dat) (mp:18 min) DEBSPE A29326 Bacillus subtilis 1423 -11528708 7500889056 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosyl aminoimidazole carboxylase i) (le:439) (re:927) (di:direct) BACPURF J02732 g143364 Bacillus subtilis 1423 -11528708 216534 pure phosphoribosylaminoimidazole carboxylase i (fn:purine biosynthesis) (db:genpept-bct1) (ec:4.1.1.21) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:97421) (re:97909) (di:direct) BSUB0004 Z99107 g2632956 Bacillus subtilis 1423 -11528708 7000686241 pure phosphoribosylaminoimidazole carboxylase:catalytic chain:phosphoribosylaminoimidazole carboxylase chain i (cl:phosphoribosylaminoimidazole carboxylase catalytic chain:phosphoribosylaminoimidazole carboxylase catalytic chain homology) (ec:4.1.1.21) (db:pir) (mp:18 min) DEBSPE D69684 Bacillus subtilis 1423 -11528708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732845	496	22652	252	83

Description

6500724851 phosphoribosylaminoimidazole carboxylase ii:phosphoribosylaminoimidazole carboxylase atpase subunit:air carboxylase:airc (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purK purK Bacillus subtilis 1423 -11528709 92462 purk (ec:4.1.1.21) (de:(air carboxylase) (airc)) (db:swissprot) PURK_BACSU P12045 BACILLUS SUBTILIS 1423 -11528709 125309 purk phosphoribosylaminoimidazole carboxylase:carbon dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase chain ii (cl:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain homology) (ec:4.1.1.21) (db:pir1.dat) (mp:18 min) DCBSPK B29326 Bacillus subtilis 1423 -11528709 7500889084 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosyl aminoimidazole carboxylase ii) (le:920) (re:2059) (di:direct) BACPURF J02732 g143365 Bacillus subtilis 1423 -11528709 216535 purk phosphoribosylaminoimidazole carboxylase ii (fn:purine biosynthesis) (db:genpept-bct1) (ec:4.1.1.21) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:97902) (re:99041) (di:direct) BSUB0004 Z99107 g2632957 Bacillus subtilis 1423 -11528709 7000686243 purk phosphoribosylaminoimidazole carboxylase:carbon dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase chain ii (cl:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain homology) (ec:4.1.1.21) (db:pir) (mp:18 min) DCBSPK G69684 Bacillus subtilis 1423 -11528709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732875	497	22653	543	180

Description

6500724852 pure:purb adenylosuccinate lyase:adenylosuccinase:asl (gtcfc:4.1:5.2) (ec:4.3.2.2) (keggfc:4.1:5.2) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purB purB Bacillus subtilis 1423 -11528710 92437 purb:pure (ec:4.3.2.2) (de:adenylosuccinate lyase, (adenylosuccinase) (asl)) (db:swissprot) PUR8_BACSU P12047 BACILLUS SUBTILIS 1423 -11528710 125629 purb adenylosuccinate lyase (cl:fumarate hydratase) (ec:4.3.2.2) (db:pir1.dat) (mp:18 min) WZBSDS C29326 Bacillus subtilis 1423 -11528710 216536 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:adenylosuccinate lyase (pur-b)) (le:2056) (re:3351) (di:direct) BACPURF J02732 g143366 Bacillus subtilis 1423 -11528710 7500889065 purb adenylosuccinate lyase (fn:purine biosynthesis) (db:genpept-bct1) (ec:4.3.2.2) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:99038) (re:100333) (di:direct) BSUB0004 Z99107 g2632958 Bacillus subtilis 1423 -11528710

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732915	498	22654	762	253

Description

6500724853 phosphoribosylaminoimidazole succinocarboxamide synthetase:phosphoribosylaminoimidazole-succinocarboxamide synthase:saicar synthetase (gtcfc:4.1) (ec:6.3.2.6) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purC purC Bacillus subtilis 1423 -11528711 92428 purc (ec:6.3.2.6) (de:(saicar synthetase) (vegetative protein 286a) (veg286a)) (db:swissprot) PUR7_BACSU P12046 BACILLUS SUBTILIS 1423 -11528711 126004 purc phosphoribosylaminoimidazolesuccinocarboxamide synthase (cl:phosphoribosylaminoimidazolesuccinocarboxamide synthase) (ec:6.3.2.6) (db:pir1.dat) (mp:18 min) CEBSSC D29326 Bacillus subtilis 1423 -11528711 216537 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosyl aminoidazole succinocarboxamide) (le:3424) (re:4149) (di:direct) BACPURF J02732 g143367 Bacillus subtilis 1423 -11528711 7500889062 purc phosphoribosylaminoimidazole succinocarboxamide (fn:purine biosynthesis) (db:genpept-bct1) (ec:6.3.2.6) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:100406) (re:101131) (di:direct) BSUB0004 Z99107 g2632959 Bacillus subtilis 1423 -11528711

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732921	499	22655	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732923	500	22656	519	173

Description

GTC ORF with score 356 to: (sr:rattus norvegicus (strain sprague-dawley) (library: charon 4a) (db:genpept-rod) (ec:1.1.3.8) (de:rat gene for l-gulono-gamma-lactone oxidase, exon 12.) (le:d12744:541:d12745:150:d12746:84) (re:543:251:209) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732927	501	22657	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732935	502	22658	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732936	503	22659	546	181

Description

6500724854 purq:purl phosphoribosylformylglycinamidine synthetase ii:phosphoribosylformylglycinamidine synthase i:fgam synthase i (gtcfc:4.1) (ec:6.3.5.3) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purL purL Bacillus subtilis 1423 -11528712 92474 purq (ec:6.3.5.3) (de:synthase i)) (db:swissprot) PURQ_BACSU P12041 BACILLUS SUBTILIS 1423 -11528712 126049 purq phosphoribosylformylglycinamidine synthase:component i (cl:phosphoribosylformylglycinamidine synthase component i) (ec:6.3.5.3) (db:pir1.dat) (mp:18 min) SYBS1G F29326 Bacillus subtilis 1423 -11528712 7500889090 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosylformyl glycinamidine synthetase i) (le:4393) (re:5076) (di:direct) BACPURF J02732 g143368 Bacillus subtilis 1423 -11528712 216538 purl phosphoribosylformylglycinamidine synthetase ii (fn:purine biosynthesis) (db:genpept-bct1) (ec:6.3.5.3) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:101375) (re:102058) (di:direct) BSUB0004 Z99107 g2632961 Bacillus subtilis 1423 -11528712 7000686245 purq phosphoribosylformylglycinamidine synthase:component i (cl:phosphoribosylformylglycinamidine synthase component i) (ec:6.3.5.3) (db:pir) (mp:18 min) SYBS1G H69684 Bacillus subtilis 1423 -11528712

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732940	504	22660	312	104

Description

6500724855 purl:purq phosphoribosylformylglycinamidine synthetase i:phosphoribosylformylglycinamidine synthase ii:fgam synthase ii (gtcfc:4.1) (ec:6.3.5.3) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purQ purQ Bacillus subtilis 1423 -11528713 92467 purl (ec:6.3.5.3) (de:synthase ii)) (db:swissprot) PURL_BACSU P12042 BACILLUS SUBTILIS 1423 -11528713 126050 purl phosphoribosylformylglycinamidine synthase:component ii:formylglycinamide ribotide amidotransferase (cl:phosphoribosylformylglycinamidine synthase component ii) (ec:6.3.5.3) (db:pir1.dat) (mp:18 min) SYBS2G G29326 Bacillus subtilis 1423 -11528713 7500889088 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosylformyl glycinamidine synthetase ii) (le:5060) (re:7288) (di:direct) BACPURF J02732 g143369 Bacillus subtilis 1423 -11528713 216539 purq phosphoribosylformylglycinamidine synthetase i (fn:purine biosynthesis) (db:genpept-bct1) (ec:6.3.5.3) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:102042) (re:104270) (di:direct) BSUB0004 Z99107 g2632962 Bacillus subtilis 1423 -11528713 7000686244 purl phosphoribosylformylglycinamidine synthase:component ii (cl:phosphoribosylformylglycinamidine synthase component ii) (ec:6.3.5.3) (db:pir) (mp:18 min) SYBS2G C69685 Bacillus subtilis 1423 -11528713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732990	505	22661	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501732992	506	22662	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733003	507	22663	864	287

Description

6500724856 purb:purf phosphoribosylpyrophosphate amidotransferase:amidophosphoribosyltransferase precursor:glutamine phosphoribosylpyrophosphate amidotransferase:atase (gtcfc:4.1:5.1) (ec:2.4.2.14) (keggfc:4.1:5.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purF purF Bacillus subtilis 1423 -11528714 92375 purf (ec:2.4.2.14) (de:phosphoribosylpyrophosphate amidotransferase) (atase) (gpatase)) (db:swissprot) PUR1_BACSU P00497 BACILLUS SUBTILIS 1423 -11528714 123441 purf amidophosphoribosyltransferase:purf:phosphoribosylpyrophosphate amidotransferase (cl:amidophosphoribosyltransferase) (ec:2.4.2.14) (db:pir1.dat) XQBS A00582 Bacillus subtilis 1423 -11528714 7500889030 (sr:b.subtilis (strain del (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosylpyrophosphate amidotransferase) (le:7264) (re:8694) (di:direct) BACPURF J02732 g143370 Bacillus subtilis 1423 -11528714 216540 purf phosphoribosylpyrophosphate amidotransferase (fn:purine biosynthesis) (db:genpept-bct1) (ec:2.4.2.14) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: purb) (le:104246) (re:105676) (di:direct) BSUB0004 Z99107 g2632963 Bacillus subtilis 1423 -11528714 7000686239 purf amidophosphoribosyltransferase:purf:phosphoribosylpyrophosphate amidotransferase (cl:amidophosphoribosyltransferase) (ec:2.4.2.14) (db:pir) XQBS E69684 Bacillus subtilis 1423 -11528714

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733004	508	22664	792	264

Description

6500724857 ath:purm phosphoribosylaminoimidazole synthetase:phosphoribosylformylglycinamidine cyclo-ligase:airs:phosphoribosyl-aminoimidazole synthetase:air synthase (gtcfc:4.1) (ec:6.3.3.1) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purM purM Bacillus subtilis 1423 -11528715 92407 purm:ath (ec:6.3.3.1) (de:(phosphoribosyl-aminoimidazole synthetase) (air synthase)) (db:swissprot) PUR5_BACSU P12043 BACILLUS SUBTILIS 1423 -11528715 126012 purm phosphoribosylformylglycinamidine cyclo-ligase::phosphoribosylaminoimidazole synthetase (cl:phosphoribosylformylglycinamidine cyclo-ligase:phosphoribosylformylglycinamidine cyclo-ligase homology) (ec:6.3.3.1) (db:pir1.dat) (mp:18 min) AJBSCL H29326 Bacillus subtilis 1423 -11528715 216541 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosyl aminoimidazole synthetase (pur-m)) (le:8796) (re:9836) (di:direct) BACPURF J02732 g143371 Bacillus subtilis 1423 -11528715 7500889054 purm phosphoribosylaminoimidazole synthetase (fn:purine biosynthesis) (db:genpept-bct1) (ec:6.3.3.1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:105778) (re:106818) (di:direct) BSUB0004 Z99107 g2632964 Bacillus subtilis 1423 -11528715

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733005	509	22665	711	236

Description

6500724858 phosphoribosylglycinamide formyltransferase:gart:gar transformylase:5-phosphoribosylglycinamide transformylase (gtcfc:4.1:9.6) (ec:2.1.2.2) (keggfc:4.1:9.8) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) (gtcfc:nucleotide metabolism-purine metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) purN purN Bacillus subtilis 1423 -11528716 92399 purn (ec:2.1.2.2) (de:transformylase) (5'-phosphoribosylglycinamide transformylase)) (db:swissprot) PUR3_BACSU P12040 BACILLUS SUBTILIS 1423 -11528716 123292 purn phosphoribosylglycinamide formyltransferase (cl:phosphoribosylglycinamide formyltransferase:phosphoribosylglycinamide formyltransferase homology) (ec:2.1.2.2) (db:pir1.dat) (mp:18 min) XYBSGF I29326 Bacillus subtilis 1423 -11528716 216542 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosyl glycinamide formyltransferase) (le:9833) (re:10420) (di:direct) BACPURF J02732 g143372 Bacillus subtilis 1423 -11528716 7500889049 purn phosphoribosylglycinamide formyltransferase (fn:purine biosynthesis) (db:genpept-bct1) (ec:2.1.2.2) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:106815) (re:107402) (di:direct) BSUB0004 Z99107 g2632965 Bacillus subtilis 1423 -11528716 5000688539 (de:(purn) (pn:phosphoribosylglycinamide formyltransferase:gart:gar transformylase:phosphoribosylglycinamide formyltransferase :gart:gar transformylase:5"-phosphoribosylglycinamide transformylase) (gtcfc:9.06) (ec:2.1.2.2) (pur3_) purN purN Bacillus subtilis 1423 10034431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733017	510	22666	378	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733019	511	22667	609	202

Description

6500724859 purj:purhj:purh phosphoribosylaminoimidazole carboxy formyl formyltransferase / inosine-monophosphate cyclohy...:phosphoribosylaminoimidazolecarboxamide formyltransferase:aicar transformylase / imp cyclohydrolase:inosinicase:imp synthetase:atic (gtcfc:4.1:9.6) (keggfc:4.1:9.8) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) (gtcfc:nucleotide metabolism-purine metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) purH purH Bacillus subtilis 1423 -11528717 92445 purh:purhj (ec:2.1.2.3:3.5.4.10) (de:(inosinicase) (imp synthetase) (atic)) (db:swissprot) PUR9_BACSU P12048 BACILLUS SUBTILIS 1423 -11528717 123294 purh:purj purh bifunctional enzyme (cl:purh bifunctional enzyme) (db:pir1.dat) (mp:18 min) DTBSPH A29183 Bacillus subtilis 1423 -11528717 216543 (sr:b.subtilis (strain del (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosyl aminoimidazole carboxy formyl) (le:10417) (re:11955) (di:direct) BACPURF J02732 g143373 Bacillus subtilis 1423 -11528717 7500889078 purh inosine-monophosphate cyclohydrolase (fn:purine biosynthesis) (db:genpept-bct1) (ec:2.1.2.3:3.5.4.10) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: purj;) (le:107399) (re:108937) (di:direct) BSUB0004 Z99107 g2632966 Bacillus subtilis 1423 -11528717 5000688538 (de:(purh) (pn:phosphoribosylaminoimidazolecarboxamide formyltransferase:aicar transformylase :phosphoribosylaminoimidazolecarboxamide formyltransferase :aicar transformylase) (gn:purhj) (gtcfc:9.06) (ec:2.1.2.3) (pur9_bacsu) (k)) purH purH Bacillus subtilis 1423 10034477

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733023	512	22668	183	61

Description

6500724860 phosphoribosylamine--glycine ligase:gars:glycinamide ribonucleotide synthetase:phosphoribosylglycinamide synthetase (gtcfc:4.1) (ec:6.3.4.13) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purD purD Bacillus subtilis 1423 -11528718 92387 purd (ec:6.3.4.13) (de:ribonucleotide synthetase) (phosphoribosylglycinamide synthetase)) (db:swissprot) PUR2_BACSU P12039 BACILLUS SUBTILIS 1423 -11528718 126037 purd phosphoribosylamine--glycine ligase::phosphoribosylglycinamide synthetase (cl:phosphoribosylamine--glycine ligase:phosphoribosylamine--glycine ligase homology) (ec:6.3.4.13) (db:pir1.dat) (mp:18 min) AJBSAG B29183 Bacillus subtilis 1423 -11528718 216544 purd phosphoribosylglycinamide synthetase (db:genpept-bct1) (de:bacillus subtilis phosphoribosylaminoimidazole-carboxamideformyltransferase (purh-j) gene, partial cds,phosphoribosylglycinamide synthetase (purd), yeca (yeca), putativeadenine deaminase (yecb), yecc (yecc), and yecd (yecd) genes,... AF011544 AF011544 g2465561 Bacillus subtilis 1423 -11528718 5500684702 (sr:b.subtilis (strain de1 (prototroph der. or w168)) dna, clone ppz) (db:genpept-bct1) (de:b.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.) (nt:phosphoribosyl glycinamide synthetase (pur-d; gtg) (le:11971) (re:13239) (di:direct) BACPURF J02732 g143374 Bacillus subtilis 1423 -11528718 7500889034 purd phosphoribosylglycinamide synthetase (fn:purine biosynthesis) (db:genpept-bct1) (ec:6.3.4.13) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:108953) (re:110221) (di:direct) BSUB0004 Z99107 g2632967 Bacillus subtilis 1423 -11528718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733028	513	22669	456	151

Description

6500724861 hypothetical protein:similar to 2:3-cyclic-nucleotide 2-phosphodiesterase (gtcfc:4.1:4.2:9.4:14.1) (keggfc:4.1:4.2:9.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkN yfkN Bacillus subtilis 1423 -11528719 7000692034 yfkn probable multifunctional phosphoesterase:yfkn (cl:probable multifunctional phosphoesterase yfkn:2',3'-cyclic-nucleotide 2'-phosphodiesterase homology:5'-nucleotidase homology:phosphoesterase core homology) (ec:3.1.-.-) (db:pir1.dat) A69809 A69809 Bacillus subtilis 1423 -11528719 6000690332 yfkn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to 2',3'-cyclic-nucleotide) (le:51801) (re:56189) (di:complement) BSUB0005 Z99108 g2633108 Bacillus subtilis 1423 -11528719 7500953282 yfkn (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:11732) (re:16120) (di:direct) D83967 D83967 g2626826 Bacillus subtilis 1423 -11528719

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733060	514	22670	921	307

Description

6500724862 hypothetical protein:hypothetical 14.9 kd protein in cspb-glpp intergenic region (gtcfc:4.1:14.1) (ec:1.1.1.205) (keggfc:4.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcV yhcV Bacillus subtilis 1423 -11528720 218985 yhcv (de:hypothetical 14.9 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCV_BACSU P54606 BACILLUS SUBTILIS 1423 -11528720 7000687951 yhcv conserved hypothetical protein yhcv (cl:conserved hypothetical protein yhcv:cbs homology) (db:pir2.dat) B69824 B69824 Bacillus subtilis 1423 -11528720 5000689182 yhcv hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to imp dehydrogenase (guab or gnab) from) (le:18055) (re:18477) (di:direct) BS75DGREG X96983 g1239998 Bacillus subtilis 1423 -11528720 308501 yhcv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:193861) (re:194283) (di:direct) BSUB0005 Z99108 g2633246 Bacillus subtilis 1423 -11528720 112707 yhcv (de:hypothetical 14.9 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCV_BACSU P54606 BACILLUS SUBTILIS 1423 -11528720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733067	515	22671	405	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733070	516	22672	621	207

Description

6500724863 hypothetical protein:similar to diadenosine tetraphosphatase (gtcfc:4.1:14.1) (ec:3.6.1.41) (keggfc:4.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbP yjbP Bacillus subtilis 1423 -11528721 7000692915 yjbp diadenosine tetraphosphatase homolog yjbp (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (db:pir2.dat) H69844 H69844 Bacillus subtilis 1423 -11528721 7500963934 yjbp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to diadenosine tetraphosphatase) (le:44468) (re:45202) (di:complement) BSUB0007 Z99110 g2633517 Bacillus subtilis 1423 -11528721

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733105	517	22673	522	173

Description

6500724864 yzad:ade:adec adenine deaminase:adenase:adenine aminase (gtcfc:4.1:4.4) (ec:3.5.4.2) (keggfc:4.1) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) adeC adeC Bacillus subtilis 1423 -11528722 58618 adec:ade (ec:3.5.4.2) (de:adenine deaminase, (adenase) (adenine aminase)) (db:swissprot) ADEC_BACSU P39761 BACILLUS SUBTILIS 1423 -11528722 7000684526 adec adenine deaminase (cl:adenine deaminase adec) (ec:3.5.4.2) (db:pir2.dat) B69583 B69583 Bacillus subtilis 1423 -11528722 7500876569 adec adenine deaminase (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to products of orf5 encoded by genbank) (le:26454) (re:28187) (di:direct) AF012285 AF012285 g3282137 Bacillus subtilis 1423 -11528722 215167 pos:5995..5997:aa:met (sr:bacillus subtilis (sub_species:marburg, strain:168) (db:genpept-bct1) (de:bacillus subtilis genes for amps, mrebh, orf1, kinc, orf3, orf4 andorf5.) (le:5995) (re:7728) (di:direct) BACAMOKOOO D37799 g1065989 Bacillus subtilis 1423 -11528722 220076 adec adenine deaminase (db:genpept-bct1) (ec:3.5.4.2) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ade, yzad) (le:125966) (re:127699) (di:direct) BSUB0008 Z99111 g2633823 Bacillus subtilis 1423 -11528722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733106	518	22674	222	74

Description

6500724865 muti:dnaf:dnap:dnae:polc dna polymerase iii:alpha subunit:dna polymerase iii:alpha chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) polC polC Bacillus subtilis 1423 -11528723 219538 polc:dnaf:muti (ec:2.7.7.7) (de:dna polymerase iii, alpha chain polc-type, (poliii)) (db:swissprot) DPO3_BACSU P13267 BACILLUS SUBTILIS 1423 -11528723 7000685083 polc:dnaf dna-directed dna polymerase:iii alpha chain polc (cl:dna-directed dna polymerase iii alpha chain polc) (ec:2.7.7.7) (db:pir2.dat) F69680 F69680 Bacillus subtilis 1423 -11528723 7500880543 (db:genpept-bct1) (de:bacillus subtilis polc gene for dna polymerase iii.) (nt:dna polymerase iii (aa 1-1437)) (le:46) (re:4359) (di:direct) BSPOLC1 X52116 g40060 Bacillus subtilis 1423 -11528723 7502851532 polc dna polymerase iii alpha subunit (fn:initation of replication cycle and dna) (db:genpept-bct1) (ec:2.7.7.7) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: muti, dnaf, dnap) (le:128104) (re:132417) (di:direct) BSUB0009 Z99112 g2634030 Bacillus subtilis 1423 -11528723 69042 polc:dnae:dnaf:muti (ec:2.7.7.7) (de:dna polymerase iii, alpha chain,) (db:swissprot) DP3A_BACSU P13267 BACILLUS SUBTILIS 1423 -11528723

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733108	519	22675	336	111

Description

6500724866 comr:pnpa polyribonucleotide nucleotidyltransferase:polynucleotide phosphorylase:pnpase (gtcfc:4.1:4.2:14.3) (ec:2.7.7.8) (keggfc:4.1:4.2) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) pnpA pnpA Bacillus subtilis 1423 -11528724 7000686157 pnpa polyribonucleotide nucleotidyltransferase:alpha chain pnpa:polynucleotide phosphorylase pnpa (cl:polyribonucleotide nucleotidyltransferase alpha chain) (ec:2.7.7.8) (db:pir2.dat) S70691 S70691 Bacillus subtilis 1423 -11528724 7500965088 pnpa polynucleotide phosphorylase pnpase (fn:necessary for competence development) (db:genpept-bct1) (ec:2.7.7.8) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: comr) (le:140354) (re:142471) (di:direct) BSUB0009 Z99112 g2634041 Bacillus subtilis 1423 -11528724 219916 pnpa polynucleotide phosphorylase (db:genpept-bct2) (de:bacillus subtilis ribosomal protein rpso (rpso) gene, partial cds,and polynucleotide phosphorylase (pnpa) gene, complete cds.) (le:224) (re:2341) (di:direct) BSU29668 U29668 g1184680 Bacillus subtilis 1423 -11528724 90175 pnp_bacsu (de:polyribonucleotide nucleotidyltransferase (ec 2.7.7.8) (polynucleotide phosphorylase) (pnpase).) P50849 P50849 Bacillus subtilis 1423 10032295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733115	520	22676	420	139

Description

6500724867 nrda:nrde ribonucleoside-diphosphate reductase:major subunit:ribonucleoside-diphosphate reductase alpha chain:ribonucleotide reductase (gtcfc:4.1:4.2:4.3:10.3) (ec:1.17.4.1) (keggfc:4.1:4.2) (bsorffc:3.3.1:4.2.1) (db:gtc-bacillus subtilis) nrdE nrdE Bacillus subtilis 1423 -11528725 219427 nrde:nrda (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR1_BACSU P50620 BACILLUS SUBTILIS 1423 -11528725 7000686334 nrde ribonucleoside-diphosphate reductase:large chain nrde (cl:salmonella typhimurium ribonucleoside-diphosphate reductase) (ec:1.17.4.1) (db:pir2.dat) B69667 B69667 Bacillus subtilis 1423 -11528725 7500889797 nrde nrde (fn:reduction of ribonucleotide diphosphates) (db:genpept-bct1) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (nt:similarity to nrde of enterobacteriaceae) (le:1291) (re:3393) (di:direct) BSNRDYMA Z68500 g1154632 Bacillus subtilis 1423 -11528725 7502851533 nrde ribonucleoside-diphosphate reductase major (db:genpept-bct1) (ec:1.17.4.1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:87010) (re:89112) (di:direct) BSUB0010 Z99113 g2634122 Bacillus subtilis 1423 -11528725 7502851534 nrde nrde (fn:reduction of ribonucleotide diphosphates) (db:genpept) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (nt:similarity to nrde of enterobacteriaceae) (le:1291) (re:3393) (di:direct) BSNRDYMA Z68500 g1154632 Bacillus subtilis 1423 -11528725 94404 nrde:nrda (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR1_BACSU P50620 BACILLUS SUBTILIS 1423 -11528725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733155	521	22677	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733158	522	22678	231	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733164	523	22679	810	270

Description

GTC ORF with score 174 to: (db:genpept-bct1) (de:bacillus licheniformis bacitracin synthetase operon includingbacitracin synthetase 1 (baca), 2 (bacb) and 3 (bacc) genes,complete cds.) (nt:peptide synthetase; ba3; bacc) (le:24119) (re:43198) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733169	524	22680	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733209	525	22681	501	166

Description

6500724868 ribonucleoside-diphosphate reductase:minor subunit:ribonucleoside-diphosphate reductase beta chain:ribonucleotide reductase (gtcfc:4.1:4.2:4.3:10.3) (ec:1.17.4.1) (keggfc:4.1:4.2) (bsorffc:3.3.1:4.2.1) (db:gtc-bacillus subtilis) nrdF nrdF Bacillus subtilis 1423 -11528726 219428 nrdf (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR2_BACSU P50621 BACILLUS SUBTILIS 1423 -11528726 7000686339 nrdf ribonucleoside-diphosphate reductase minor subunit nrdf (cl:ribonucleoside-diphosphate reductase beta) (db:pir2.dat) C69667 C69667 Bacillus subtilis 1423 -11528726 7500889805 nrdf nrdf (fn:reduction of ribonucleotide diphosphates) (db:genpept-bct1) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (nt:similarity to nrdf of enterobacteriaceae) (le:3411) (re:4400) (di:direct) BSNRDYMA Z68500 g1154633 Bacillus subtilis 1423 -11528726 7502851535 nrdf ribonucleoside-diphosphate reductase minor (db:genpept-bct1) (ec:1.17.4.1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:89130) (re:90119) (di:direct) BSUB0010 Z99113 g2634123 Bacillus subtilis 1423 -11528726 7502851536 nrdf nrdf (fn:reduction of ribonucleotide diphosphates) (db:genpept) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (nt:similarity to nrdf of enterobacteriaceae) (le:3411) (re:4400) (di:direct) BSNRDYMA Z68500 g1154633 Bacillus subtilis 1423 -11528726 94437 nrdf (ec:1.17.4.1) (de:(ribonucleotide reductase)) (db:swissprot) RIR2_BACSU P50621 BACILLUS SUBTILIS 1423 -11528726

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733213	526	22682	735	245

Description

6500724869 purine nucleoside phosphorylase (gtcfc:4.1:4.2:4.3:9.4) (ec:2.4.2.1) (keggfc:4.1:4.2:9.4) (bsorffc:3.3.1) (db:gtc-bacillus subtilis) deoD deoD Bacillus subtilis 1423 -11528727 7000694472 deod purine nucleoside phosphorylase deod (cl:purine-nucleoside phosphorylase pnp) (db:pir2.dat) D69614 D69614 Bacillus subtilis 1423 -11528727 5500687375 yoky yoky (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:similar to the punb (purine nucleoside) (le:20019) (re:20720) (di:direct) AF006665 AF006665 g2529472 Bacillus subtilis 1423 -11528727 5500687376 deod purine nucleoside phosphorylase (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415397 Bacillus subtilis 1423 -11528727 7500965120 deod purine nucleoside phosphorylase (fn:purine nucleoside salvage) (db:genpept-bct1) (ec:2.4.2.1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:134544) (re:135245) (di:complement) BSUB0011 Z99114 g2634355 Bacillus subtilis 1423 -11528727

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733247	527	22683	303	100

Description

6500724870 hypothetical protein:similar to ribonucleoside-diphosphate reductase:beta subunit (gtcfc:4.1:4.2:14.1) (ec:1.17.4.1) (keggfc:4.1:4.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosP yosP Bacillus subtilis 1423 -11528728 7000694519 yosp ribonucleoside-diphosphate reductase beta homolog yosp (db:pir2.dat) B69927 B69927 Bacillus subtilis 1423 -11528728 7500965151 yosp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to ribonucleoside-diphosphate reductase) (le:160264) (re:160851) (di:complement) BSUB0011 Z99114 g2634397 Bacillus subtilis 1423 -11528728

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733258	528	22684	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733311	529	22685	198	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733327	530	22686	225	75

Description

GTC ORF with score 330 to: (db:genpept-pln1) (de:aspergillus oryzae putative dna binding protein facb (facb) gene,complete cds.) (nt:description: homologue of the emericella nidulans) (le:1680:2223:2597:2927) (re:2148:2536:2877:3284) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733391	531	22687	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733445	532	22688	717	238

Description

6500724871 nucleoside diphosphate kinase:ndk:ndp kinase (gtcfc:4.1:4.2:4.3) (ec:2.7.4.6) (keggfc:4.1:4.2) (bsorffc:3.3.1) (db:gtc-bacillus subtilis) ndk ndk Bacillus subtilis 1423 -11528729 85483 ndk (ec:2.7.4.6) (de:nucleoside diphosphate kinase, (ndk) (ndp kinase)) (db:swissprot) NDK_BACSU P31103 BACILLUS SUBTILIS 1423 -11528729 7000685951 ndk nucleoside diphosphate kinase ndk (cl:nucleoside-diphosphate kinase) (db:pir2.dat) D69666 D69666 Bacillus subtilis 1423 -11528729 217030 ndk ndk (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:3947) (re:4396) (di:direct) BACVARGNS M80245 g143804 Bacillus subtilis 1423 -11528729 7500886371 ndk nucleoside diphosphate kinase (db:genpept-bct1) (ec:2.7.4.6) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:185052) (re:185501) (di:complement) BSUB0012 Z99115 g2634691 Bacillus subtilis 1423 -11528729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733446	533	22689	264	88

Description

6500724872 yqko:deod:pnp purine nucleoside phosphorylase:inosine phosphorylase:pnp (gtcfc:4.1:4.2:4.4:9.4) (ec:2.4.2.1) (keggfc:4.1:4.2:9.4) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) pnp pnp Bacillus subtilis 1423 -11528730 68259 deod:pnp (ec:2.4.2.1) (de:(pnp)) (db:swissprot) DEOD_BACSU P46354 BACILLUS SUBTILIS 1423 -11528730 7000685011 pnp purine-nucleoside phosphorylase:pnp (cl:purine-nucleoside phosphorylase) (ec:2.4.2.1) (db:pir2.dat) D69680 D69680 Bacillus subtilis 1423 -11528730 216240 yqko (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:272417) (re:273232) (di:direct) BACJH642 D84432 g1303996 Bacillus subtilis 1423 -11528730 219959 pnp purine nucleoside phosphorylase (fn:cleavage of guanosine or inosine to respective) (db:genpept-bct1) (de:bacillus subtilis ripx (ripx) gene, partial cds, purine nucleosidephosphorylase (pnp) and phosphopentomutase (drm) genes, completecds.) (nt:involved in purine nucleoside salvage)... BSU32685 U32685 g944944 Bacillus subtilis 1423 -11528730 7500880172 pnp purine nucleoside phosphorylase (fn:cleavage of guanosine or inosine to respective) (db:genpept-bct1) (ec:2.4.2.1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqko) (le:50387) (re:51202) (di:complement) BSUB0013 Z99116 g2634784 Bacillus subtilis 1423 -11528730

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733447	534	22690	1158	386

Description

6500724873 adenine phosphoribosyltransferase (gtcfc:4.1) (ec:2.4.2.7) (keggfc:4.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) apt apt Bacillus subtilis 1423 -11528731 7000692156 apt adenine phosphoribosyltransferase::amp pyrophosphorylase:transphosphoribosidase (cl:adenine phosphoribosyltransferase) (ec:2.4.2.7) (db:pir2.dat) B69587 B69587 Bacillus subtilis 1423 -11528731 5500698951 apt adenine phosphoribosyltransferase (db:genpept-bct1) (ec:2.4.2.7) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:27036) (re:27548) (di:complement) BSUB0015 Z99118 g2635225 Bacillus subtilis 1423 -11528731 7500954017 apt (db:genpept-bct2) (de:bacillus subtilis (p)ppgpp synthetase (rela) and adeninephosphoribosyltransferase (apt) genes, complete cds.) (nt:adenine phosphoribosyltransferase; apt) (le:222) (re:734) (di:direct) BSU86377 U86377 g2580524 Bacillus subtilis 1423 -11528731

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733448	535	22691	231	77

Description

6500724874 dna polymerase i (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) polA polA Bacillus subtilis 1423 -11528732 7502851537 pola (ec:2.7.7.7) (de:dna polymerase i, (pol i)) (db:swissprot) DPO1_BACSU O34996 BACILLUS SUBTILIS 1423 -11528732 7000692936 pola dna polymerase i pola (cl:dna-directed dna polymerase i) (db:pir2.dat) E69680 E69680 Bacillus subtilis 1423 -11528732 4000714264 pola dna-polymerase i (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:203300) (re:205942) (di:direct) AF008220 AF008220 g2293272 Bacillus subtilis 1423 -11528732 7500963950 pola dna polymerase i (fn:replication and dna repair) (db:genpept-bct1) (ec:2.7.7.7) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:177125) (re:179767) (di:complement) BSUB0015 Z99118 g2635374 Bacillus subtilis 1423 -11528732

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733449	536	22692	252	83

Description

6500724875 dna polymerase iii:alpha subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaE dnaE Bacillus subtilis 1423 -11528733 7502851538 dnae (ec:2.7.7.7) (de:dna polymerase iii, alpha chain,) (db:swissprot) DP3A_BACSU O34623 BACILLUS SUBTILIS 1423 -11528733 7000692937 dnae dna polymerase iii alpha subunit dnae (cl:dna-directed dna polymerase iii alpha chain) (db:pir2.dat) D69617 D69617 Bacillus subtilis 1423 -11528733 4000714254 dnae dna-polymerase iii alpha-chain (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:184508) (re:187855) (di:direct) AF008220 AF008220 g2293260 Bacillus subtilis 1423 -11528733 7500963951 dnae dna polymerase iii alpha subunit (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:195212) (re:198559) (di:complement) BSUB0015 Z99118 g2635388 Bacillus subtilis 1423 -11528733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733485	537	22693	267	88

Description

GTC ORF with score 198 to: (fn:catalyzes the phosphorylation of pyruvate) (db:genpept-pln2) (ec:2.7.1.99) (de:zea mays pyruvate dehydrogenase kinase isoform 2 mrna, nuclear geneencoding mitochondrial protein, complete cds.) (nt:pdk2) (le:78) (re:1172) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733489	538	22694	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733490	539	22695	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733494	540	22696	921	307

Description

GTC ORF with score 966 to: (sr:neurospora crassa strain=74-or23-1va) (db:genpept-pln1) (de:neurospora crassa 74-or23-1va two-component histidine kinase nik-1(nik-1) mrna, complete cds.) (nt:two-component histidine kinase) (le:869) (re:4765) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733529	541	22697	300	99

Description

6500724876 hypothetical protein:similar to allantoinase (gtcfc:4.1:14.1) (ec:3.5.2.5) (keggfc:4.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yunH yunH Bacillus subtilis 1423 -11528734 7500876767 yunh (ec:3.5.2.5) (de:putative allantoinase,) (db:swissprot) ALLA_BACSU O32137 BACILLUS SUBTILIS 1423 -11528734 7000692178 yunh allantoinase homolog yunh (cl:allantoinase:bacillus dihydroorotase homology) (db:pir2.dat) C70016 C70016 Bacillus subtilis 1423 -11528734 7500876769 yunh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to allantoinase) (le:129305) (re:130645) (di:complement) BSUB0017 Z99120 g2635738 Bacillus subtilis 1423 -11528734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733536	542	22698	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733550	543	22699	513	170

Description

6500724877 urease:alpha subunit:urease alpha subunit:urea amidohydrolase (gtcfc:4.1:5.16:5.4) (ec:3.5.1.5) (keggfc:4.1:5.16) (bsorffc:3.1.7) (db:gtc-bacillus subtilis) ureC ureC Bacillus subtilis 1423 -11528735 4000709979 urec (ec:3.5.1.5) (de:urease alpha subunit, (urea amidohydrolase)) (db:swissprot) URE1_BACSU P77837 BACILLUS SUBTILIS 1423 -11528735 7000686898 urec urease alpha subunit urec (cl:urease 62k chain:urease 62k chain homology) (db:pir2.dat) D69729 D69729 Bacillus subtilis 1423 -11528735 220219 urec urease alpha subunit (db:genpept-bct1) (ec:3.5.1.5) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:168678) (re:170387) (di:complement) BSUB0019 Z99122 g2636189 Bacillus subtilis 1423 -11528735 7500893839 urec urease (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:844) (re:2553) (di:direct) BSUEROP Y08559 g1592696 Bacillus subtilis 1423 -11528735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733612	544	22700	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733629	545	22701	414	138

Description

6500724878 urease:beta subunit:urease beta subunit:urea amidohydrolase (gtcfc:4.1:5.16:5.4) (ec:3.5.1.5) (keggfc:4.1:5.16) (bsorffc:3.1.7) (db:gtc-bacillus subtilis) ureB ureB Bacillus subtilis 1423 -11528736 5500686120 ureb (ec:3.5.1.5) (de:urease beta subunit, (urea amidohydrolase)) (db:swissprot) URE2_BACSU P71035 BACILLUS SUBTILIS 1423 -11528736 7000686900 ureb urease beta subunit ureb (cl:urease 12k chain:urease 12k chain homology) (db:pir2.dat) C69729 C69729 Bacillus subtilis 1423 -11528736 220218 ureb urease beta subunit (db:genpept-bct1) (ec:3.5.1.5) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:170384) (re:170758) (di:complement) BSUB0019 Z99122 g2636190 Bacillus subtilis 1423 -11528736 7500893842 ureb urease (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:473) (re:847) (di:direct) BSUEROP Y08559 g1592695 Bacillus subtilis 1423 -11528736

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733633	546	22702	582	193

Description

6500724879 urease:gamma subunit:urease gamma subunit:urea amidohydrolase (gtcfc:4.1:5.16:5.4) (ec:3.5.1.5) (keggfc:4.1:5.16) (bsorffc:3.1.7) (db:gtc-bacillus subtilis) ureA ureA Bacillus subtilis 1423 -11528737 5500686124 urea (ec:3.5.1.5) (de:urease gamma subunit, (urea amidohydrolase)) (db:swissprot) URE3_BACSU P75030 BACILLUS SUBTILIS 1423 -11528737 7000686901 urea urease gamma subunit urea (cl:urease 11k chain:urease 11k chain homology) (db:pir2.dat) B69729 B69729 Bacillus subtilis 1423 -11528737 219037 urea urease gamma subunit (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:12095) (re:12412) (di:direct) BSATPC Z81356 g1648860 Bacillus subtilis 1423 -11528737 220217 urea urease gamma subunit (db:genpept-bct1) (ec:3.5.1.5) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:170755) (re:171072) (di:complement) BSUB0019 Z99122 g2636191 Bacillus subtilis 1423 -11528737 304090 urea urease (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:159) (re:476) (di:direct) BSUEROP Y08559 g1592694 Bacillus subtilis 1423 -11528737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733638	547	22703	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733690	548	22704	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733691	549	22705	381	126

Description

6500724880 rna polymerase:delta subunit:dna-directed rna polymerase delta subunit (gtcfc:4.1:4.2:10.3) (ec:2.7.7.6) (keggfc:4.1:4.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rpoE rpoE Bacillus subtilis 1423 -11528738 304110 rpoe (ec:2.7.7.6) (de:dna-directed rna polymerase delta subunit,) (db:swissprot) RPOE_BACSU P12464 BACILLUS SUBTILIS 1423 -11528738 123966 rpoe dna-directed rna polymerase:delta chain rpoe (cl:dna-directed rna polymerase delta chain) (ec:2.7.7.6) (db:pir1.dat) JT0302 JT0302 Bacillus subtilis 1423 -11528738 216640 (sr:b.subtilis (strain 168) dna, clone mml11) (db:genpept-bct1) (de:b.subtilis rna polymerase delta subunit (rpoe) gene, complete cds.) (nt:rpoe protein (ttg start codon)) (le:101) (re:622) (di:direct) BACRPOE M21677 g143456 Bacillus subtilis 1423 -11528738 219138 rpoe rna polymerase delta subunit (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:ttg start codon) (le:8717) (re:9238) (di:direct) BSDNA320D Z49782 g853761 Bacillus subtilis 1423 -11528738 7502851539 rpoe rna polymerase delta subunit (db:genpept-bct1) (ec:2.7.7.6) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:13195) (re:13716) (di:complement) BSUB0020 Z99123 g2636253 Bacillus subtilis 1423 -11528738 96271 rpoe (ec:2.7.7.6) (de:dna-directed rna polymerase delta subunit,) (db:swissprot) RPOE_BACSU P12464 BACILLUS SUBTILIS 1423 -11528738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733711	550	22706	876	292

Description

6500724881 adenylosuccinate synthetase:imp--aspartate ligase (gtcfc:4.1:5.2) (ec:6.3.4.4) (keggfc:4.1:5.2) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purA purA Bacillus subtilis 1423 -11528739 206155 pura adenylosuccinate synthase:pura:imp--aspartate ligase (cl:adenylosuccinate synthase) (ec:6.3.4.4) (db:pir2.dat) A42280 S65968 Bacillus subtilis 1423 -11528739 7500954507 pura adenylosuccinate synthetase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:3429) (re:4721) (di:complement) BAC180K D26185 g467328 Bacillus subtilis 1423 -11528739 214928 pura adenylosuccinate synthetase (fn:amp biosynthesis) (db:genpept-bct1) (ec:6.3.4.4) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:155361) (re:156653) (di:complement) BSUB0021 Z99124 g2636589 Bacillus subtilis 1423 -11528739 7000689225 pura adenylosuccinate synthase:pura:imp--aspartate ligase (cl:adenylosuccinate synthase) (ec:6.3.4.4) (db:pir) A42280 A42280 Bacillus subtilis 1423 -11528739

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733747	551	22707	201	66

Description

6500724882 phosphoribosylglycinamide formyltransferase 2:gart 2:gar transformylase 2:5-phosphoribosylglycinamide transformylase 2:formate-dependent gar transformylase (gtcfc:4.1) (ec:2.1.2.-) (keggfc:14.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) purT purT Bacillus subtilis 1423 -11528740 7502851540 purt (ec:2.1.2.-) (de:2) (formate-dependent gar transformylase)) (db:swissprot) PURT_BACSU P39771 BACILLUS SUBTILIS 1423 -11528740 7000694421 purt phosphoribosylglycinamide formyltransferase:2:5-phosphoribosyl-1-glycinamide transformylase t (cl:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain homology) (ec:2.1.2.-) (db:pir2.dat) E69685 E69685 Bacillus subtilis 1423 -11528740 7500954388 purt phosphoribosylglycinamide formyltransferase 2 (fn:purine biosynthesis) (db:genpept-bct1) (ec:2.1.2.-) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:49231) (re:50385) (di:direct) BSUB0002 Z99105 g2632509 Bacillus subtilis 1423 -11528740 7500954389 purt phosphoribosylglycinamide formyltransferase 2 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:46882) (re:48036) (di:direct) AB006424 AB006424 g3599645 Bacillus subtilis 1423 -11528740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733748	552	22708	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733754	553	22709	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733755	554	22710	483	160

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733790	555	22711	273	90

Description

6500724883 phosphoadenosine phosphosulfate (gtcfc:4.1) (ec:1.8.99.4) (keggfc:14.1) (bsorffc:3.2.1) (db:gtc-bacillus subtilis) cysH cysH Bacillus subtilis 1423 -11528741 7000694404 cysh 3-phosphoadenosine 5-phosphosulfate reductase:cysh:3-phosphoadenylylsulfate reductase:thioredoxin dependent:paps reductase:paps sulfotransferase (ec:1.8.99.4) (db:pir2.dat) H69611 H69611 Bacillus subtilis 1423 -11528741 5500687774 cysh putative phospho-adenylylsulphate (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (le:548) (re:1249) (di:direct) BSPYREYLO AJ000974 g2462956 Bacillus subtilis 1423 -11528741 7500965067 cysh phosphoadenosine phosphosulfate (fn:cysteine biosynthesis) (db:genpept-bct1) (ec:1.8.99.4) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:31361) (re:32062) (di:direct) BSUB0009 Z99112 g2633930 Bacillus subtilis 1423 -11528741

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733792	556	22712	882	293

Description

6500724884 yaap:tmk thymidylate kinase:dtmp kinase (gtcfc:4.2) (ec:2.7.4.9) (keggfc:4.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) tmk tmk Bacillus subtilis 1423 -11528742 81195 tmk (ec:2.7.4.9) (de:thymidylate kinase, (dtmp kinase)) (db:swissprot) KTHY_BACSU P37537 BACILLUS SUBTILIS 1423 -11528742 7000685704 tmk thymidylate kinase tmk (cl:dtmp kinase) (db:pir2.dat) S66058 S66058 Bacillus subtilis 1423 -11528742 7500884756 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:102759) (re:103397) (di:direct) BAC180K D26185 g467418 Bacillus subtilis 1423 -11528742 215018 tmk thymidylate kinase (db:genpept-bct1) (ec:2.7.4.9) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yaap) (le:39157) (re:39795) (di:direct) BSUB0001 Z99104 g2632295 Bacillus subtilis 1423 -11528742 206224 tmk thymidylate kinase tmk (cl:dtmp kinase) (db:pir) S66058 S66058 Bacillus subtilis 1423 -11528742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733846	557	22713	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733850	558	22714	534	178

Description

6500724885 aspartate carbamoyltransferase:aspartate transcarbamylase:atcase (gtcfc:4.2:5.2) (ec:2.1.3.2) (keggfc:4.2:5.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) pyrB pyrB Bacillus subtilis 1423 -11528743 92596 pyrb (ec:2.1.3.2) (de:transcarbamylase) (atcase)) (db:swissprot) PYRB_BACSU P05654 BACILLUS SUBTILIS 1423 -11528743 123304 pyrb aspartate carbamoyltransferase:catalytic chain:aspartate transcarbamoylase (cl:ornithine carbamoyltransferase:aspartate/ornithine carbamoyltransferase homology) (ec:2.1.3.2) (db:pir1.dat) (mp:37 min) OWBSAC A25015 Bacillus subtilis 1423 -11528743 216556 (sr:b.subtilis (strain jh861) dna, clone pls201) (db:genpept-bct1) (de:b.subtilis pyrb gene encoding aspartate transcarbamoylase, completecds.) (nt:aspartate transcarbamoylase (ec 2.1.3.2)) (le:96) (re:1010) (di:direct) BACPYRB M13128 g143384 Bacillus subtilis 1423 -11528743 216559 pyrb aspartate transcarbamylase (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (le:2859) (re:3773) (di:direct) BACPYROP M59757 g143387 Bacillus subtilis 1423 -11528743 7500889139 pyrb aspartate carbamoyltransferase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:2.1.3.2) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:21455) (re:22369) (di:direct) BSUB0009 Z99112 g2633922 Bacillus subtilis 1423 -11528743

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733853	559	22715	675	225

Description

6500724886 dihydroorotase:dhoase (gtcfc:4.2) (ec:3.5.2.3) (keggfc:4.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) pyrC pyrC Bacillus subtilis 1423 -11528744 92602 pyrc (ec:3.5.2.3) (de:dihydroorotase, (dhoase)) (db:swissprot) PYRC_BACSU P25995 BACILLUS SUBTILIS 1423 -11528744 125040 pyrc dihydroorotase (cl:bacillus dihydroorotase:bacillus dihydroorotase homology) (ec:3.5.2.3) (db:pir1.dat) DEBSO D39845 Bacillus subtilis 1423 -11528744 216560 pyrc dihydroorotase (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (le:3757) (re:5043) (di:direct) BACPYROP M59757 g143388 Bacillus subtilis 1423 -11528744 7500889147 pyrc dihydroorotase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:3.5.2.3) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:22353) (re:23639) (di:direct) BSUB0009 Z99112 g2633923 Bacillus subtilis 1423 -11528744

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733858	560	22716	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733859	561	22717	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733955	562	22718	537	178

Description

6500724887 pyrdi:pyrda:pyrd dihydroorotate dehydrogenase:dihydroorotate oxidase:dhodehase (gtcfc:4.2) (keggfc:4.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) pyrD pyrD Bacillus subtilis 1423 -11528745 92611 pyrdi:pyrda:pyrd (ec:1.3.3.1) (de:(dhodehase)) (db:swissprot) PYRD_BACSU P25996 BACILLUS SUBTILIS 1423 -11528745 122679 pyrd dihydroorotate oxidase:pyrd:dihydroorotate dehydrogenase (cl:dihydroorotate oxidase) (ec:1.3.3.1) (db:pir1.dat) H39845 H39845 Bacillus subtilis 1423 -11528745 216564 pyrd dihydroorotase dehydrogenase (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (le:10101) (re:11036) (di:direct) BACPYROP M59757 g143392 Bacillus subtilis 1423 -11528745 7500889161 pyrd dihydroorotate dehydrogenase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:1.3.3.1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:28697) (re:29632) (di:direct) BSUB0009 Z99112 g2633927 Bacillus subtilis 1423 -11528745

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501733963	563	22719	897	299

Description

6500724888 orotidine 5-phosphate decarboxylase:omp decarboxylase (gtcfc:4.2) (ec:4.1.1.23) (keggfc:4.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) pyrF pyrF Bacillus subtilis 1423 -11528746 68051 pyrf (ec:4.1.1.23) (de:decarboxylase)) (db:swissprot) DCOP_BACSU P25971 BACILLUS SUBTILIS 1423 -11528746 7000684991 pyrf orotidine-5-phosphate decarboxylase:pyrf:omp decarboxylase (cl:orotidine-5'-phosphate decarboxylase:orotidine-5'-phosphate decarboxylase homology) (ec:4.1.1.23) (db:pir2.dat) I39845 I39845 Bacillus subtilis 1423 -11528746 7500880058 pyrf omp decarboxylase (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (le:11005) (re:11724) (di:direct) BACPYROP M59757 g143393 Bacillus subtilis 1423 -11528746 216565 pyrf orotidine 5-phosphate decarboxylase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:4.1.1.23) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:29601) (re:30320) (di:direct) BSUB0009 Z99112 g2633928 Bacillus subtilis 1423 -11528746 170409 pyrf orotidine-5-phosphate decarboxylase:pyrf:omp decarboxylase (ec:4.1.1.23) (db:pir) I39845 I39845 Bacillus subtilis 1423 -11528746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734022	564	22720	426	142

Description

6500724889 pyrx:pyre orotate phosphoribosyltransferase:oprt:oprtase (gtcfc:4.2) (ec:2.4.2.10) (keggfc:4.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) pyrE pyrE Bacillus subtilis 1423 -11528747 92622 pyre:pyrx (ec:2.4.2.10) (de:orotate phosphoribosyltransferase, (oprt) (oprtase)) (db:swissprot) PYRE_BACSU P25972 BACILLUS SUBTILIS 1423 -11528747 7000686251 pyre orotate phosphoribosyltransferase (cl:orotate phosphoribosyltransferase:orotate phosphoribosyltransferase homology) (ec:2.4.2.10) (db:pir1.dat) F69686 F69686 Bacillus subtilis 1423 -11528747 216566 pyre omp-prpp transferase (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (le:11703) (re:12353) (di:direct) BACPYROP M59757 g143394 Bacillus subtilis 1423 -11528747 7500889166 pyre orotate phosphoribosyltransferase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:2.4.2.10) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: pyrx) (le:30299) (re:30949) (di:direct) BSUB0009 Z99112 g2633929 Bacillus subtilis 1423 -11528747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734025	565	22721	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734032	566	22722	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734035	567	22723	1137	378

Description

GTC ORF with score 1483 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmids 9379, 9581, andlambda clone 4678.) (nt:similar to hypothetical protein f42a10.1 from) (le:5607) (re:7439) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734040	568	22724	1053	350

Description

6500724890 hypothetical protein:similar to deoxyuridine 5-triphosphate pyrophosphatase (gtcfc:4.2:14.1) (ec:3.6.1.23) (keggfc:4.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yncF yncF Bacillus subtilis 1423 -11528748 7000692914 yncf deoxyuridine 5-triphosphate pyrophosphata homolog yncf (db:pir2.dat) H69888 H69888 Bacillus subtilis 1423 -11528748 7500963933 yncf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to deoxyuridine 5'-triphosphate) (le:118134) (re:118568) (di:direct) BSUB0010 Z99113 g2634150 Bacillus subtilis 1423 -11528748

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734094	569	22725	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734106	570	22726	456	152

Description

6500724891 thymidylate synthase a:ts a:tsase a (gtcfc:4.2:4.4:9.6) (ec:2.1.1.45) (keggfc:4.2:9.7:9.8) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) (gtcfc:nucleotide metabolism-pyrimidine metabolism:nucleotide metabolism-salvage and interconversion:metabolism of cofactors and vitamins-biotin metabolis... thyA thyA Bacillus subtilis 1423 -11528749 7500893619 thya (ec:2.1.1.45) (de:thymidylate synthase a, (ts a) (tsase a)) (db:swissprot) TYSA_BACSU P42326 BACILLUS SUBTILIS 1423 -11528749 7000686842 thya thymidylate synthase:a (cl:thymidylate synthase:thymidylate synthase homology) (ec:2.1.1.45) (db:pir1.dat) I40494 I40494 Bacillus subtilis 1423 -11528749 5000688540 thya thymidylate synthetase (fn:enzyme involved in pyrimidine metabolism) (db:genpept-bct1) (de:b.subtilis (168 trpc2) thya gene for thymidylate synthetase.) (nt:thya gene from b.subtilis is highly related to) (le:460) (re:1299) (di:direct) BSTHYAGE X78560 g607048 Bacillus subtilis 1423 -11528749 219721 thya thymidylate synthase a (fn:deoxyribonucleotide biosynthesis) (db:genpept-bct1) (ec:2.1.1.45) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:120274) (re:121113) (di:direct) BSUB0010 Z99113 g2634152 Bacillus subtilis 1423 -11528749 102936 thya (ec:2.1.1.45) (de:thymidylate synthase a, (ts a) (tsase a)) (db:swissprot) TYSA_BACSU P42326 BACILLUS SUBTILIS 1423 -11528749 137761 thya thymidylate synthase:a thya (cl:thymidylate synthase:thymidylate synthase homology) (ec:2.1.1.45) (db:pir) I40494 I40494 Bacillus subtilis 1423 -11528749

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734117	571	22727	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734118	572	22728	399	133

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734168	573	22729	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734172	574	22730	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734252	575	22731	183	60

Description

6500724892 hypothetical protein:similar to deoxyuridine 5-triphosphate nucleotidohydrolase (gtcfc:4.2:14.1) (ec:3.6.1.23) (keggfc:4.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosS yosS Bacillus subtilis 1423 -11528750 7000692912 yoss deoxyuridine 5-triphosphate nucleotidohyd homolog yoss (db:pir2.dat) E69927 E69927 Bacillus subtilis 1423 -11528750 5500698556 yoju dutpase homolog (db:genpept-bct1) (de:bacillus subtilis yojp gene, partial cds; yojq/s, yojr, yojt,yoju, yojv, yojw, yojx, yojy, yojz, and yoka genes, complete cds.) (nt:yoju; similar to dutpase of the temperate) (le:4398) (re:4826) (di:direct) AF012906 AF012906 g2522313 Bacillus subtilis 1423 -11528750 7000692913 yoss (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to deoxyuridine 5'-triphosphate) (le:158341) (re:158769) (di:complement) BSUB0011 Z99114 g2634394 Bacillus subtilis 1423 -11528750 7500963932 yoss putative dutpase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:126751) (re:127179) (di:direct) AF020713 AF020713 g3025643 Bacteriophage SPBc2 66797 -11528750

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734253	576	22732	438	145

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734257	577	22733	555	184

Description

6500724893 thymidylate synthase b:ts b:tsase b (gtcfc:4.2:4.4:9.6) (ec:2.1.1.45) (keggfc:4.2:9.7:9.8) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) (gtcfc:nucleotide metabolism-pyrimidine metabolism:nucleotide metabolism-salvage and interconversion:metabolism of cofactors and vitamins-biotin metabolis... thyB thyB Bacillus subtilis 1423 -11528751 102937 thyb (ec:2.1.1.45) (de:thymidylate synthase b, (ts b) (tsase b)) (db:swissprot) TYSB_BACSU P11044 BACILLUS SUBTILIS 1423 -11528751 216964 (sr:b.subtilis dna) (db:genpept-bct1) (de:b.subtilis thymidylate synthase b and dihydrofolate reductasegenes.) (nt:thymidylate synthase b (thyb)) (le:798) (re:1592) (di:direct) BACTHYDA M20012 g143741 Bacillus subtilis 1423 -11528751 217097 thyb thymidylate synthase (fn:thymidine biosynthesis) (db:genpept-bct1) (ec:2.1.1.45) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (le:23551) (re:24345) (di:direct) BACYACA L77246 g1256640 Bacillus subtilis 1423 -11528751 7500893620 thyb thymidylate synthase b (fn:deoxyribonucleotide biosynthesis) (db:genpept-bct1) (ec:2.1.1.45) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:100807) (re:101601) (di:complement) BSUB0012 Z99115 g2634602 Bacillus subtilis 1423 -11528751 7000686843 thyb thymidylate synthase b thyb (cl:thymidylate synthase:thymidylate synthase homology) (db:pir) E69723 E69723 Bacillus subtilis 1423 -11528751 5000688541 (de:(thyb) (pn:thymidylate synthase b:ts b:tsase b:thymidylate synthase b :tsase b) (gtcfc:9.06) (ec:2.1.1.45) (tysb_bacsu) (keggfc:4.2:9.8) (bsorffc:3.2.3) (db:gtc-bacillus subtilis)) thyB thyB Bacillus subtilis 1423 10044749

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734268	578	22734	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734278	579	22735	705	234

Description

6500724894 jofc:ypfc:cmk cytidylate kinase:probable cytidylate kinase:ck:cytidine monophosphate kinase:cmp kinase (gtcfc:4.2:4.4) (ec:2.7.4.14) (keggfc:4.2) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) cmk cmk Bacillus subtilis 1423 -11528752 80552 cmk:jofc (ec:2.7.4.14) (de:(cmp kinase)) (db:swissprot) KCY_BACSU P38493 BACILLUS SUBTILIS 1423 -11528752 7000685666 cmk cytidylate kinase cmk (cl:cytidylate kinase cmk) (db:pir2.dat) F69601 F69601 Bacillus subtilis 1423 -11528752 219797 jofc unknown (db:genpept-bct1) (de:bacillus subtilis 168 jofa, jofb, mssa homolog (jofc) and ribosomalprotein s1 homolog (jofd) genes, complete cds, and joeb gene,partial cds.) (nt:similar to the escherichia coli mssa gene product) (le:1744) (re:2418) (di:direct) BSU11687 U11687 g533105 Bacillus subtilis 1423 -11528752 6000684839 cmk cytidylate kinase (db:genpept-bct1) (ec:2.7.4.14) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jofc, ypfc) (le:199742) (re:200416) (di:complement) BSUB0012 Z99115 g2634707 Bacillus subtilis 1423 -11528752 7500884539 cmk cytidylate kinase (db:genpept-bct1) (ec:2.7.4.14) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: jofc, ypfc) (le:22) (re:696) (di:complement) BSUB0013 Z99116 g2634724 Bacillus subtilis 1423 -11528752 216720 cmk cytidine monophosphate kinase (fn:cytidine diphosphate biosynthesis) (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic en... BACSERA L47648 g1146214 Bacillus subtilis 1423 -11528752 7502851541 cmk cytidine monophosphate kinase (fn:cytidine diphosphate biosynthesis) (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme ... BACSERA L47648 g1146214 Bacillus subtilis 1423 -11528752

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734317	580	22736	804	267

Description

6500724895 cytidine/deoxycytidine deaminase:cytidine deaminase:cytidine aminohydrolase:cda (gtcfc:4.2:4.4) (ec:3.5.4.5) (keggfc:4.2) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) cdd cdd Bacillus subtilis 1423 -11528753 63641 cdd (ec:3.5.4.5) (de:cytidine deaminase, (cytidine aminohydrolase) (cda)) (db:swissprot) CDD_BACSU P19079 BACILLUS SUBTILIS 1423 -11528753 7000684780 cdd cytidine/deoxycytidine deaminase:cdd:cytidine 12-deoxycytidine aminohydrolase:p43 protein (cl:cytidine deaminase) (ec:3.5.4.-) (db:pir2.dat) (mp:225 (degrees)) JE0022 JE0022 Bacillus subtilis 1423 -11528753 7500878427 cdd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:108267) (re:108677) (di:direct) BACJH642 D84432 g1303825 Bacillus subtilis 1423 -11528753 216069 cdd cytidine deaminase (db:genpept-bct1) (de:bacillus subtilis cytidine deaminase (cdd) gene and g-protein bex(bex) gene, complete cds.) (le:112) (re:522) (di:direct) BSU18532 U18532 g606744 Bacillus subtilis 1423 -11528753 219853 cdd cytidine/deoxycytidine deaminase (db:genpept-bct1) (ec:3.5.4.5) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:214943) (re:215353) (di:complement) BSUB0013 Z99116 g2634962 Bacillus subtilis 1423 -11528753 6000684559 cdd cytidine/deoxycytidine deaminase (db:genpept-bct1) (ec:3.5.4.5) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:10753) (re:11163) (di:complement) BSUB0014 Z99117 g2634976 Bacillus subtilis 1423 -11528753 169945 cdd cytidine/deoxycytidine deaminase:cdd:cytidine 12-deoxycytidine aminohydrolase:p43 protein (cl:cytidine deaminase) (ec:3.5.4.-) (db:pir) (mp:225 (degrees)) JE0022 JE0022 Bacillus subtilis 1423 -11528753

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734322	581	22737	684	227

Description

6500724896 comd:come2:comeb hypothetical protein:come operon protein 2 (gtcfc:4.2:13.12) (ec:3.5.4.12) (keggfc:4.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comEB comEB Bacillus subtilis 1423 -11528754 64869 comeb:come2 (de:come operon protein 2) (db:swissprot) CME2_BACSU P32393 BACILLUS SUBTILIS 1423 -11528754 7000684845 comeb late competence operon required for dna binding and uptake comeb (cl:archaeoglobus probable dcmp deaminase) (db:pir2.dat) S39864 S39864 Bacillus subtilis 1423 -11528754 7500878902 comeb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:79168) (re:79737) (di:direct) BACJH642 D84432 g1303797 Bacillus subtilis 1423 -11528754 215369 comeb (fn:required for dna binding and uptake) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: comd) (le:39693) (re:40262) (di:complement) BSUB0014 Z99117 g2635004 Bacillus subtilis 1423 -11528754 216041 (sr:bacillus subtilis dna) (db:genpept-bct2) (de:bacillus subtilis come operon encoding orf1, orf2, orf3 andreverse-orf genes, complete cds.) (le:2030) (re:2599) (di:direct) BACCOME L15202 g289261 Bacillus subtilis 1423 -11528754 169925 comeb late competence operon required for dna binding and uptake comeb (db:pir) S39864 S39864 Bacillus subtilis 1423 -11528754 5000689911 (de:(comeb) (pn:come operon protein 2:come operon protein 2) (gn:come2) (gtcfc:13.12) (ec:) (cme2_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comEB comEB Bacillus subtilis 1423 10007530

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734333	582	22738	573	190

Description

6500724897 uridine kinase (gtcfc:4.2) (ec:2.7.1.48) (keggfc:4.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) udk udk Bacillus subtilis 1423 -11528755 7000694893 udk uridine kinase udk (cl:uridine kinase) (db:pir2.dat) G69728 G69728 Bacillus subtilis 1423 -11528755 7500965430 udk uridine kinase (fn:pyrimidine salvage) (db:genpept-bct1) (ec:2.7.1.48) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:192038) (re:192673) (di:complement) BSUB0014 Z99117 g2635179 Bacillus subtilis 1423 -11528755

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734382	583	22739	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734393	584	22740	546	182

Description

GTC ORF with score 210 to: (sr:soybean) (db:genpept-pln1) (ec:2.7.7.6) (de:soybean rpb1-b1 gene for the largest subunit of rna polymerase ii(ec 2.7.7.6).) (nt:largest subunit of rna polymerase ii) (le:<1:2062:2196) (re:1736:2133:2265) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734400	585	22741	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734408	586	22742	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734412	587	22743	348	115

Description

6500724898 ipc-35d:upp uracil phosphoribosyltransferase:ump pyrophosphorylase:uprtase (gtcfc:4.2:4.4) (ec:2.4.2.9) (keggfc:4.2) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) upp upp Bacillus subtilis 1423 -11528756 7500893825 upp:ipc-35d (ec:2.4.2.9) (de:(uprtase)) (db:swissprot) UPP_BACSU P39149 BACILLUS SUBTILIS 1423 -11528756 7000686897 upp uracil phosphoribosyltransferase:upp (cl:uracil phosphoribosyltransferase upp) (ec:2.4.2.9) (db:pir2.dat) I40484 I40484 Bacillus subtilis 1423 -11528756 219668 upp uracil phosphoribosyltransferase (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:6881) (re:7510) (di:direct) BSSPORUPP Z38002 g556887 Bacillus subtilis 1423 -11528756 7502851542 upp uracil phosphoribosyltransferase (fn:pyrimidine salvage) (db:genpept-bct1) (ec:2.4.2.9) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-35d) (le:190391) (re:191020) (di:complement) BSUB0019 Z99122 g2636214 Bacillus subtilis 1423 -11528756 103782 upp:ipc-35d (ec:2.4.2.9) (de:(uprtase)) (db:swissprot) UPP_BACSU P39149 BACILLUS SUBTILIS 1423 -11528756 170659 upp uracil phosphoribosyltransferase upp (db:pir) I40484 I40484 Bacillus subtilis 1423 -11528756

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734421	588	22744	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734473	589	22745	405	134

Description

6500724899 thymidine kinase (gtcfc:4.2:4.4) (ec:2.7.1.21) (keggfc:4.2) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) tdk tdk Bacillus subtilis 1423 -11528757 304120 tdk (ec:2.7.1.21) (de:thymidine kinase,) (db:swissprot) KITH_BACSU Q03221 BACILLUS SUBTILIS 1423 -11528757 7000685691 tdk thymidine kinase:tdk (cl:thymidine kinase) (ec:2.7.1.21) (db:pir2.dat) S55432 S55432 Bacillus subtilis 1423 -11528757 7500884635 tdk thymidine kinase (sr:bacillus subtilis (transposon tn917 insertional library) dna) (db:genpept-bct1) (de:bacillus subtilis orfr, 3' end; orfq; transcriptional terminator(rho) gene; ribosomal protein l31; thymidine kinase (tdk) gene,complete cds.) (nt:incorrect sequence... BACRHOTDKX M97678 g405819 Bacillus subtilis 1423 -11528757 6000684851 tdk thymidine kinase (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:18786) (re:19373) (di:direct) BSDNA320D Z49782 g853771 Bacillus subtilis 1423 -11528757 216592 tdk thymidine kinase (db:genpept-bct1) (ec:2.7.1.21) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:204370) (re:204957) (di:complement) BSUB0019 Z99122 g2636231 Bacillus subtilis 1423 -11528757 219148 tdk thymidine kinase (db:genpept-bct1) (ec:2.7.1.21) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:3060) (re:3647) (di:complement) BSUB0020 Z99123 g2636243 Bacillus subtilis 1423 -11528757 80744 tdk (ec:2.7.1.21) (de:thymidine kinase,) (db:swissprot) KITH_BACSU Q03221 BACILLUS SUBTILIS 1423 -11528757 170628 tdk thymidine kinase:tdk (cl:thymidine kinase) (ec:2.7.1.21) (db:pir) S55432 S55432 Bacillus subtilis 1423 -11528757

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734474	590	22746	207	68

Description

6500724900 pyrg:ctra ctp synthase:utp--ammonia ligase:ctp synthetase (gtcfc:4.2) (ec:6.3.4.2) (keggfc:4.2) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) ctrA ctrA Bacillus subtilis 1423 -11528758 304111 ctra (ec:6.3.4.2) (de:ctp synthase, (utp--ammonia ligase) (ctp synthetase)) (db:swissprot) PYRG_BACSU P13242 BACILLUS SUBTILIS 1423 -11528758 126017 ctra:pyrg ctp synthase::ctp-synthetase:utp--ammonia ligase (cl:ctp synthase) (ec:6.3.4.2) (db:pir1.dat) (mp:37 min) SYBSTP A32354 Bacillus subtilis 1423 -11528758 216853 ctra ctp synthetase (sr:bacillus subtilis (strains jh642 and uot0550) dna) (db:genpept-bct1) (de:bacillus subtillis spo0f, ctp synthetase (ctra), andfructose-bisphosphate aldolase (orfy-tsr) genes, complete cds.) (le:339) (re:1946) (di:direct) BACSPO0FA M22039 g143597 Bacillus subtilis 1423 -11528758 219139 pyrg ctp synthase (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:9480) (re:11087) (di:direct) BSDNA320D Z49782 g853762 Bacillus subtilis 1423 -11528758 7502851543 ctra ctp synthetase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:6.3.4.2) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: pyrg) (le:11346) (re:12953) (di:complement) BSUB0020 Z99123 g2636252 Bacillus subtilis 1423 -11528758 92636 ctra (ec:6.3.4.2) (de:ctp synthase, (utp--ammonia ligase) (ctp synthetase)) (db:swissprot) PYRG_BACSU P13242 BACILLUS SUBTILIS 1423 -11528758

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734475	591	22747	270	90

Description

6500724901 pyrimidine-nucleoside phosphorylase (gtcfc:4.2:4.4) (ec:2.4.2.2) (keggfc:4.2) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) pdp pdp Bacillus subtilis 1423 -11528759 7500887767 pdp (ec:2.4.2.2) (de:pyrimidine-nucleoside phosphorylase,) (db:swissprot) PDP_BACSU P39142 BACILLUS SUBTILIS 1423 -11528759 7000686106 pdp pyrimidine-nucleoside phosphorylase:pdp (cl:thymidine phosphorylase) (ec:2.4.2.2) (db:pir1.dat) S49457 S49457 Bacillus subtilis 1423 -11528759 222540 pdp pyrimidine nucleoside phosphorylase (db:genpept-bct1) (de:b.subtilis operon contg. dra, nupc and pdp genes.) (le:3433) (re:4737) (di:direct) BSDNPOP X82174 g558559 Bacillus subtilis 1423 -11528759 219176 pdp pyrimidine-nucleoside phosphorylase (db:genpept-bct1) (ec:2.4.2.2) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:48518) (re:49822) (di:complement) BSUB0021 Z99124 g2636486 Bacillus subtilis 1423 -11528759 7502851544 pdp pyrimidine nucleoside phosphorylase (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (le:21654) (re:22958) (di:direct) D45912 D45912 g1408508 Bacillus subtilis 1423 -11528759 7502851545 pdp pyrimidine nucleoside phosphorylase (db:genpept) (de:b.subtilis operon contg. dra, nupc and pdp genes.) (le:3433) (re:4737) (di:direct) BSDNPOP X82174 g558559 Bacillus subtilis 1423 -11528759 88884 pdp (ec:2.4.2.2) (de:pyrimidine-nucleoside phosphorylase,) (db:swissprot) PDP_BACSU P39142 BACILLUS SUBTILIS 1423 -11528759 170470 pdp pyrimidine nucleoside phosphorylase pdp (db:pir) S49457 S49457 Bacillus subtilis 1423 -11528759

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734491	592	22748	891	296

Description

6500724902 ybah:trua pseudouridylate synthase i (gtcfc:4.2) (ec:4.2.1.70) (keggfc:14.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) truA truA Bacillus subtilis 1423 -11528760 7502851546 trua (ec:4.2.1.70) (de:i) (pseudouridine synthase i) (uracil hydrolyase)) (db:swissprot) TRUA_BACSU P70973 BACILLUS SUBTILIS 1423 -11528760 7000694464 trua pseudouridylate synthase i trua (cl:trna-pseudouridine synthase i) (db:pir2.dat) F69726 F69726 Bacillus subtilis 1423 -11528760 222736 trua pseudouridylate synthase i (db:genpept-bct1) (ec:4.2.1.70) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybah) (le:152935) (re:153678) (di:direct) BSUB0001 Z99104 g2632415 Bacillus subtilis 1423 -11528760 7500965114 orf8 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:2496) (re:3239) (di:direct) D64126 D64126 g1644206 Bacillus subtilis 1423 -11528760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734493	593	22749	411	137

Description

6500724903 cpa:cpaa:cara carbamoyl-phosphate transferase-arginine:subunit a:carbamoyl-phosphate synthase:arginine-specific:small chain:carbamoyl-phosphate synthetase glutamine chain (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) carA carA Bacillus subtilis 1423 -11528761 7500878183 cara:cpaa (ec:6.3.5.5) (de:(ec 6.3.5.5) (carbamoyl-phosphate synthetase glutamine chain)) (db:swissprot) CARX_BACSU P36838 BACILLUS SUBTILIS 1423 -11528761 7000684750 cara carbamoylphosphate synthetase chain a cara (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology:trpg homology) (db:pir2.dat) I40376 I40376 Bacillus subtilis 1423 -11528761 6000684549 cara carbamoylphosphate synthetase subunit a (db:genpept-bct1) (de:b.subtilis (168) dna for argc-f citrulline biosynthetic operon.) (le:4417) (re:5478) (di:direct) BSCITBO Z26919 g408118 Bacillus subtilis 1423 -11528761 219066 cara carbamoyl-phosphate transferase-arginine (fn:arginine biosynthesis) (db:genpept-bct1) (ec:6.3.5.5) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: cpa) (le:199302) (re:200363) (di:direct) BSUB0006 Z99109 g2633460 Bacillus subtilis 1423 -11528761 308605 cara carbamoyl-phosphate transferase-arginine (fn:arginine biosynthesis) (db:genpept-bct1) (ec:6.3.5.5) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: cpa) (le:4412) (re:5473) (di:direct) BSUB0007 Z99110 g2633477 Bacillus subtilis 1423 -11528761 62825 cara:cpaa (ec:6.3.5.5) (de:(ec 6.3.5.5) (carbamoyl-phosphate synthetase glutamine chain)) (db:swissprot) CARX_BACSU P36838 BACILLUS SUBTILIS 1423 -11528761 169894 cara carbamoylphosphate synthetase chain a cara (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology:trpg homology) (db:pir) I40376 I40376 Bacillus subtilis 1423 -11528761

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734500	594	22750	495	165

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734550	595	22751	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734562	596	22752	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734642	597	22753	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734643	598	22754	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734655	599	22755	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734661	600	22756	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734715	601	22757	726	241

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734716	602	22758	783	261

Description

6500724904 cpa:cpab:carb carbamoyl-phosphate transferase-arginine:subunit b:carbamoyl-phosphate synthase:arginine-specific:large chain:carbamoyl-phosphate synthetase ammonia chain (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) carB carB Bacillus subtilis 1423 -11528762 7500878184 carb:cpab (ec:6.3.5.5) (de:(ec 6.3.5.5) (carbamoyl-phosphate synthetase ammonia chain)) (db:swissprot) CARY_BACSU P18185 BACILLUS SUBTILIS 1423 -11528762 7000684751 carb:cpa carbamoyl-phosphate synthase glutamine-hydrolyzing::arginine-repressible:large chain carb:carbamoylphosphate synthetase chain b (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology) (ec:6.3.5.5) (db:pir2.dat) (mp:100 (degrees)) I40377 I40377 Bacillus subtilis 1423 -11528762 6000684551 carb carbamoylphosphate synthetase subunit b (db:genpept-bct1) (de:b.subtilis (168) dna for argc-f citrulline biosynthetic operon.) (le:5471) (re:8554) (di:direct) BSCITBO Z26919 g408119 Bacillus subtilis 1423 -11528762 219067 carb carbamoyl-phosphate transferase-arginine (fn:arginine biosynthesis) (db:genpept-bct1) (ec:6.3.5.5) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: cpa) (le:200356) (re:203439) (di:direct) BSUB0006 Z99109 g2633461 Bacillus subtilis 1423 -11528762 308606 carb carbamoyl-phosphate transferase-arginine (fn:arginine biosynthesis) (db:genpept-bct1) (ec:6.3.5.5) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: cpa) (le:5466) (re:8549) (di:direct) BSUB0007 Z99110 g2633478 Bacillus subtilis 1423 -11528762 62826 carb:cpab (ec:6.3.5.5) (de:(ec 6.3.5.5) (carbamoyl-phosphate synthetase ammonia chain)) (db:swissprot) CARY_BACSU P18185 BACILLUS SUBTILIS 1423 -11528762 142436 carb:cpa carbamoyl-phosphate synthase glutamine-hydrolyzing::arginine-repressible:large chain carb:carbamoylphosphate synthetase chain b (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology) (ec:6.3.5.5) (db:pir) (mp:100 (degrees)) I40377 I40377 Bacillus subtilis 1423 -11528762

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734729	603	22759	438	145

Description

6500724905 carbamoyl-phosphate synthetase:glutaminase subunit:carbamoyl-phosphate synthase:pyrimidine-specific:small chain:carbamoyl-phosphate synthetase glutamine chain (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) pyrAA pyrAA Bacillus subtilis 1423 -11528763 62787 pyraa (ec:6.3.5.5) (de:(ec 6.3.5.5) (carbamoyl-phosphate synthetase glutamine chain)) (db:swissprot) CARA_BACSU P25993 BACILLUS SUBTILIS 1423 -11528763 7000684748 pyraa carbamoyl-phosphate synthase glutamine-hydrolyzing::pyrimidine-repressible:small chain pyraa:carbamoyl-phosphate synthetase glutaminase subunit pyraa (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology:trpg homology) (ec:6.3.5.5) (db:pir2.dat) E39845 E39845 Bacillus subtilis 1423 -11528763 7500878173 pyraa glutaminase of carbamyl phosphate synthetase (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (le:5040) (re:6134) (di:direct) BACPYROP M59757 g143389 Bacillus subtilis 1423 -11528763 216561 pyraa carbamoyl-phosphate synthetase glutaminase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:6.3.5.5) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:23636) (re:24730) (di:direct) BSUB0009 Z99112 g2633924 Bacillus subtilis 1423 -11528763 169893 pyraa carbamoyl-phosphate synthase glutamine-hydrolyzing::pyrimidine-repressible:small chain pyraa:carbamoyl-phosphate synthetase glutaminase subunit pyraa (cl:trpd homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology:trpg homology) (ec:6.3.5.5) (db:pir) E39845 E39845 Bacillus subtilis 1423 -11528763

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734837	604	22760	219	72

Description

6500724906 carbamoyl-phosphate synthetase:catalytic subunit:carbamoyl-phosphate synthase:pyrimidine-specific:large chain:carbamoyl-phosphate synthetase ammonia chain (gtcfc:4.2:5.1) (ec:6.3.5.5) (keggfc:5.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) pyrAB pyrAB Bacillus subtilis 1423 -11528764 62796 pyrab (ec:6.3.5.5) (de:(ec 6.3.5.5) (carbamoyl-phosphate synthetase ammonia chain)) (db:swissprot) CARB_BACSU P25994 BACILLUS SUBTILIS 1423 -11528764 7000684749 pyrab carbamoyl-phosphate synthase glutamine-hydrolyzing::pyrimidine-repressible:large chain pyrab:carbamoyl-phosphate synthetase catalytic chain pyrab (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology) (ec:6.3.5.5) (db:pir2.dat) F39845 F39845 Bacillus subtilis 1423 -11528764 7500878178 pyrab carbamyl phosphate synthetase (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (le:6119) (re:9334) (di:direct) BACPYROP M59757 g143390 Bacillus subtilis 1423 -11528764 216562 pyrab carbamoyl-phosphate synthetase catalytic (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:6.3.5.5) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:24715) (re:27930) (di:direct) BSUB0009 Z99112 g2633925 Bacillus subtilis 1423 -11528764 142435 pyrab carbamoyl-phosphate synthase glutamine-hydrolyzing::pyrimidine-repressible:large chain pyrab:carbamoyl-phosphate synthetase catalytic chain pyrab (cl:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology) (ec:6.3.5.5) (db:pir) F39845 F39845 Bacillus subtilis 1423 -11528764

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734858	605	22761	363	121

Description

6500724907 uridylate kinase (gtcfc:4.2) (ec:2.7.4.-) (keggfc:14.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) smbA smbA Bacillus subtilis 1423 -11528765 7000694894 smba uridylate kinase smba (cl:uridine 5'-monophosphate kinase) (db:pir2.dat) F69708 F69708 Bacillus subtilis 1423 -11528765 7500965431 smba uridylate kinase (fn:pyrimidine biosynthesis) (db:genpept-bct1) (ec:2.7.4.-) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:120774) (re:121496) (di:direct) BSUB0009 Z99112 g2634023 Bacillus subtilis 1423 -11528765

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734936	606	22762	639	212

Description

5000689745 ywdb:ipa-52r:thid phosphomethylpyrimidine kinase:hmp-p kinase (gtcfc:4.2) (ec:2.7.4.7) (keggfc:14.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) thiD thiD Bacillus subtilis 1423 -11528766 7500893057 thid:ipa-52r (ec:2.7.4.7) (de:(hmp-p kinase)) (db:swissprot) THID_BACSU P39610 BACILLUS SUBTILIS 1423 -11528766 7000686787 thid phosphomethylpyrimidine kinase thid:protein ipa-52r (cl:phosphomethylpyrimidine phosphate kinase) (db:pir2.dat) S39707 S39707 Bacillus subtilis 1423 -11528766 6500724908 ipa-52r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:55788) (re:56603) (di:complement) BSGENR X73124 g413976 Bacillus subtilis 1423 -11528766 219289 thid phosphomethylpyrimidine kinase (fn:thiamin biosynthesis) (db:genpept-bct1) (ec:2.7.4.7) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ywdb, ipa-52r) (le:101359) (re:102174) (di:direct) BSUB0020 Z99123 g2636337 Bacillus subtilis 1423 -11528766 116684 thid:ipa-52r (ec:2.7.4.7) (de:(hmp-p kinase)) (db:swissprot) THID_BACSU P39610 BACILLUS SUBTILIS 1423 -11528766 170132 thid phosphomethylpyrimidine kinase thid (db:pir) S39707 S39707 Bacillus subtilis 1423 -11528766

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734952	607	22763	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734960	608	22764	570	190

Description

GTC ORF with score 351 to: (fn:catalyzes the biosynthesis of d-erythroascorbic) (db:genpept) (ec:1.1.3.24) (de:candida albicans d-arabinono-1,4-lactone oxidase (alo) gene,complete cds.) (nt:l-galactono-gamma-lactone oxidase) (le:1464) (re:3137) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734968	609	22765	318	106

Description

6500724909 ipa-26d:ywbk:thie:thic thiamine-phosphate pyrophosphorylase:thiamin-phosphate pyrophosphorylase:tmp pyrophosphorylase:tmp-ppase:thiamin-phosphate synthase (gtcfc:4.2) (ec:2.5.1.3) (keggfc:14.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) thiC thiC Bacillus subtilis 1423 -11528767 7500893059 thie:thic:ipa-26d (ec:2.5.1.3) (de:pyrophosphorylase) (tmp-ppase) (thiamin-phosphate synthase)) (db:swissprot) THIE_BACSU P39594 BACILLUS SUBTILIS 1423 -11528767 7000686789 thic thiamin-phosphate pyrophosphorylase:thic:protein ipa-26d (cl:thie protein:thiamin-phosphate pyrophosphorylase homology) (ec:2.5.1.3) (db:pir2.dat) S39681 S39681 Bacillus subtilis 1423 -11528767 5000689731 ipa-26d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:26188) (re:26856) (di:direct) BSGENR X73124 g413950 Bacillus subtilis 1423 -11528767 219263 thic thiamine-phosphate pyrophosphorylase (fn:substitution of the pyrophosphate of) (db:genpept-bct1) (ec:2.5.1.3) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-26d, ywbk) (le:131103) (re:131771) (di:complement) BSUB0020 Z99123 g2636364 Bacillus subtilis 1423 -11528767 116668 thie:thic:ipa-26d (ec:2.5.1.3) (de:pyrophosphorylase) (tmp-ppase) (thiamin-phosphate synthase)) (db:swissprot) THIE_BACSU P39594 BACILLUS SUBTILIS 1423 -11528767 170115 thic thiamin-phosphate pyrophosphorylase:thic (cl:thie protein:thiamin-phosphate pyrophosphorylase homology) (ec:2.5.1.3) (db:pir) S39681 S39681 Bacillus subtilis 1423 -11528767

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734969	610	22766	201	66

Description

6500724910 ipa-25d:ywbj:thim:thik hydroxyethylthiazole kinase:4-methyl-5-beta-hydroxyethylthiazole kinase:th kinase (gtcfc:4.2) (ec:2.7.1.50) (keggfc:14.1) (bsorffc:3.2.2) (db:gtc-bacillus subtilis) thiK thiK Bacillus subtilis 1423 -11528768 7500893075 thim:thik:ipa-25d (ec:2.7.1.50) (de:hydroxyethylthiazole kinase) (thz kinase) (th kinase)) (db:swissprot) THIM_BACSU P39593 BACILLUS SUBTILIS 1423 -11528768 7000686794 thik hydroxyethylthiazole kinase:thik:protein ipa-25d (cl:hydroxyethylthiazole kinase:hydroxyethylthiazole kinase homology) (ec:2.7.1.50) (db:pir2.dat) S39680 S39680 Bacillus subtilis 1423 -11528768 5000689730 ipa-25d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:25373) (re:26191) (di:direct) BSGENR X73124 g413949 Bacillus subtilis 1423 -11528768 219262 thik hydroxyethylthiazole kinase (fn:phosphorylation of) (db:genpept-bct1) (ec:2.7.1.50) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-25d, ywbj) (le:131768) (re:132586) (di:complement) BSUB0020 Z99123 g2636365 Bacillus subtilis 1423 -11528768 116667 thim:thik:ipa-25d (ec:2.7.1.50) (de:hydroxyethylthiazole kinase) (thz kinase) (th kinase)) (db:swissprot) THIM_BACSU P39593 BACILLUS SUBTILIS 1423 -11528768 170114 thik hydroxyethylthiazole kinase thik (cl:hypothetical protein hi0415:hydroxyethylthiazole kinase homology) (db:pir) S39680 S39680 Bacillus subtilis 1423 -11528768

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734977	611	22767	315	104

Description

5000688428 xanthine phosphoribosyltransferase (gtcfc:4.4) (keggfc:14.1) (bsorffc:3.2.3) (db:gtc-bacillus subtilis) xpt xpt Bacillus subtilis 1423 -11528769 220236 xpt (ec:2.4.2.-) (de:xanthine phosphoribosyltransferase,) (db:swissprot) XPT_BACSU P42085 BACILLUS SUBTILIS 1423 -11528769 7000687049 xpt xanthine phosphoribosyltransferase xpt (db:pir2.dat) S51309 S51309 Bacillus subtilis 1423 -11528769 7500894477 xpt adenine phosphoribosyltransferase (fn:purine biosynthesis) (db:genpept-bct1) (ec:2.4.2.7) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:27% identity with e.coli adenine) (le:1426) (re:2010) (di:direct) BACYACA L77246 g1256617 Bacillus subtilis 1423 -11528769 217074 xpt xanthine phosphoribosyltransferase (fn:purine biosynthesis) (db:genpept-bct1) (ec:2.4.2.7) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:123142) (re:123726) (di:complement) BSUB0012 Z99115 g2634626 Bacillus subtilis 1423 -11528769 6500724911 xpt xanthine phosphoribosyltransferase (db:genpept-bct1) (de:b.subtilis xpt and pbux genes.) (le:357) (re:941) (di:direct) BSXPTPBUX X83878 g633169 Bacillus subtilis 1423 -11528769 108160 xpt (ec:2.4.2.-) (de:xanthine phosphoribosyltransferase,) (db:swissprot) XPT_BACSU P42085 BACILLUS SUBTILIS 1423 -11528769 170666 xpt xanthine phosphoribosyltransferase xpt (db:pir) S51309 S51309 Bacillus subtilis 1423 -11528769

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501734978	612	22768	486	161

Description

6500724912 glutamyl-trna synthetase:glutamate--trna ligase:glurs (gtcfc:10.6) (ec:6.1.1.17) (keggfc:5.1:9.10:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) gltX gltX Bacillus subtilis 1423 -11528770 100018 gltx (ec:6.1.1.17) (de:(glurs)) (db:swissprot) SYE_BACSU P22250 BACILLUS SUBTILIS 1423 -11528770 125922 gltx glutamate--trna ligase:gltx:glutamyl-trna synthetase gltx (cl:glutamate--trna ligase:glutamine--trna ligase homology) (ec:6.1.1.17) (db:pir1.dat) SYBSET A36090 Bacillus subtilis 1423 -11528770 7500892372 gltx glutamyl-trna synthetase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:174646) (re:176097) (di:direct) BAC180K D26185 g467480 Bacillus subtilis 1423 -11528770 215080 gltx transfer rna-gln synthetase (sr:bacillus subtilis 168t dna) (db:genpept-bct1) (ec:6.1.1.17) (de:bacillus subtilis glutamyl-trna synthetase gene, complete cds.) (le:1) (re:1452) (di:direct) BACGLTXA M55073 g143006 Bacillus subtilis 1423 -11528770 215692 gltx glutamyl-trna synthetase (sr:bacillus subtilis (strain 168t) dna) (db:genpept-bct1) (de:bacillus subtilis glutamyl-trna transferase (gltx), serineacetyltransferase (cyse), and cysteinyl-trna synthetase (cyss)genes, complete cds's.) (le:1706) (re:3157) (di:direct) BACGLUSYN L14580 g289282 Bacillus subtilis 1423 -11528770 215699 gltx glutamyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.17) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:111044) (re:112495) (di:direct) BSUB0001 Z99104 g2632359 Bacillus subtilis 1423 -11528770 6000685240 glutamyl-trna synthetase (db:genpept-bct2) (de:bacillus subtilis glutamyl-trna synthetase gene, complete cds.) (le:1) (re:1452) (di:direct) U49789 U49789 g2653659 Bacillus subtilis 1423 -11528770 7000686706 gltx glutamate--trna ligase:gltx:glutamyl-trna synthetase gltx (cl:glutamate--trna ligase) (ec:6.1.1.17) (db:pir) SYBSET S66121 Bacillus subtilis 1423 -11528770 5000688543 (de:(gltx) (pn:glutamyl-trna synthetase:glutamate--trna ligase:glurs:glutamyl-trna synthetase :glutamate-trna ligase:glurs) (gtcfc:9.10:10.06) (ec:6.1.1.17) (sye_bacsu) (keggfc:5.1:9.10:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacill) gltX gltX Bacillus subtilis 1423 10041872

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501734981	613	22769	285	95

Description

6500724913 outb:tscbgh:gsp-81:nade nh3-dependent nad+ synthetase:nh:3-dependent nad:synthetase:spore outgrowth factor b:sporulation protein outb:general stress protein 38:gsp38 (gtcfc:5.1:9.3:9.4) (ec:6.3.5.1) (keggfc:5.1:9.4) (bsorffc:3.4.2) (db:gtc-bacillus subtilis) (gtcfc:1-amino acid metabolism-glutamate metabolism:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6):metabolism of cofactors and vitamin... nadE nadE Bacillus subtilis 1423 -11528771 85145 nade:outb (ec:6.3.5.1) (de:b) (sporulation protein outb) (general stress protein 38) (gsp38)) (db:swissprot) NADE_BACSU P08164 BACILLUS SUBTILIS 1423 -11528771 131075 nade:outb nad+ synthase::32k phosphoprotein outb:nh3-dependent nad+ synthetase nade:spore outgrowth factor b (cl:spore outgrowth factor b) (ec:6.3.1.5) (db:pir1.dat) A26936 A26936 Bacillus subtilis 1423 -11528771 216427 (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis outb gene encoding a sporulation protein,complete cds.) (nt:outb) (le:141) (re:959) (di:direct) BACOUTB M15811 g143279 Bacillus subtilis 1423 -11528771 222579 nade nh3-dependent nad+ synthetase (fn:nad biosynthesis) (db:genpept-bct1) (ec:6.3.5.1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: outb, tscbgh, gsp-81) (le:143210) (re:144028) (di:direct) BSUB0002 Z99105 g2632599 Bacillus subtilis 1423 -11528771 7500886247 outb spore outgrowth factor b (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:17513) (re:18331) (di:direct) D50453 D50453 g1805385 Bacillus subtilis 1423 -11528771

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735045	614	22770	894	297

Description

6500724914 hypothetical protein:similar to glutamate racemase (gtcfc:5.1:6.7:14.1) (ec:5.1.1.3) (keggfc:5.1:6.6) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrpC yrpC Bacillus subtilis 1423 -11528772 7000693045 yrpc glutamate racemase homolog yrpc (cl:glutamate racemase) (db:pir2.dat) C69978 C69978 Bacillus subtilis 1423 -11528772 1500692676 yrpc yrpc (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934638 Bacillus subtilis 1423 -11528772 7500964022 yrpc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to glutamate racemase) (le:138127) (re:138924) (di:direct) BSUB0014 Z99117 g2635126 Bacillus subtilis 1423 -11528772

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735049	615	22771	915	304

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735068	616	22772	747	249

Description

6500724915 glutamate racemase (gtcfc:5.1:6.7) (ec:5.1.1.3) (keggfc:5.1:6.6) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) racE racE Bacillus subtilis 1423 -11528773 4000707585 race (ec:5.1.1.3) (de:glutamate racemase,) (db:swissprot) MURI_BACSU P94556 BACILLUS SUBTILIS 1423 -11528773 7000685889 race glutamate racemase (cl:glutamate racemase) (ec:5.1.1.3) (db:pir2.dat) B69688 B69688 Bacillus subtilis 1423 -11528773 220333 race glutamate racemase (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:5.1.1.3) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:107188) (re:108006) (di:complement) BSUB0015 Z99118 g2635304 Bacillus subtilis 1423 -11528773 304206 race glutamate racemase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (le:61901) (re:62719) (di:direct) BSZ75208 Z75208 g1770057 Bacillus subtilis 1423 -11528773

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735073	617	22773	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735074	618	22774	327	108

Description

GTC ORF with score 91 to: (fn:putative lectin-like protein involved in) (sr:saccharomyces cerevisiae (sub_species:pastorianus, strain:kms004) (db:genpept) (de:saccharomyces cerevisiae gene for flocculin, partial cds.) (le:<1) (re:2550) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735099	619	22775	720	239

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735105	620	22776	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735109	621	22777	312	104

Description

6500724916 ipa-76d:roca pyrroline-5 carboxylate dehydrogenase:1-pyrroline-5-carboxylate dehydrogenase:p5c dehydrogenase (gtcfc:5.1:5.10:10.11) (ec:1.5.1.12) (keggfc:5.1:5.10) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) rocA rocA Bacillus subtilis 1423 -11528774 7500890485 roca:ipa-76d (ec:1.5.1.12) (de:dehydrogenase)) (db:swissprot) ROCA_BACSU P39634 BACILLUS SUBTILIS 1423 -11528774 7000686433 roca pyrroline-5 carboxylate dehydrogenase roca:protein ipa-76d (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) S39731 S39731 Bacillus subtilis 1423 -11528774 5000688418 ipa-76d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:77047) (re:78594) (di:direct) BSGENR X73124 g414000 Bacillus subtilis 1423 -11528774 219313 roca pyrroline-5 carboxylate dehydrogenase (fn:arginine and ornithine utilization) (db:genpept-bct1) (ec:1.5.1.12) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-76d) (le:79365) (re:80912) (di:complement) BSUB0020 Z99123 g2636314 Bacillus subtilis 1423 -11528774 95879 roca:ipa-76d (ec:1.5.1.12) (de:dehydrogenase)) (db:swissprot) ROCA_BACSU P39634 BACILLUS SUBTILIS 1423 -11528774 170154 roca pyrroline-5 carboxylate dehydrogenase roca (db:pir) S39731 S39731 Bacillus subtilis 1423 -11528774

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735162	622	22778	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735174	623	22779	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735176	624	22780	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735182	625	22781	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735183	626	22782	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735234	627	22783	801	267

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735254	628	22784	861	287

Description

GTC ORF with score 176 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completecds.) (nt:similar to salicylate hydroxylase; orf7) (le:10288) (re:11433) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735310	629	22785	195	64

Description

6500724917 glutamate-1-semialdehyde aminotransferase (gtcfc:5.1:9.10) (ec:5.4.3.8) (keggfc:9.10) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) gsaB gsaB Bacillus subtilis 1423 -11528775 7000693049 gsab glutamate-1-semialdehyde aminotransferase gsab (db:pir2.dat) G69637 G69637 Bacillus subtilis 1423 -11528775 7500964026 gsab glutamate-1-semialdehyde aminotransferase (db:genpept-bct1) (ec:5.4.3.8) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:139134) (re:140312) (di:complement) BSUB0005 Z99108 g2633194 Bacillus subtilis 1423 -11528775

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735317	630	22786	675	224

Description

6500724918 yhfg:gltt proton/sodium-glutamate symport protein (gtcfc:5.1:12.1) (keggfc:14.2) (bsorffc:1.1.1:3.1.1) (db:gtc-bacillus subtilis) gltT gltT Bacillus subtilis 1423 -11528776 7000693082 gltt h+/na+-glutamate symport protein gltt (db:pir2.dat) D69635 D69635 Bacillus subtilis 1423 -11528776 4000714638 gltt proton/sodium-glutamate symport protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yhfg) (le:96532) (re:97821) (di:complement) BSUB0006 Z99109 g2633358 Bacillus subtilis 1423 -11528776 7500964046 yhfg hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to glutamate-aspartate carrier proteins) (le:16391) (re:17680) (di:complement) BSY14083 Y14083 g2226240 Bacillus subtilis 1423 -11528776

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735338	631	22787	366	121

Description

6500724919 n-acetylglutamate gamma-semialdehyde dehydrogenase:n-acetyl-gamma-glutamyl-phosphate reductase:agpr:n-acetyl-glutamate semialdehyde dehydrogenase:nagsa dehydrogenase (gtcfc:5.1:5.16) (ec:1.2.1.38) (keggfc:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argC argC Bacillus subtilis 1423 -11528777 218954 argc (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:9035) (re:10075) (di:direct) BS168NPRB Z79580 g1620932 Bacillus subtilis 1423 -11528777 304074 argc n-acetylglutamate gamma-semialdehyde (fn:arginine biosynthesis) (db:genpept-bct1) (ec:1.2.1.38) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:195006) (re:196046) (di:direct) BSUB0006 Z99109 g2633456 Bacillus subtilis 1423 -11528777 3500684476 argc n-acetylglutamate gamma-semialdehyde (fn:arginine biosynthesis) (db:genpept-bct1) (ec:1.2.1.38) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:116) (re:1156) (di:direct) BSUB0007 Z99110 g2633473 Bacillus subtilis 1423 -11528777 6000689695 argc (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (le:52232) (re:53272) (di:direct) BSY09476 Y09476 g2145421 Bacillus subtilis 1423 -11528777 7000694277 argc n-acetylglutamate gamma-semialdehyde dehydrogenase argc (db:pir) F69588 F69588 Bacillus subtilis 1423 -11528777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735340	632	22788	234	77

Description

6500724920 arga:arge:argj ornithine acetyltransferase / amino-acid acetyltransferase:glutamate n-acetyltransferase:ornithine acetyltransferase:ornithine transacetylase:oatase / amino-acid acetyltransferase:n-acetylglutamate synthase:ags (gtcfc:5.1:5.16) (keggfc:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argJ argJ Bacillus subtilis 1423 -11528778 7500877141 argj (ec:2.3.1.35:2.3.1.1) (de:acetyltransferase, (n-acetylglutamate synthase) (ags)) (db:swissprot) ARGJ_BACSU P36843 BACILLUS SUBTILIS 1423 -11528778 7000684613 argj ornithine acetyltransferase / amino-acid acetyltransferase argj (cl:glutamate n-acetyltransferase argj) (db:pir2.dat) I40373 I40373 Bacillus subtilis 1423 -11528778 5000688466 argj ornithine acetyltransferase (db:genpept-bct1) (de:b.subtilis (168) dna for argc-f citrulline biosynthetic operon.) (le:1181) (re:2401) (di:direct) BSCITBO Z26919 g408115 Bacillus subtilis 1423 -11528778 219063 argj amino-acid acetyltransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.3.1.35:2.3.1.1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: arga, arge; ornithine) (le:196066) (re:197286) (di:direct) BSUB0006 Z99109 g2633457 Bacillus subtilis 1423 -11528778 6000684505 argj amino-acid acetyltransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.3.1.35:2.3.1.1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: arga, arge; ornithine) (le:1176) (re:2396) (di:direct) BSUB0007 Z99110 g2633474 Bacillus subtilis 1423 -11528778 60096 argj (ec:2.3.1.35:2.3.1.1) (de:acetyltransferase, (n-acetylglutamate synthase) (ags)) (db:swissprot) ARGJ_BACSU P36843 BACILLUS SUBTILIS 1423 -11528778 170408 argj ornithine acetyltransferase / amino-acid acetyltransferase argj (db:pir) I40373 I40373 Bacillus subtilis 1423 -11528778 308602 argj amino-acid acetyltransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.3.1.35:2.3.1.1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: arga, arge; ornithine) (le:1176) (re:2396) (di:direct) BSUB0007 Z99110 g2633474 Bacillus subtilis 1423 -11528778

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501735397	633	22789	186	61

Description

6500724921 n-acetylglutamate 5-phosphotransferase:acetylglutamate kinase:nag kinase:agk:n-acetylglutamate 5-phosphotransferase (gtcfc:5.1:5.16) (ec:2.7.2.8) (keggfc:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argB argB Bacillus subtilis 1423 -11528779 7500877111 argb (ec:2.7.2.8) (de:(n-acetylglutamate 5-phosphotransferase)) (db:swissprot) ARGB_BACSU P36840 BACILLUS SUBTILIS 1423 -11528779 7000684609 argb n-acetylglutamate 5-phosphotransferase argb (db:pir2.dat) I40374 I40374 Bacillus subtilis 1423 -11528779 5000688463 argb n-acetylglutamate 5-phosphotransferase (db:genpept-bct1) (de:b.subtilis (168) dna for argc-f citrulline biosynthetic operon.) (le:2416) (re:3192) (di:direct) BSCITBO Z26919 g408116 Bacillus subtilis 1423 -11528779 219064 argb n-acetylglutamate 5-phosphotransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.7.2.8) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:197301) (re:198077) (di:direct) BSUB0006 Z99109 g2633458 Bacillus subtilis 1423 -11528779 6000684500 argb n-acetylglutamate 5-phosphotransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.7.2.8) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:2411) (re:3187) (di:direct) BSUB0007 Z99110 g2633475 Bacillus subtilis 1423 -11528779 7502851547 argb n-acetylglutamate-5-phosphotransferase (db:genpept) (de:bacillus amyloliquefaciens n-acetylglutamate-5-phosphotransferase(argb) gene, partial cds.) (nt:regulatory protein for the arginine biosynthetic) (le:1) (re:774) (di:direct) AF001832 AF001832 g4100638 Bacillus amyloliquefaciens 1390 -11528779 60063 argb (ec:2.7.2.8) (de:(n-acetylglutamate 5-phosphotransferase)) (db:swissprot) ARGB_BACSU P36840 BACILLUS SUBTILIS 1423 -11528779 170360 argb n-acetylglutamate 5-phosphotransferase argb (db:pir) I40374 I40374 Bacillus subtilis 1423 -11528779 308603 argb n-acetylglutamate 5-phosphotransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.7.2.8) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:2411) (re:3187) (di:direct) BSUB0007 Z99110 g2633475 Bacillus subtilis 1423 -11528779

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735398	634	22790	453	150

Description

6500724922 n-acetylornithine aminotransferase:acetylornithine aminotransferase:acoat (gtcfc:5.1:5.16) (ec:2.6.1.11) (keggfc:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argD argD Bacillus subtilis 1423 -11528780 7500877129 argd (ec:2.6.1.11) (de:acetylornithine aminotransferase, (acoat)) (db:swissprot) ARGD_BACSU P36839 BACILLUS SUBTILIS 1423 -11528780 7000684610 argd n-acetylornithine aminotransferase argd (db:pir2.dat) I40375 I40375 Bacillus subtilis 1423 -11528780 5000688465 argd n-acetylornithine aminotransferase (db:genpept-bct1) (de:b.subtilis (168) dna for argc-f citrulline biosynthetic operon.) (le:3189) (re:4346) (di:direct) BSCITBO Z26919 g408117 Bacillus subtilis 1423 -11528780 219065 argd n-acetylornithine aminotransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.6.1.11) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:198074) (re:199231) (di:direct) BSUB0006 Z99109 g2633459 Bacillus subtilis 1423 -11528780 6000684502 argd n-acetylornithine aminotransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.6.1.11) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:3184) (re:4341) (di:direct) BSUB0007 Z99110 g2633476 Bacillus subtilis 1423 -11528780 60076 argd (ec:2.6.1.11) (de:acetylornithine aminotransferase, (acoat)) (db:swissprot) ARGD_BACSU P36839 BACILLUS SUBTILIS 1423 -11528780 170365 argd n-acetylornithine aminotransferase argd (db:pir) I40375 I40375 Bacillus subtilis 1423 -11528780 308604 argd n-acetylornithine aminotransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.6.1.11) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:3184) (re:4341) (di:direct) BSUB0007 Z99110 g2633476 Bacillus subtilis 1423 -11528780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735400	635	22791	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735402	636	22792	594	197

Description

6500724923 ornithine carbamoyltransferase:ornithine carbamoyltransferase chain f:otcase-2 (gtcfc:5.1:5.10:5.16) (ec:2.1.3.3) (keggfc:5.10:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argF argF Bacillus subtilis 1423 -11528781 219068 argf (ec:2.1.3.3) (de:ornithine carbamoyltransferase, anabolic, (otcase)) (db:swissprot) OTCA_BACSU P18186 BACILLUS SUBTILIS 1423 -11528781 123317 argf ornithine carbamoyltransferase::citrulline phosphorylase:ornithine transcarbamylase (cl:ornithine carbamoyltransferase:aspartate/ornithine carbamoyltransferase homology) (ec:2.1.3.3) (db:pir1.dat) (mp:100 (degrees)) OWBS S11000 Bacillus subtilis 1423 -11528781 219008 (db:genpept-bct1) (de:b.subtilis argf gene for ornithine carbamoyltransferase and partialcpa gene for carbamoyl phosphate synthase (ec 2.1.3.3, ec 6.3.5.5).) (nt:argf protein (aa 1 - 319)) (le:477) (re:1436) (di:direct) BSARGCPA X53360 g39811 Bacillus subtilis 1423 -11528781 5000688415 argf ornithine carbamoyltransferase (db:genpept-bct1) (de:b.subtilis (168) dna for argc-f citrulline biosynthetic operon.) (nt:see also embl accession number x53360) (le:8542) (re:9501) (di:direct) BSCITBO Z26919 g408120 Bacillus subtilis 1423 -11528781 308607 argf ornithine carbamoyltransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.1.3.3) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:203427) (re:204386) (di:direct) BSUB0006 Z99109 g2633462 Bacillus subtilis 1423 -11528781 6000684965 argf ornithine carbamoyltransferase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:2.1.3.3) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:8537) (re:9496) (di:direct) BSUB0007 Z99110 g2633479 Bacillus subtilis 1423 -11528781 87953 argf (ec:2.1.3.3) (de:ornithine carbamoyltransferase, anabolic, (otcase)) (db:swissprot) OTCA_BACSU P18186 BACILLUS SUBTILIS 1423 -11528781

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735409	637	22793	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735411	638	22794	513	171

Description

6500724924 gamma-glutamyl kinase (gtcfc:5.1:5.16) (ec:2.7.2.11) (keggfc:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) proB proB Bacillus subtilis 1423 -11528782 7500888522 prob (ec:2.7.2.11) (de:glutamate 5-kinase, (gamma-glutamyl kinase) (gk)) (db:swissprot) PROB_BACSU P39820 BACILLUS SUBTILIS 1423 -11528782 7000693015 prob gamma-glutamyl kinase prob (cl:glutamate 5-kinase) (db:pir2.dat) D69682 D69682 Bacillus subtilis 1423 -11528782 6000689762 prob gamma-glutamyl kinase (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:30621) (re:31718) (di:direct) BSAJ2571 AJ002571 g2632032 Bacillus subtilis 1423 -11528782 7500888525 prob gamma-glutamyl kinase (fn:proline biosynthesis) (db:genpept-bct1) (ec:2.7.2.11) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:183570) (re:184667) (di:direct) BSUB0007 Z99110 g2633666 Bacillus subtilis 1423 -11528782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735423	639	22795	537	178

Description

6500724925 gamma-glutamyl phosphate reductase (gtcfc:5.1:5.16:9.10) (ec:1.2.1.41) (keggfc:5.16:9.10) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) proA proA Bacillus subtilis 1423 -11528783 7000693016 proa gamma-glutamyl phosphate reductase proa (cl:glutamate-5-semialdehyde dehydrogenase) (db:pir2.dat) C69682 C69682 Bacillus subtilis 1423 -11528783 6000689764 proa gamma-glutamylphosphate reductase (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:31730) (re:32977) (di:direct) BSAJ2571 AJ002571 g2632033 Bacillus subtilis 1423 -11528783 7500964000 proa gamma-glutamyl phosphate reductase (fn:proline biosynthesis) (db:genpept-bct1) (ec:1.2.1.41) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:184679) (re:185926) (di:direct) BSUB0007 Z99110 g2633667 Bacillus subtilis 1423 -11528783

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735429	640	22796	525	174

Description

6500724926 glutamate synthase:large subunit (gtcfc:5.1) (ec:1.4.1.13) (keggfc:14.1) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) gltA gltA Bacillus subtilis 1423 -11528784 7502851548 gltb:glta (ec:1.4.1.13) (de:glutamate synthase (nadph) large chain, (nadph-gogat)) (db:swissprot) GLTB_BACSU P39812 BACILLUS SUBTILIS 1423 -11528784 7000693047 glta glutamate synthase large subunit glta (cl:glutamate synthase (nadph)) (db:pir2.dat) G69634 G69634 Bacillus subtilis 1423 -11528784 6000690966 glta glutamate synthase large subunit (fn:glutamate biosynthesis) (db:genpept-bct1) (ec:1.4.1.13) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:228126) (re:232688) (di:complement) BSUB0010 Z99113 g2634228 Bacillus subtilis 1423 -11528784 7500964024 glta glutamate synthase large subunit (fn:glutamate biosynthesis) (db:genpept-bct1) (ec:1.4.1.13) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:9156) (re:13718) (di:complement) BSUB0011 Z99114 g2634239 Bacillus subtilis 1423 -11528784

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735496	641	22797	279	93

Description

6500724927 acetylornitine deacetylase (gtcfc:5.1) (ec:3.5.1.16) (keggfc:14.1) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argE argE Bacillus subtilis 1423 -11528785 7000692142 arge acetylornithine deacetylase arge (db:pir2.dat) H69588 H69588 Bacillus subtilis 1423 -11528785 5500687384 arge acetylornitine deacetylase (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415403 Bacillus subtilis 1423 -11528785 7500963371 arge acetylornitine deacetylase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:3.5.1.16) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:140776) (re:142086) (di:complement) BSUB0011 Z99114 g2634363 Bacillus subtilis 1423 -11528785

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735502	642	22798	783	260

Description

6500724928 lys:lysa diaminopimelate decarboxylase:dap decarboxylase (gtcfc:5.1:5.8) (ec:4.1.1.20) (keggfc:5.8) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) lysA lysA Bacillus subtilis 1423 -11528786 169960 lysa diaminopimelate decarboxylase:lysa (cl:diaminopimelate decarboxylase) (ec:4.1.1.20) (db:pir2.dat) JU0471 S45535 Bacillus subtilis 1423 -11528786 7500963935 lysa diaminopimelate decarboxylase (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:1345) (re:2664) (di:direct) BACDIA L09228 g410117 Bacillus subtilis 1423 -11528786 215496 lysa diaminopimelate decarboxylase (fn:lysine biosynthesis) (db:genpept-bct1) (ec:4.1.1.20) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:40919) (re:42238) (di:complement) BSUB0013 Z99116 g2634773 Bacillus subtilis 1423 -11528786 7000692916 lysa diaminopimelate decarboxylase:lysa (ec:4.1.1.20) (db:pir) JU0471 JU0471 Bacillus subtilis 1423 -11528786

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735508	643	22799	825	275

Description

6500724929 hemk:heml glutamate-1-semialdehyde 2:1-aminotransferase:glutamate-1-semialdehyde 2:1-aminomutase:gsa:glutamate-1-semialdehyde aminotransferase:gsa-at (gtcfc:5.1:9.10) (ec:5.4.3.8) (keggfc:9.10) (bsorffc:3.1.1:3.4.7) (db:gtc-bacillus subtilis) hemL hemL Bacillus subtilis 1423 -11528787 74595 heml:hemk (ec:5.4.3.8) (de:(glutamate-1-semialdehyde aminotransferase) (gsa-at)) (db:swissprot) GSA_BACSU P30949 BACILLUS SUBTILIS 1423 -11528787 7000685458 heml glutamate-1-semialdehyde 2:1-aminomutase:heml:glutamate-1-semialdehyde 2:1-aminotransferase heml (ec:5.4.3.8) (db:pir2.dat) D42728 D42728 Bacillus subtilis 1423 -11528787 7500882782 heml glutamate-1-semialdehyde 2:1-aminotransferase (fn:5-aminolevulinic acid synthesis) (sr:b.subtilis dna) (db:genpept-bct1) (ec:5.4.3.8) (de:bacillus subtilis hemaxcdbl gene cluster.) (le:5193) (re:6485) (di:direct) BACHEMAXC M57676 g143040 Bacillus subtilis 1423 -11528787 215828 heml glutamate-1-semialdehyde 2:1-aminotransferase (fn:porphyrin biosynthesis) (db:genpept-bct1) (ec:5.4.3.8) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: hemk) (le:76850) (re:78142) (di:complement) BSUB0015 Z99118 g2635277 Bacillus subtilis 1423 -11528787 170019 heml glutamate-1-semialdehyde 2:1-aminomutase:heml:glutamate-1-semialdehyde 2:1-aminotransferase heml (ec:5.4.3.8) (db:pir) D42728 D42728 Bacillus subtilis 1423 -11528787 5000688550 (de:(heml) (pn:glutamate-1-semialdehyde 2,1-aminomutase:gsa:glutamate-1- semialdehyde aminotransferase:glutamate-1-semialdehyde 2,1-aminomutase :gsa:glutamate-1-semialdehyde aminotransferase:gsa-at) (gn:hemk) (gtcfc:9.10) (ec:5.4.3.8)) hemL hemL Bacillus subtilis 1423 10017109

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735511	644	22800	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735514	645	22801	642	214

Description

6500724930 aeca:ask hypothetical protein:aspartokinase ii leader peptide:attenuator peptide (gtcfc:5.1) (keggfc:14.2) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) ask ask Bacillus subtilis 1423 -11528788 82371 ask:aeca (de:aspartokinase ii leader peptide (attenuator peptide)) (db:swissprot) LPA2_BACSU P08497 BACILLUS SUBTILIS 1423 -11528788 7000685760 ask aspartokinase ii attenuator ask (db:pir2.dat) G69590 G69590 Bacillus subtilis 1423 -11528788 215193 aspartokinase ii attenuator (sr:bacillus subtilis (strain 168) (tissue library: atcc 6633) dna) (db:genpept-bct1) (de:bacillus subtilis thioredoxin (trx), uvrb and aspartokinase iigenes, complete cds.) (le:2352) (re:2426) (di:direct) BACAPKII J03294 g142522 Bacillus subtilis 1423 -11528788 220322 ask (fn:aspartokinase ii attenuator) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:114895) (re:114969) (di:complement) BSUB0015 Z99118 g2635313 Bacillus subtilis 1423 -11528788 304195 ask 24 residue peptide (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:aspartokinase ii attenuator) (le:54938) (re:55012) (di:direct) BSZ75208 Z75208 g1770046 Bacillus subtilis 1423 -11528788 5000688412 (de:(ask) (pn:aspartokinase ii leader peptide:attenuator peptide) (gn:aeca) (gtcfc:5.01) (ec:) (lpa2_bacsu) (keggfc:11.2) (bsorffc:3.1.1) (db:gtc-bacillus subtilis)) ask ask Bacillus subtilis 1423 10024601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735518	646	22802	567	188

Description

6500724931 argininosuccinate lyase (gtcfc:5.1:5.10:5.16:5.2) (ec:4.3.2.1) (keggfc:5.2:5.10:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argH argH Bacillus subtilis 1423 -11528789 7000692224 argh argininosuccinate lyase argh (cl:argininosuccinate lyase) (db:pir2.dat) C69589 C69589 Bacillus subtilis 1423 -11528789 4000714234 argh arginine succinate lyase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:165989) (re:167374) (di:direct) AF008220 AF008220 g2293243 Bacillus subtilis 1423 -11528789 6000689047 argh argininosuccinate lyase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:4.3.2.1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:215693) (re:217078) (di:complement) BSUB0015 Z99118 g2635409 Bacillus subtilis 1423 -11528789 7500963427 argh argininosuccinate lyase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:4.3.2.1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:13053) (re:14438) (di:complement) BSUB0016 Z99119 g2635428 Bacillus subtilis 1423 -11528789

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735527	647	22803	618	205

Description

6500724932 argininosuccinate synthase (gtcfc:5.1:5.10:5.16:5.2) (ec:6.3.4.5) (keggfc:5.2:5.10:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) argG argG Bacillus subtilis 1423 -11528790 7000692225 argg argininosuccinate synthase argg (cl:argininosuccinate synthase) (db:pir2.dat) B69589 B69589 Bacillus subtilis 1423 -11528790 4000714233 argg arginine succinate synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:164781) (re:165992) (di:direct) AF008220 AF008220 g2293242 Bacillus subtilis 1423 -11528790 6000689045 argg argininosuccinate synthase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:6.3.4.5) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:217075) (re:218286) (di:complement) BSUB0015 Z99118 g2635410 Bacillus subtilis 1423 -11528790 7500954508 argg argininosuccinate synthase (fn:arginine biosynthesis) (db:genpept-bct1) (ec:6.3.4.5) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:14435) (re:15646) (di:complement) BSUB0016 Z99119 g2635429 Bacillus subtilis 1423 -11528790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735576	648	22804	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735582	649	22805	294	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735585	650	22806	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735596	651	22807	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735607	652	22808	324	107

Description

6500724933 ornithine aminotransferase:ornithine--oxo-acid aminotransferase (gtcfc:5.1:5.10:5.16) (ec:2.6.1.13) (keggfc:5.10:5.16) (bsorffc:3.1.1) (db:gtc-bacillus subtilis) rocD rocD Bacillus subtilis 1423 -11528791 219596 rocd (ec:2.6.1.13) (de:aminotransferase)) (db:swissprot) OAT_BACSU P38021 BACILLUS SUBTILIS 1423 -11528791 7000686025 rocd ornithine--oxo-acid transaminase:rocd:ornithine aminotransferase:ornithine--oxo-acid aminotransferase (cl:ornithine--oxo-acid aminotransferase) (ec:2.6.1.13) (db:pir2.dat) S55793 S55793 Bacillus subtilis 1423 -11528791 215786 rocd orthinine aminotransferase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:25845) (re:27050) (di:complement) BACGNTZA D78193 g1064807 Bacillus subtilis 1423 -11528791 5000688419 rocd ornithine aminotransferase (db:genpept-bct1) (de:b.subtilis rocd, roce and rocf genes.) (le:241) (re:1446) (di:direct) BSROCDEF X81802 g550311 Bacillus subtilis 1423 -11528791 302082 rocd ornithine aminotransferase (fn:arginine and ornithine utilization) (db:genpept-bct1) (ec:2.6.1.13) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:144229) (re:145434) (di:complement) BSUB0021 Z99124 g2636581 Bacillus subtilis 1423 -11528791 87376 rocd (ec:2.6.1.13) (de:aminotransferase)) (db:swissprot) OAT_BACSU P38021 BACILLUS SUBTILIS 1423 -11528791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735608	653	22809	690	229

Description

6500724934 prolyl-trna synthetase (gtcfc:10.6) (ec:6.1.1.15) (keggfc:5.10:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) proS proS Bacillus subtilis 1423 -11528792 7000694454 pros proline--trna ligase:pros:prolyl-trna synthetase (cl:proline--trna ligase) (ec:6.1.1.15) (db:pir2.dat) G69682 G69682 Bacillus subtilis 1423 -11528792 7500954484 pros prolyl-trna synthetase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:126301) (re:127995) (di:direct) BSUB0009 Z99112 g2634029 Bacillus subtilis 1423 -11528792

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735654	654	22810	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735661	655	22811	408	135

Description

GTC ORF with score 173 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completecds.) (nt:similar to salicylate hydroxylase; orf7) (le:10288) (re:11433) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735663	656	22812	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735669	657	22813	1125	375

Description

GTC ORF with score 156 to: (sr:hordeum vulgare (strain himalaya) (library: lambda zap ii) 24 hou) (db:genpept-pln1) (de:hordeum vulgare seed imbitition protein (sip1) gene, complete cds.) (le:1042:1596:1951:2136) (re:1232:1855:2041:2184) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735699	658	22814	411	136

Description

6500724935 hypothetical protein:similar to hypothetical proteins (gtcfc:5.10:14.1) (ec:2.3.1.57) (keggfc:5.10) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaD ynaD Bacillus subtilis 1423 -11528793 7000692649 ynad conserved hypothetical protein ynad (db:pir2.dat) D69887 D69887 Bacillus subtilis 1423 -11528793 220169 ynad ynad (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750115 Bacillus subtilis 1423 -11528793 7500963757 ynad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins) (le:101220) (re:101732) (di:direct) BSUB0010 Z99113 g2634136 Bacillus subtilis 1423 -11528793

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735764	659	22815	597	198

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735766	660	22816	201	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735769	661	22817	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735771	662	22818	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735780	663	22819	240	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735789	664	22820	978	326

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735791	665	22821	219	73

Description

6500724936 arginyl-trna synthetase (gtcfc:10.6) (ec:6.1.1.19) (keggfc:5.10:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) argS argS Bacillus subtilis 1423 -11528794 4000714663 args (ec:6.1.1.19) (de:arginyl-trna synthetase, (arginine--trna ligase) (argrs)) (db:swissprot) SYR_BACSU P46906 BACILLUS SUBTILIS 1423 -11528794 7000692226 args arginine--trna ligase:args:arginyl-trna synthetase (cl:bacillus arginine--trna ligase) (ec:6.1.1.19) (db:pir2.dat) E69589 E69589 Bacillus subtilis 1423 -11528794 7500892560 args arginyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.19) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:34303) (re:35973) (di:complement) BSUB0020 Z99123 g2636270 Bacillus subtilis 1423 -11528794 7502851549 args arginyl trna synthetase (db:genpept-bct1) (de:bacillus subtilis ywia, sbo, ywib, args and nark genes.) (le:1680) (re:3350) (di:direct) BSZ97024 Z97024 g2224756 Bacillus subtilis 1423 -11528794 7500892558 args (ec:6.1.1.19) (de:arginyl-trna synthetase, (arginine--trna ligase) (argrs)) (db:swissprot) SYR_BACSU P46906 BACILLUS SUBTILIS 1423 -11528794

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735797	666	22822	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735846	667	22823	660	220

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735850	668	22824	807	268

Description

6500724937 hypothetical protein:similar to agmatinase (gtcfc:5.10:14.1) (ec:3.5.3.11) (keggfc:5.10) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhG ywhG Bacillus subtilis 1423 -11528795 7000692161 ywhg agmatinase homolog ywhg (cl:methanococcus jannaschii agmatinase) (db:pir2.dat) H70057 H70057 Bacillus subtilis 1423 -11528795 7500963385 ywhg unknown:highly similar to several agmatinases (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:7336) (re:8208) (di:direct) BSTHRZ Z80360 g1565242 Bacillus subtilis 1423 -11528795 219707 ywhg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to agmatinase) (le:48506) (re:49378) (di:complement) BSUB0020 Z99123 g2636285 Bacillus subtilis 1423 -11528795

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735853	669	22825	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735860	670	22826	342	114

Description

6500724938 hypothetical protein:similar to spermidine synthase (gtcfc:5.10:5.16:6.1:14.1) (ec:2.5.1.16) (keggfc:5.10:5.16:6.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywhF ywhF Bacillus subtilis 1423 -11528796 7000694600 ywhf spermidine synthase homolog ywhf (cl:spermidine synthase) (db:pir2.dat) G70057 G70057 Bacillus subtilis 1423 -11528796 7500965197 ywhf unknown:highly similar to several spermidine (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:6445) (re:7275) (di:direct) BSTHRZ Z80360 g1565241 Bacillus subtilis 1423 -11528796 219706 ywhf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to spermidine synthase) (le:49439) (re:50269) (di:complement) BSUB0020 Z99123 g2636286 Bacillus subtilis 1423 -11528796

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735862	671	22827	813	270

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735865	672	22828	615	204

Description

6500724939 arginase (gtcfc:5.10:5.16:10.11) (ec:3.5.3.1) (keggfc:5.10:5.16) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) rocF rocF Bacillus subtilis 1423 -11528797 215784 rocf (ec:3.5.3.1) (de:arginase,) (db:swissprot) ARGI_BACSU P39138 BACILLUS SUBTILIS 1423 -11528797 7000684612 rocf arginase:rocf (cl:arginase 1) (ec:3.5.3.1) (db:pir2.dat) S55795 S55795 Bacillus subtilis 1423 -11528797 302080 rocf arginase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:23255) (re:24145) (di:complement) BACGNTZA D78193 g1064805 Bacillus subtilis 1423 -11528797 5000688420 rocf arginase (db:genpept-bct1) (de:b.subtilis rocd, roce and rocf genes.) (le:3146) (re:4036) (di:direct) BSROCDEF X81802 g550313 Bacillus subtilis 1423 -11528797 219598 rocf arginase (fn:arginine and ornithine utilization) (db:genpept-bct1) (ec:3.5.3.1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:141639) (re:142529) (di:complement) BSUB0021 Z99124 g2636579 Bacillus subtilis 1423 -11528797 60087 rocf (ec:3.5.3.1) (de:arginase,) (db:swissprot) ARGI_BACSU P39138 BACILLUS SUBTILIS 1423 -11528797 169869 rocf arginase:rocf (ec:3.5.3.1) (db:pir) S55795 S55795 Bacillus subtilis 1423 -11528797

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735869	673	22829	576	191

Description

GTC ORF with score 121 to: (fn:helicase, helicase-primase complex) (db:genpept-vrl) (de:human herpesvirus 6 serotype b putative major immediate-earlygenes.) (nt:similar to hhv6a u86, region ie-b) (le:16386) (re:19235) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735870	674	22830	264	87

Description

6500724940 histidyl-trna synthetase (gtcfc:10.6) (ec:6.1.1.21) (keggfc:5.11:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) hisS hisS Bacillus subtilis 1423 -11528798 7500892436 hiss (ec:6.1.1.21) (de:(hisrs)) (db:swissprot) SYH_BACSU O32039 BACILLUS SUBTILIS 1423 -11528798 7000693099 hiss histidine--trna ligase:hiss:histidyl-trna synthetase (cl:histidine--trna ligase:amino acid--trna ligase repeat homology:histidine--trna ligase homology) (ec:6.1.1.21) (db:pir2.dat) G69641 G69641 Bacillus subtilis 1423 -11528798 7500892438 hiss histidyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.21) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:20670) (re:21944) (di:complement) BSUB0015 Z99118 g2635220 Bacillus subtilis 1423 -11528798

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735938	675	22831	732	243

Description

6500724941 hisie:hisi phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyrophosphohydrolase:phosphoribosyl-atp pyrophosphohydrolase (gtcfc:5.11:14.3) (keggfc:5.11) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) hisI hisI Bacillus subtilis 1423 -11528799 5500701777 hisi:hisie (ec:3.5.4.19:3.6.1.31) (de:pyrophosphohydrolase,) (db:swissprot) HIS2_BACSU O34912 BACILLUS SUBTILIS 1423 -11528799 7000694418 hisi phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyropho hisi (cl:hisi bifunctional enzyme:hisi bifunctional enzyme homology:hisi protein homology) (db:pir2.dat) E69641 E69641 Bacillus subtilis 1423 -11528799 7502851550 hisi phosphoribosyl-atp pyrophosphohydrolase (fn:histidine biosynthesis) (db:genpept-bct1) (ec:3.5.4.19:3.6.1.31) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: hisie; phosphoribosyl-amp) (le:182446) (re:183075) (di:complement) BSUB0018 Z99121 g2635999 Bacillus subtilis 1423 -11528799 7500954325 hisie phosphoribosyl-amp cyclohydrolase / (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:44758) (re:45387) (di:direct) AF017113 AF017113 g2618871 Bacillus subtilis 1423 -11528799

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735949	676	22832	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735957	677	22833	387	128

Description

6500724942 phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (gtcfc:5.11) (ec:5.3.1.16) (keggfc:5.11) (db:gtc-bacillus subtilis) hisA hisA Bacillus subtilis 1423 -11528800 7502851551 hisa (ec:5.3.1.16) (de:isomerase,) (db:swissprot) HIS4_BACSU O35006 BACILLUS SUBTILIS 1423 -11528800 7000694420 hisa phosphoribosylformimino-5-aminoimidazole carboxamide ribotide hisa (cl:n-(5'-phospho-d-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidazolecarboxamide isomerase) (db:pir2.dat) F69640 F69640 Bacillus subtilis 1423 -11528800 5500701775 hisa phosphoribosylformimino-5-aminoimidazole (fn:histidine biosynthesis) (db:genpept-bct1) (ec:5.3.1.16) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:183827) (re:184564) (di:complement) BSUB0018 Z99121 g2636001 Bacillus subtilis 1423 -11528800 7500965076 hisa phosphoribosylformimino-5-aminoimidazole (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:43269) (re:44006) (di:direct) AF017113 AF017113 g2618869 Bacillus subtilis 1423 -11528800

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735971	678	22834	219	73

Description

6500724943 amidotransferase (gtcfc:5.11:5.12:5.13:5.15) (keggfc:5.11:5.12:5.13:5.15) (bsorffc:3.1.6) (db:gtc-bacillus subtilis) hisH hisH Bacillus subtilis 1423 -11528801 7500883298 hish (ec:2.4.2.-) (de:amidotransferase hish,) (db:swissprot) HIS5_BACSU O34565 BACILLUS SUBTILIS 1423 -11528801 7000692185 hish amidotransferase hish (cl:amidotransferase hish) (db:pir2.dat) D69641 D69641 Bacillus subtilis 1423 -11528801 7500883300 hish amidotransferase (fn:histidine biosynthesis) (db:genpept-bct1) (ec:2.4.2.-) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:184561) (re:185199) (di:complement) BSUB0018 Z99121 g2636002 Bacillus subtilis 1423 -11528801 5500701774 hish amidotransferase hish (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:42634) (re:43272) (di:direct) AF017113 AF017113 g2618868 Bacillus subtilis 1423 -11528801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501735974	679	22835	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736035	680	22836	384	127

Description

6500724944 histidinol dehydrogenase (gtcfc:5.11) (ec:1.1.1.23) (keggfc:5.11) (bsorffc:3.1.6) (db:gtc-bacillus subtilis) hisD hisD Bacillus subtilis 1423 -11528802 7500883342 hisd (ec:1.1.1.23) (de:histidinol dehydrogenase, (hdh)) (db:swissprot) HISX_BACSU O34651 BACILLUS SUBTILIS 1423 -11528802 7000693097 hisd histidinol dehydrogenase hisd (cl:histidinol dehydrogenase:histidinol dehydrogenase homology) (db:pir2.dat) A69641 A69641 Bacillus subtilis 1423 -11528802 7500883344 hisd histidinol dehydrogenase (fn:histidine biosynthesis) (db:genpept-bct1) (ec:1.1.1.23) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:185781) (re:187064) (di:complement) BSUB0018 Z99121 g2636004 Bacillus subtilis 1423 -11528802 5500701772 hisd histidinol dehydrogenase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:40769) (re:42052) (di:direct) AF017113 AF017113 g2618866 Bacillus subtilis 1423 -11528802

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736040	681	22837	486	161

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736044	682	22838	192	63

Description

6500724945 atp phosphoribosyltransferase (gtcfc:5.11:14.3) (ec:2.4.2.17) (keggfc:5.11) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) hisG hisG Bacillus subtilis 1423 -11528803 7500883263 hisg (ec:2.4.2.17) (de:atp phosphoribosyltransferase,) (db:swissprot) HIS1_BACSU O34520 BACILLUS SUBTILIS 1423 -11528803 7000692243 hisg atp phosphoribosyltransferase hisg (db:pir2.dat) C69641 C69641 Bacillus subtilis 1423 -11528803 7500883265 hisg atp phosphoribosyltransferase (fn:histidine biosynthesis) (db:genpept-bct1) (ec:2.4.2.17) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:187061) (re:187702) (di:complement) BSUB0018 Z99121 g2636005 Bacillus subtilis 1423 -11528803 5500701771 hisg atp phosphoribosyltransferase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:40131) (re:40772) (di:direct) AF017113 AF017113 g2618865 Bacillus subtilis 1423 -11528803

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736048	683	22839	612	203

Description

6500724946 ee57a:hutu urocanate hydratase:urocanase:imidazolonepropionate hydrolase (gtcfc:5.11:10.11) (ec:4.2.1.49) (keggfc:5.11) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) hutU hutU Bacillus subtilis 1423 -11528804 78097 hutu:ee57a (ec:4.2.1.49) (de:hydrolase)) (db:swissprot) HUTU_BACSU P25503 BACILLUS SUBTILIS 1423 -11528804 7000685574 hutu urocanate hydratase:hutu:urocanase (cl:urocanate hydratase) (ec:4.2.1.49) (db:pir2.dat) G69643 G69643 Bacillus subtilis 1423 -11528804 215863 ee57a::hutu hutu protein:urocanase (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:4094) (re:5752) (di:complement) BACHUTWAPA D31856 g603769 Bacillus subtilis 1423 -11528804 7500883636 hutu urocanase (fn:histidine utilization) (db:genpept-bct1) (ec:4.2.1.49) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:43083) (re:44741) (di:direct) BSUB0021 Z99124 g2636482 Bacillus subtilis 1423 -11528804 5000688425 (de:(hutu) (pn:urocanate hydratase:imidazolonepropionate hydrolase:urocanate hydratase :urocanase) (gn:ee57a) (gtcfc:5.11) (ec:4.2.1.49) (hutu_bacsu) (keggfc:5.11) (bsorffc:2.2.0) (db:gtc-bacillus subtilis)) hutU hutU Bacillus subtilis 1423 10020436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736057	684	22840	858	285

Description

6500724947 ee57b:huti imidazolonepropionase:imidazolone-5-propionate hydrolase (gtcfc:5.11:10.11) (ec:3.5.2.7) (keggfc:5.11) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) hutI hutI Bacillus subtilis 1423 -11528805 78093 huti:ee57b (ec:3.5.2.7) (de:hydrolase)) (db:swissprot) HUTI_BACSU P42084 BACILLUS SUBTILIS 1423 -11528805 7000685572 huti imidazolone-5-propionate hydrolase huti (db:pir2.dat) D69643 D69643 Bacillus subtilis 1423 -11528805 215862 ee57b::huti huti protein:imidazolone-5-propionate (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:2816) (re:4081) (di:complement) BACHUTWAPA D31856 g603768 Bacillus subtilis 1423 -11528805 7500883633 huti imidazolone-5-propionate hydrolase (fn:histidine utilization) (db:genpept-bct1) (ec:3.5.2.7) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:44754) (re:46019) (di:direct) BSUB0021 Z99124 g2636483 Bacillus subtilis 1423 -11528805 5000688424 (de:(huti) (pn:imidazolonepropionase:imidazolonepropionase :imidazolone-5-propionate hydrolase) (gn:ee57b) (gtcfc:5.11) (ec:3.5.2.7) (huti_bacsu) (keggfc:5.11) (bsorffc:2.2.0) (db:gtc-bacillus subtilis)) hutI hutI Bacillus subtilis 1423 10020432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736059	685	22841	744	248

Description

6500724948 ee57c:hutg formiminoglutamase:formiminoglutamate hydrolase (gtcfc:5.11:10.11) (ec:3.5.3.8) (keggfc:5.11) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) hutG hutG Bacillus subtilis 1423 -11528806 78085 hutg:ee57c (ec:3.5.3.8) (de:formiminoglutamase, (formiminoglutamate hydrolase)) (db:swissprot) HUTG_BACSU P42068 BACILLUS SUBTILIS 1423 -11528806 7000685571 hutg formiminoglutamate hydrolase hutg (db:pir2.dat) B69643 B69643 Bacillus subtilis 1423 -11528806 215861 ee57c::hutg hutg protein:formiminoglutamete hydrolase (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:1864) (re:2823) (di:complement) BACHUTWAPA D31856 g603767 Bacillus subtilis 1423 -11528806 7500883627 hutg formiminoglutamate hydrolase (fn:histidine utilization) (db:genpept-bct1) (ec:3.5.3.8) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:46012) (re:46971) (di:direct) BSUB0021 Z99124 g2636484 Bacillus subtilis 1423 -11528806 5000688422 (de:(hutg) (pn:formiminoglutamase:formiminoglutamase :formiminoglutamate hydrolase) (gn:ee57c) (gtcfc:5.11) (ec:3.5.3.8) (hutg_bacsu) (keggfc:5.11) (bsorffc:2.2.0) (db:gtc-bacillus subtilis)) hutG hutG Bacillus subtilis 1423 10020424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736061	686	22842	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736062	687	22843	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736122	688	22844	477	158

Description

GTC ORF with score 395 to: (fn:hydrolyzes acetyl groups from xylan) (db:genpept-pln2) (ec:3.1.1.6.) (de:penicillium purporogenum acetyl xylan esterase ii precursor (axe-2)mrna, complete cds.) (nt:axe ii; belongs to xylanolytic system; protein) (le:187)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736123	689	22845	201	67

Description

GTC ORF with score 215 to: (fn:hydrolyzes acetyl groups from xylan) (db:genpept-pln2) (ec:3.1.1.6.) (de:penicillium purporogenum acetyl xylan esterase ii precursor (axe-2)mrna, complete cds.) (nt:axe ii; belongs to xylanolytic system; protein) (le:187)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736133	690	22846	612	204

Description

6500724949 aminotransferase:putative aminotransferase b (gtcfc:5.11) (ec:2.6.1.-) (keggfc:14.1) (bsorffc:3.1.6) (db:gtc-bacillus subtilis) patB patB Bacillus subtilis 1423 -11528807 88675 patb (ec:2.6.1.-) (de:putative aminotransferase b,) (db:swissprot) PATB_BACSU Q08432 BACILLUS SUBTILIS 1423 -11528807 7000686089 patb aminotransferase patb (db:pir2.dat) S32934 S32934 Bacillus subtilis 1423 -11528807 4000707241 patb patb (db:genpept-bct1) (de:bacillus subtilis putative aminotransferase (patb), atp-dependentprotein kinase b (kinb), kinase-associated protein b (kapb) andkapd (kapd) genes, complete cds.) (nt:putative aminotransferase) (le:288) (re:1451) (di:direct) BSU63302 U63302 g2231218 Bacillus subtilis 1423 -11528807 219967 patb aminotransferase (db:genpept-bct1) (ec:2.6.1.-) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:30855) (re:32018) (di:direct) BSUB0017 Z99120 g2635640 Bacillus subtilis 1423 -11528807 1500685371 patb aminotransferase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuga to yugd.) (nt:putative) (le:288) (re:1451) (di:direct) BSZ93933 Z93933 g1934779 Bacillus subtilis 1423 -11528807 1500685372 patb aminotransferase (db:genpept-bct1) (de:b.subtilis genomic dna fragment from patb to yugk.) (nt:putative) (le:122) (re:1285) (di:complement) BSZ93934 Z93934 g1934787 Bacillus subtilis 1423 -11528807 170414 patb aminotransferase patb (db:pir) S32934 S32934 Bacillus subtilis 1423 -11528807 5000688427 (de:(patb) (pn:putative aminotransferase b:putative aminotransferase b) (gtcfc:5.11) (ec:2.6.1.-) (patb_bacsu) (keggfc:5.8:5.11) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) patB patB Bacillus subtilis 1423 10030802

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736142	691	22847	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736143	692	22848	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736146	693	22849	792	263

Description

6500724950 scob:n15l:yxje hypothetical protein:probable succinyl-coa:3-ketoacid-coenzyme a transferase subunit b:succinyl coa:3-oxoacid coa-transferase:oxct b (gtcfc:5.13:14.1) (keggfc:5.13) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjE yxjE Bacillus subtilis 1423 -11528808 88784 scob:n15l (ec:2.8.3.5) (de:(ec 2.8.3.5) (succinyl coa:3-oxoacid coa-transferase) (oxct b)) (db:swissprot) SCOB_BACSU P42316 BACILLUS SUBTILIS 1423 -11528808 7000686571 yxje 3-oxoadipate coa-transferase homolog yxje (cl:3-oxoadipate coa-transferase beta chain:3-oxoadipate coa-transferase beta chain homology) (db:pir2.dat) C70079 C70079 Bacillus subtilis 1423 -11528808 222855 yxje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to 3-oxoadipate coa-transferase) (le:201717) (re:202367) (di:complement) BSUB0020 Z99123 g2636433 Bacillus subtilis 1423 -11528808 301522 yxje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to 3-oxoadipate coa-transferase) (le:837) (re:1487) (di:complement) BSUB0021 Z99124 g2636444 Bacillus subtilis 1423 -11528808 6000684988 yxje (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to 3-oxoadipate coa-transferase (ec) (le:22098) (re:22748) (di:direct) D83026 D83026 g666003 Bacillus subtilis 1423 -11528808 5000688434 (de:(yxje) (pn:probable 3-oxoadipate coa-transferase subunit b:probable 3-oxoadipate coa-transferase subunit b) (gn:n15l) (gtcfc:5.13) (ec:2.8.3.6) (pcaj_bacsu) (keggfc:5.13) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxjE yxjE Bacillus subtilis 1423 10030911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736151	694	22850	660	219

Description

6500724951 scoa:n15k:yxjd hypothetical protein:probable succinyl-coa:3-ketoacid-coenzyme a transferase subunit a:succinyl coa:3-oxoacid coa-transferase:oxct a (gtcfc:5.13:14.1) (keggfc:5.13) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yxjD yxjD Bacillus subtilis 1423 -11528809 88782 scoa:n15k (ec:2.8.3.5) (de:(ec 2.8.3.5) (succinyl coa:3-oxoacid coa-transferase) (oxct a)) (db:swissprot) SCOA_BACSU P42315 BACILLUS SUBTILIS 1423 -11528809 7000686569 yxjd 3-oxoadipate coa-transferase homolog yxjd (cl:3-oxoadipate coa-transferase alpha chain:3-oxoadipate coa-transferase alpha chain homology) (db:pir2.dat) B70079 B70079 Bacillus subtilis 1423 -11528809 222854 yxjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:similar to 3-oxoadipate coa-transferase) (le:202364) (re:203080) (di:complement) BSUB0020 Z99123 g2636434 Bacillus subtilis 1423 -11528809 301521 yxjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:similar to 3-oxoadipate coa-transferase) (le:1484) (re:2200) (di:complement) BSUB0021 Z99124 g2636445 Bacillus subtilis 1423 -11528809 6000684986 yxjd (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to 3-oxoadipate coa-transferase (ec) (le:21385) (re:22101) (di:direct) D83026 D83026 g666002 Bacillus subtilis 1423 -11528809 5000688433 (de:(yxjd) (pn:probable 3-oxoadipate coa-transferase subunit a:probable 3-oxoadipate coa-transferase subunit a) (gn:n15k) (gtcfc:5.13) (ec:2.8.3.6) (pcai_bacsu) (keggfc:5.13) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yxjD yxjD Bacillus subtilis 1423 10030909

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501736215	695	22851	306	101

Description

6500724952 tryptophanyl-trna synthetase:tryptophan--trna ligase:trprs (gtcfc:10.6) (ec:6.1.1.2) (keggfc:5.14:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) trpS trpS Bacillus subtilis 1423 -11528810 100228 trps (ec:6.1.1.2) (de:(trprs)) (db:swissprot) SYW_BACSU P21656 BACILLUS SUBTILIS 1423 -11528810 125879 trps tryptophan--trna ligase::tryptophanyl-trna synthetase (cl:tryptophan--trna ligase) (ec:6.1.1.2) (db:pir1.dat) YWBS JT0481 Bacillus subtilis 1423 -11528810 217004 (sr:b.subtilis (strain qb928) dna, clone ptsq2) (db:genpept-bct1) (de:b.subtilis trps gene encoding tryptophanyl-trna synthetase,complete cds.) (nt:tryptophanyl-trna synthetase (ec 6.1.1.2)) (le:171) (re:1163) (di:direct) BACTRPSA M24068 g143786 Bacillus subtilis 1423 -11528810 7500892635 trps tryptophanyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.2) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:23195) (re:24187) (di:complement) BSUB0007 Z99110 g2633496 Bacillus subtilis 1423 -11528810 5000688438 (de:(trps) (pn:tryptophanyl-trna synthetase:tryptophan--trna ligase:trprs:tryptophanyl-trna synthetase :tryptophan-trna ligase:trprs) (gtcfc:5.14:10.06) (ec:6.1.1.2) (syw_bacsu) (keggfc:5.14:10.1:10.2) (bsorffc:4.3.1) (db:gtc-b) trpS trpS Bacillus subtilis 1423 10042082

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736228	696	22852	645	214

Description

6500724953 trpg:trpx:paba para-aminobenzoate synthase glutamine amidotransferase:subunit b / anthranilate synthase:subunit ii:para-aminobenzoate synthase glutamine amidotransferase component ii:adc synthase / anthranilate synthase component ii (gtcfc:5.15:9.12:9.6) (keggfc:5.15:9.13) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:l-amino acid metabolism-phenylalanine--tyrosine and tryptophan biosynthesis:metabolism of cofactors and vitamins-quinone biosynthesis:metabolism of cofactors and... pabA pabA Bacillus subtilis 1423 -11528811 88409 paba:trpg (ec:4.1.3.-:4.1.3.27) (de:(ec 4.1.3.27)) (db:swissprot) PABA_BACSU P28819 BACILLUS SUBTILIS 1423 -11528811 7000686073 paba:trpg para-aminobenzoate synthase:glutamine amidotransferase chain b / anthranilate synthase chain ii paba:anthranilate synthase:component ii:glutamine amidotransferase::glutamine aminotransferase (cl:glutamine amidotransferase:trpg homology) (ec:4.1.3.-:4.1.3.27:2.4.2.-) (db:pir2.dat) B37854 B37854 Bacillus subtilis 1423 -11528811 7500887587 trpg glutamine aminotransferase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:147889) (re:148473) (di:direct) BAC180K D26185 g467464 Bacillus subtilis 1423 -11528811 215064 (sr:b.subtilis (strain vb157) vegetative cell dna, clones pjs(1,2)) (db:genpept-bct1) (de:b.subtilis folic acid biosynthetic operon encodingpara-aminobenzoic acid synthase, component i (pab), glutamineamidotransferase (trpg), pot. p-aminobenzoate synth... BACRFOLA M34053 g143408 Bacillus subtilis 1423 -11528811 216579 paba anthranilate synthase subunit ii (fn:folate and tryptophan biosynthesis) (db:genpept-bct1) (ec:4.1.3.-:4.1.3.27) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: trpg, trpx; para-aminobenzoate) (le:84287) (re:84871) (di:direct) BSUB0001 Z99104 g2632342 Bacillus subtilis 1423 -11528811 141741 paba:trpg para-aminobenzoate synthase:glutamine amidotransferase chain b / anthranilate synthase chain ii paba:anthranilate synthase:component ii:glutamine amidotransferase::glutamine aminotransferase (cl:glutamine amidotransferase:trpg homology) (ec:4.1.3.-:4.1.3.27:2.4.2.-) (db:pir) B37854 B37854 Bacillus subtilis 1423 -11528811 5000688447 (de:(paba) (pn:para-aminobenzoate synthase glutamine amidotransferase component ii:adc synthase :para-aminobenzoate synthase glutamine amidotransferase component ii :adc synthase) (gn:trpg) (gtcfc:5.15:9.12) (ec:4.1.3.-) (paba_ba) pabA pabA Bacillus subtilis 1423 10030538

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736238	697	22853	1026	342

Description

6500724954 shikimate kinase:sk (gtcfc:5.15) (ec:2.7.1.71) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroI aroI Bacillus subtilis 1423 -11528812 60221 aroi (ec:2.7.1.71) (de:shikimate kinase, (sk)) (db:swissprot) AROK_BACSU P37944 BACILLUS SUBTILIS 1423 -11528812 7000684633 aroi shikimate kinase aroi (cl:shikimate kinase:shikimate kinase homology) (db:pir2.dat) I39782 I39782 Bacillus subtilis 1423 -11528812 7500877190 aroi shikimate kinase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis aroi gene for shikimate kinase, complete cds.) (le:427) (re:987) (di:direct) BACAROI1 D63474 g474964 Bacillus subtilis 1423 -11528812 215208 aroi shikimate kinase (fn:shikimate pathway) (db:genpept-bct1) (ec:2.7.1.71) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:144947) (re:145507) (di:direct) BSUB0002 Z99105 g2632601 Bacillus subtilis 1423 -11528812 222581 aroi sikimate kinase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:19250) (re:19810) (di:direct) D50453 D50453 g1805387 Bacillus subtilis 1423 -11528812 170525 aroi shikimate kinase aroi (cl:shikimate kinase:shikimate kinase homology) (db:pir) I39782 I39782 Bacillus subtilis 1423 -11528812 5000688446 (de:(aroi) (pn:shikimate kinase:sk:shikimate kinase :sk) (gtcfc:5.15) (ec:2.7.1.71) (arok_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) aroI aroI Bacillus subtilis 1423 10002947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736240	698	22854	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736287	699	22855	741	246

Description

6500724955 5-enolpyruvoylshikimate-3-phosphate synthase:putative 3-phosphoshikimate 1-carboxyvinyltransferase:5-enolpyruvylshikimate-3-phosphate synthase:epsp synthase (gtcfc:5.15) (ec:2.5.1.19) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroE aroE Bacillus subtilis 1423 -11528813 60154 aroe (ec:2.5.1.19) (de:(5-enolpyruvylshikimate-3-phosphate synthase) (epsp synthase)) (db:swissprot) AROA_BACSU P20691 BACILLUS SUBTILIS 1423 -11528813 7000684619 aroe 5-enolpyruvoylshikimate-3-phosphate synthase aroe (cl:3-phosphoshikimate 1-carboxyvinyltransferase:3-phosphoshikimate 1-carboxyvinyltransferase homology) (db:pir2.dat) C26532 C26532 Bacillus subtilis 1423 -11528813 7500877161 aroe aroe (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:16507) (re:17793) (di:direct) BACVARGNS M80245 g143816 Bacillus subtilis 1423 -11528813 217042 aroe 5-enolpyruvoylshikimate-3-phosphate synthase (fn:shikimate pathway) (db:genpept-bct1) (ec:2.5.1.19) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:171655) (re:172941) (di:complement) BSUB0012 Z99115 g2634678 Bacillus subtilis 1423 -11528813 138359 aroe 5-enolpyruvoylshikimate-3-phosphate synthase aroe (cl:3-phosphoshikimate 1-carboxyvinyltransferase:3-phosphoshikimate 1-carboxyvinyltransferase homology) (db:pir) C26532 C26532 Bacillus subtilis 1423 -11528813 5000688443 (de:(aroe) (pn:putative 3-phosphoshikimate 1-carboxyvinyltransferase:5- enolpyruvylshikimate-3-phosphate synthase:epsp synthase:putative 3-phosphoshikimate 1-carboxyvinyltransferase :5-enolpyruvylshikimate-3-phosphate synthase:epsp synt) aroE aroE Bacillus subtilis 1423 10002880

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736300	700	22856	816	272

Description

6500724956 prephenate dehydrogenase:pdh (gtcfc:5.15) (ec:1.3.1.12) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) tyrA tyrA Bacillus subtilis 1423 -11528814 7000694441 tyra prephenate dehydrogenase:tyra (cl:prephenate dehydrogenase tyra) (ec:1.3.1.12) (db:pir2.dat) B26532 B26532 Bacillus subtilis 1423 -11528814 7500965096 tyra tyra (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:15381) (re:16496) (di:direct) BACVARGNS M80245 g143815 Bacillus subtilis 1423 -11528814 217041 tyra prephenate dehydrogenase (fn:tyrosine biosynthesis) (db:genpept-bct1) (ec:1.3.1.12) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:172952) (re:174067) (di:complement) BSUB0012 Z99115 g2634679 Bacillus subtilis 1423 -11528814 170653 tyra prephenate dehydrogenase:tyra (ec:1.3.1.12) (db:pir) B26532 B26532 Bacillus subtilis 1423 -11528814

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736304	701	22857	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736381	702	22858	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736383	703	22859	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736391	704	22860	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736399	705	22861	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736413	706	22862	603	200

Description

5000688453 tryptophan synthase:alpha subunit:tryptophan synthase alpha chain (gtcfc:5.15) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) trpA trpA Bacillus subtilis 1423 -11528815 102295 trpa (ec:4.2.1.20) (de:tryptophan synthase alpha chain,) (db:swissprot) TRPA_BACSU P07601 BACILLUS SUBTILIS 1423 -11528815 7000686828 trpa tryptophan synthase:alpha chain trpa (cl:tryptophan synthase alpha chain:tryptophan synthase alpha chain homology) (ec:4.2.1.20) (db:pir2.dat) (mp:205 (degrees)) F22794 F22794 Bacillus subtilis 1423 -11528815 7500893436 (sr:b.subtilis (strain w168 and derivative strain bg2001) dna, clone) (db:genpept-bct1) (de:b.subtilis tryptophan (trp) operon, complete cds.) (nt:trpa protein) (le:5722) (re:6525) (di:direct) BACTRP K01391 g143773 Bacillus subtilis 1423 -11528815 216993 trpa trpa (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:13436) (re:14239) (di:direct) BACVARGNS M80245 g143813 Bacillus subtilis 1423 -11528815 217039 trpa tryptophan synthase alpha subunit (fn:tryptophan biosynthesis) (db:genpept-bct1) (ec:4.2.1.10) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:175209) (re:176012) (di:complement) BSUB0012 Z99115 g2634681 Bacillus subtilis 1423 -11528815 141898 trpa tryptophan synthase:alpha chain trpa (cl:tryptophan synthase alpha chain:tryptophan synthase alpha chain homology) (ec:4.2.1.20) (db:pir) (mp:205 (degrees)) F22794 F22794 Bacillus subtilis 1423 -11528815 6500724957 tryptophan synthase:alpha subunit:tryptophan synthase alpha chain (gtcfc:5.15) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) trpA trpA Bacillus subtilis 1423 -11528815

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736420	707	22863	387	129

Description

6500724958 tryptophan synthase:beta subunit:tryptophan synthase beta chain (gtcfc:5.15) (ec:4.2.1.20) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) trpB trpB Bacillus subtilis 1423 -11528816 102320 trpb (ec:4.2.1.20) (de:tryptophan synthase beta chain,) (db:swissprot) TRPB_BACSU P07600 BACILLUS SUBTILIS 1423 -11528816 7000686830 trpb tryptophan synthase:beta chain (cl:tryptophan synthase beta chain:tryptophan synthase beta chain homology) (ec:4.2.1.20) (db:pir2.dat) (mp:205 (degrees)) E22794 E22794 Bacillus subtilis 1423 -11528816 7500893446 (sr:b.subtilis (strain w168 and derivative strain bg2001) dna, clone) (db:genpept-bct1) (de:b.subtilis tryptophan (trp) operon, complete cds.) (nt:trpb protein) (le:4527) (re:5729) (di:direct) BACTRP K01391 g143772 Bacillus subtilis 1423 -11528816 216992 trpb trpb (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:12241) (re:13443) (di:direct) BACVARGNS M80245 g143812 Bacillus subtilis 1423 -11528816 217038 trpb tryptophan synthase beta subunit (fn:tryptophan biosynthesis) (db:genpept-bct1) (ec:4.2.1.20) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:176005) (re:177207) (di:complement) BSUB0012 Z99115 g2634682 Bacillus subtilis 1423 -11528816 141902 trpb tryptophan synthase:beta chain trpb (cl:tryptophan synthase beta chain:tryptophan synthase beta chain homology) (ec:4.2.1.20) (db:pir) (mp:205 (degrees)) E22794 E22794 Bacillus subtilis 1423 -11528816 5000688454 (de:(trpb) (pn:tryptophan synthase beta chain) (gtcfc:5.15) (ec:4.2.1.20) (trpb_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) trpB trpB Bacillus subtilis 1423 10044139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736427	708	22864	624	208

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736428	709	22865	1194	397

Description

6500724959 phosphoribosyl anthranilate isomerase:n-:5-phosphoribosylanthranilate isomerase:prai (gtcfc:5.15) (ec:5.3.1.24) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) trpF trpF Bacillus subtilis 1423 -11528817 102418 trpf (ec:5.3.1.24) (de:n-(5'-phosphoribosyl)anthranilate isomerase, (prai)) (db:swissprot) TRPF_BACSU P20167 BACILLUS SUBTILIS 1423 -11528817 125593 trpf phosphoribosylanthranilate isomerase (cl:phosphoribosylanthranilate isomerase:trpf homology) (ec:5.3.1.24) (db:pir1.dat) (mp:205 (degrees)) D22794 D22794 Bacillus subtilis 1423 -11528817 216991 (sr:b.subtilis (strain w168 and derivative strain bg2001) dna, clone) (db:genpept-bct1) (de:b.subtilis tryptophan (trp) operon, complete cds.) (nt:trpf protein) (le:3899) (re:4546) (di:direct) BACTRP K01391 g143771 Bacillus subtilis 1423 -11528817 217037 trpf trpf (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:11613) (re:12260) (di:direct) BACVARGNS M80245 g143811 Bacillus subtilis 1423 -11528817 7500893489 trpf phosphoribosyl anthranilate isomerase (fn:tryptophan biosynthesis) (db:genpept-bct1) (ec:5.3.1.24) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:177188) (re:177835) (di:complement) BSUB0012 Z99115 g2634683 Bacillus subtilis 1423 -11528817 5000688458 (de:(trpf) (pn:5"-phosphoribosylanthranilate isomerase:prai:n-:5"-phosphoribosylanthranilate isomerase :prai) (gtcfc:5.15) (ec:5.3.1.24) (trpf_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) trpF trpF Bacillus subtilis 1423 10044237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736439	710	22866	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736445	711	22867	552	184

Description

6500724960 indol-3-glycerol phosphate synthase:indole-3-glycerol phosphate synthase:igps (gtcfc:5.15) (ec:4.1.1.48) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) trpC trpC Bacillus subtilis 1423 -11528818 102347 trpc (ec:4.1.1.48) (de:indole-3-glycerol phosphate synthase, (igps)) (db:swissprot) TRPC_BACSU P03964 BACILLUS SUBTILIS 1423 -11528818 125590 trpc indole-3-glycerol-phosphate synthase::1-2-carboxyphenylamino -1-decarboxy-d-ribulose-5-phosphate carboxy-lyase cyclizing (cl:indole-3-glycerol-phosphate synthase:trpc homology) (ec:4.1.1.48) (db:pir1.dat) (mp:205 (degrees)) GWBS A01134 Bacillus subtilis 1423 -11528818 216990 (sr:b.subtilis (strain w168 and derivative strain bg2001) dna, clone) (db:genpept-bct1) (de:b.subtilis tryptophan (trp) operon, complete cds.) (nt:trpc protein) (le:3142) (re:3894) (di:direct) BACTRP K01391 g143770 Bacillus subtilis 1423 -11528818 7500893456 trpc indol-3-glycerol phosphate synthase (fn:tryptophan biosynthesis) (db:genpept-bct1) (ec:4.1.1.48) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:177840) (re:178592) (di:complement) BSUB0012 Z99115 g2634684 Bacillus subtilis 1423 -11528818 5000688455 (de:(trpc) (pn:indole-3-glycerol phosphate synthase:igps:indole-3-glycerol phosphate synthase :igps) (gtcfc:5.15) (ec:4.1.1.48) (trpc_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) trpC trpC Bacillus subtilis 1423 10044166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736515	712	22868	1035	345

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736528	713	22869	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736538	714	22870	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736543	715	22871	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736625	716	22872	390	129

Description

GTC ORF with score 141 to: (or:Candida tropicalis) (sr:candida tropicalis (tissue library: atcc 20336) dna) (db:genpept-pln1) (de:candida tropicalis (atcc 20336)small aleate-inducible peroxisomalprotein gene, complete cds.) (le:592) (re:975) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736627	717	22873	318	105

Description

6500724961 anthranilate phosphoribosyltransferase (gtcfc:5.15) (ec:2.4.2.18) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) trpD trpD Bacillus subtilis 1423 -11528819 102371 trpd (ec:2.4.2.18) (de:anthranilate phosphoribosyltransferase,) (db:swissprot) TRPD_BACSU P03947 BACILLUS SUBTILIS 1423 -11528819 123446 trpd anthranilate phosphoribosyltransferase (cl:anthranilate phosphoribosyltransferase:trpd homology) (ec:2.4.2.18) (db:pir1.dat) (mp:205) NPBS A00586 Bacillus subtilis 1423 -11528819 216989 (sr:b.subtilis (strain w168 and derivative strain bg2001) dna, clone) (db:genpept-bct1) (de:b.subtilis tryptophan (trp) operon, complete cds.) (nt:trpd protein) (le:2136) (re:3149) (di:direct) BACTRP K01391 g143769 Bacillus subtilis 1423 -11528819 217036 trpd trpd (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:9850) (re:10863) (di:direct) BACVARGNS M80245 g143810 Bacillus subtilis 1423 -11528819 7500893463 trpd anthranilate phosphoribosyltransferase (fn:tryptophan biosynthesis) (db:genpept-bct1) (ec:2.4.2.18) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:178585) (re:179598) (di:complement) BSUB0012 Z99115 g2634685 Bacillus subtilis 1423 -11528819 5000688456 (de:(trpd) (pn:anthranilate phosphoribosyltransferase) (gtcfc:5.15) (ec:2.4.2.18) (trpd_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) trpD trpD Bacillus subtilis 1423 10044190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736630	718	22874	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736646	719	22875	342	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736691	720	22876	192	63

Description

6500724962 anthranilate synthase:anthranilate synthase component i (gtcfc:5.15:9.12) (ec:4.1.3.27) (keggfc:5.15:9.13) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) trpE trpE Bacillus subtilis 1423 -11528820 102393 trpe (ec:4.1.3.27) (de:anthranilate synthase component i,) (db:swissprot) TRPE_BACSU P03963 BACILLUS SUBTILIS 1423 -11528820 125565 trpe anthranilate synthase:component i (cl:anthranilate synthase component i) (ec:4.1.3.27) (db:pir1.dat) (mp:205 (degrees)) NNBS1 A01119 Bacillus subtilis 1423 -11528820 216988 (sr:b.subtilis (strain w168 and derivative strain bg2001) dna, clone) (db:genpept-bct1) (de:b.subtilis tryptophan (trp) operon, complete cds.) (nt:trpe protein) (le:617) (re:2164) (di:direct) BACTRP K01391 g143768 Bacillus subtilis 1423 -11528820 217035 trpe trpe (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:8331) (re:9878) (di:direct) BACVARGNS M80245 g143809 Bacillus subtilis 1423 -11528820 7500893477 trpe anthranilate synthase (fn:tryptophan biosynthesis) (db:genpept-bct1) (ec:4.1.3.27) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:179570) (re:181117) (di:complement) BSUB0012 Z99115 g2634686 Bacillus subtilis 1423 -11528820 5000688457 (de:(trpe) (pn:anthranilate synthase component i) (gtcfc:5.15:9.12) (ec:4.1.3.27) (trpe_bacsu) (keggfc:5.15:9.13) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) trpE trpE Bacillus subtilis 1423 10044212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736692	721	22877	258	85

Description

6500724963 isozymes 1 and 2:chorismate mutase:cm (gtcfc:5.15) (ec:5.4.99.5) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroH aroH Bacillus subtilis 1423 -11528821 217034 aroh aroh (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:7732) (re:8115) (di:direct) BACVARGNS M80245 g143808 Bacillus subtilis 1423 -11528821 7500963533 aroh chorismate mutase isozymes 1 and 2 (fn:aromatic amino acids biosynthesis) (db:genpept-bct1) (ec:5.4.99.5) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:181333) (re:181716) (di:complement) BSUB0012 Z99115 g2634687 Bacillus subtilis 1423 -11528821 7000692371 aroh chorismate mutase isozymes 1 and 2 aroh (db:pir) D69590 D69590 Bacillus subtilis 1423 -11528821

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736693	722	22878	225	74

Description

6500724964 3-dehydroquinate synthase (gtcfc:5.15) (ec:4.6.1.3) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroB aroB Bacillus subtilis 1423 -11528822 60174 arob (ec:4.6.1.3) (de:3-dehydroquinate synthase,) (db:swissprot) AROB_BACSU P31102 BACILLUS SUBTILIS 1423 -11528822 7000684624 arob 3-dehydroquinate synthase arob (cl:3-dehydroquinate synthase:3-dehydroquinate synthase homology) (db:pir2.dat) G69589 G69589 Bacillus subtilis 1423 -11528822 217033 arob arob (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:6647) (re:7735) (di:direct) BACVARGNS M80245 g143807 Bacillus subtilis 1423 -11528822 7500877167 arob 3-dehydroquinate synthase (fn:shikimate pathway) (db:genpept-bct1) (ec:4.6.1.3) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:181713) (re:182801) (di:complement) BSUB0012 Z99115 g2634688 Bacillus subtilis 1423 -11528822 5000688440 (de:(arob) (pn:3-dehydroquinate synthase) (gtcfc:5.15) (ec:4.6.1.3) (arob_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) aroB aroB Bacillus subtilis 1423 10002900

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736698	723	22879	303	100

Description

6500724965 chorismate synthase:5-enolpyruvylshikimate-3-phosphate phospholyase (gtcfc:5.15) (ec:4.6.1.4) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroF aroF Bacillus subtilis 1423 -11528823 60179 arof (ec:4.6.1.4) (de:phospholyase) (vegetative protein 216) (veg216)) (db:swissprot) AROC_BACSU P31104 BACILLUS SUBTILIS 1423 -11528823 7000684626 arof chorismate synthase arof (db:pir2.dat) C69590 C69590 Bacillus subtilis 1423 -11528823 217032 arof arof (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:5479) (re:6585) (di:direct) BACVARGNS M80245 g143806 Bacillus subtilis 1423 -11528823 7500877173 arof chorismate synthase (fn:shikimate pathway) (db:genpept-bct1) (ec:4.6.1.4) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:182863) (re:183969) (di:complement) BSUB0012 Z99115 g2634689 Bacillus subtilis 1423 -11528823 5000688444 (de:(arof) (pn:chorismate synthase:chorismate synthase :5-enolpyruvylshikimate-3-phosphate phospholyase) (gtcfc:5.15) (ec:4.6.1.4) (aroc_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) aroF aroF Bacillus subtilis 1423 10002905

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736706	724	22880	459	152

Description

6500724966 3-dehydroquinate dehydratase:3-dehydroquinase (gtcfc:5.15) (ec:4.2.1.10) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroC aroC Bacillus subtilis 1423 -11528824 60190 aroc (ec:4.2.1.10) (de:3-dehydroquinate dehydratase, (3-dehydroquinase)) (db:swissprot) AROD_BACSU P35146 BACILLUS SUBTILIS 1423 -11528824 7000684628 aroc 3-dehydroquinate dehydratase:aroc (cl:3-dehydroquinate dehydratase:3-dehydroquinate dehydratase homology) (ec:4.2.1.10) (db:pir2.dat) S45563 S45563 Bacillus subtilis 1423 -11528824 7500877177 aroc dehydroquinate dehydratase (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:26136) (re:26903) (di:direct) BACDIA L09228 g410145 Bacillus subtilis 1423 -11528824 215524 aroc 3-dehydroquinate dehydratase (fn:shikimate pathway) (db:genpept-bct1) (ec:4.2.1.10) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:16680) (re:17447) (di:complement) BSUB0013 Z99116 g2634743 Bacillus subtilis 1423 -11528824 141814 aroc 3-dehydroquinate dehydratase:aroc (cl:3-dehydroquinate dehydratase:3-dehydroquinate dehydratase homology) (ec:4.2.1.10) (db:pir) S45563 S45563 Bacillus subtilis 1423 -11528824 5000688441 (de:(aroc) (pn:3-dehydroquinate dehydratase:3-dehydroquinate dehydratase :3-dehydroquinase) (gtcfc:5.15) (ec:4.2.1.10) (arod_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) aroC aroC Bacillus subtilis 1423 10002916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736707	725	22881	225	74

Description

Hypothetical protein

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501736711	726	22882	822	273

Description

6500724967 hypothetical protein:putative catabolic 3-dehydroquinate dehydratase:3-dehydroquinase (gtcfc:5.15:14.1) (ec:4.2.1.10) (keggfc:5.15) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhS yqhS Bacillus subtilis 1423 -11528825 57512 yqhs (ec:4.2.1.10) (de:dehydroquinase)) (db:swissprot) 3DHQ_BACSU P54517 BACILLUS SUBTILIS 1423 -11528825 7000684464 yqhs 3-dehydroquinate dehydratase homolog yqhs (cl:catabolic 3-dehydroquinate dehydratase) (db:pir2.dat) B69960 B69960 Bacillus subtilis 1423 -11528825 216144 yqhs (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:179404) (re:179850) (di:direct) BACJH642 D84432 g1303900 Bacillus subtilis 1423 -11528825 7500876103 yqhs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to 3-dehydroquinate dehydratase) (le:143771) (re:144217) (di:complement) BSUB0013 Z99116 g2634881 Bacillus subtilis 1423 -11528825 5000688462 (de:(yqhs) (pn:putative catabolic 3-dehydroquinate dehydratase:3-dehydroquinase) (gtcfc:5.15) (ec:4.2.1.10) (3dhq_bacsu) (keggfc:5.15) (db:gtc-bacillus subtilis)) yqhS yqhS Bacillus subtilis 1423 10000295

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501736714	727	22883	645	214

Description

6500724968 shikimate 5-dehydrogenase (gtcfc:5.15) (ec:1.1.1.25) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroD aroD Bacillus subtilis 1423 -11528826 60196 arod (ec:1.1.1.25) (de:shikimate 5-dehydrogenase,) (db:swissprot) AROE_BACSU P54374 BACILLUS SUBTILIS 1423 -11528826 7000684630 arod shikimate 5-dehydrogenase arod (cl:shikimate dehydrogenase:shikimate dehydrogenase homology) (db:pir2.dat) A69590 A69590 Bacillus subtilis 1423 -11528826 216033 arod (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:74142) (re:74984) (di:direct) BACJH642 D84432 g1303789 Bacillus subtilis 1423 -11528826 7500877180 arod shikimate 5-dehydrogenase (fn:shikimate pathway) (db:genpept-bct1) (ec:1.1.1.25) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:44446) (re:45288) (di:complement) BSUB0014 Z99117 g2635012 Bacillus subtilis 1423 -11528826 5000688442 (de:(arod) (pn:shikimate 5-dehydrogenase) (gtcfc:5.15) (ec:1.1.1.25) (aroe_bacsu) (keggfc:5.15) (db:gtc-bacillus subtilis)) aroD aroD Bacillus subtilis 1423 10002922

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736718	728	22884	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736729	729	22885	537	178

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736805	730	22886	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736806	731	22887	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736813	732	22888	285	94

Description

6500724969 quinolinate synthetase (gtcfc:5.15:9.12) (ec:4.6.1.3) (keggfc:5.15) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) nadA nadA Bacillus subtilis 1423 -11528827 7000694487 nada quinolinate synthetase nada (cl:helicobacter pylori quinolinate synthetase a) (db:pir2.dat) E69663 E69663 Bacillus subtilis 1423 -11528827 7500965126 nada quinolinate synthetase (fn:quinolinate biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:50085) (re:51191) (di:complement) BSUB0015 Z99118 g2635250 Bacillus subtilis 1423 -11528827

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736816	733	22889	477	158

Description

6500724970 prephenate dehydratase:pdt (gtcfc:5.15) (ec:4.2.1.51) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) pheA pheA Bacillus subtilis 1423 -11528828 89520 phea (ec:4.2.1.51) (de:prephenate dehydratase, (pdt)) (db:swissprot) PHEA_BACSU P21203 BACILLUS SUBTILIS 1423 -11528828 125676 phea prephenate dehydratase (cl:prephenate dehydratase:prephenate dehydratase homology) (ec:4.2.1.51) (db:pir1.dat) C32804 C32804 Bacillus subtilis 1423 -11528828 215818 phea prephenate dehydratase (fn:phenylalanine biosynthesis) (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtillis sporulation protein (spoob), gtp-binding protein(obg), phenylalanine biosynthesis associated protein (pheb), andmonofunctional prephenate dehydratase (p... BACGTPBP M24537 g508981 Bacillus subtilis 1423 -11528828 7500888015 phea prephenate dehydratase (fn:phenylalanine biosynthesis) (db:genpept-bct1) (ec:4.2.1.51) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:55414) (re:56271) (di:complement) BSUB0015 Z99118 g2635255 Bacillus subtilis 1423 -11528828 5000688449 (de:(phea) (pn:prephenate dehydratase:pdt:prephenate dehydratase :pdt) (gtcfc:5.15) (ec:4.2.1.51) (phea_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) pheA pheA Bacillus subtilis 1423 10031642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736817	734	22890	234	77

Description

GTC ORF with score 288 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f55a12.) (nt:strong similarity to c. elegans unc-101 and other) (le:3614:3758:3927) (re:3712:3882:4027) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736822	735	22891	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736845	736	22892	729	242

Description

6500724971 chorismate mutase:possible chorismate mutase:cm (gtcfc:5.15) (ec:5.4.99.5) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) pheB pheB Bacillus subtilis 1423 -11528829 89540 pheb (ec:5.4.99.5) (de:possible chorismate mutase, (cm)) (db:swissprot) PHEB_BACSU P21204 BACILLUS SUBTILIS 1423 -11528829 7000686131 pheb chorismate mutase:pheb:phenyalanine biosynthesis protein pheb (ec:5.4.99.5) (db:pir2.dat) D32804 D32804 Bacillus subtilis 1423 -11528829 7500888018 pheb (fn:phenylalanine biosynthesis) (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtillis sporulation protein (spoob), gtp-binding protein(obg), phenylalanine biosynthesis associated protein (pheb), andmonofunctional prephenate dehydratase (p... BACGTPBP M24537 g508980 Bacillus subtilis 1423 -11528829 215817 pheb chorismate mutase (fn:phenylalanine biosynthesis) (db:genpept-bct1) (ec:5.4.99.5) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:56288) (re:56731) (di:complement) BSUB0015 Z99118 g2635256 Bacillus subtilis 1423 -11528829 170435 pheb chorismate mutase:pheb:phenyalanine biosynthesis protein pheb (ec:5.4.99.5) (db:pir) D32804 D32804 Bacillus subtilis 1423 -11528829 5000688450 (de:(pheb) (pn:possible chorismate mutase:cm:possible chorismate mutase :cm) (gtcfc:5.15) (ec:5.4.99.5) (pheb_bacsu) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis)) pheB pheB Bacillus subtilis 1423 10031662

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736847	737	22893	765	255

Description

6500724972 phenylalanyl-trna synthetase:beta subunit:phenylalanyl-trna synthetase beta chain:phenylalanine--trna ligase beta chain:phers (gtcfc:10.6) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) pheT pheT Bacillus subtilis 1423 -11528830 7500892390 phet (ec:6.1.1.20) (de:trna ligase beta chain) (phers)) (db:swissprot) SYFB_BACSU P17922 BACILLUS SUBTILIS 1423 -11528830 7000694392 phet phenylalanine--trna ligase:beta chain:phenylalanyl-trna synthetase beta chain (cl:phenylalanine--trna ligase beta chain) (ec:6.1.1.20) (db:pir1.dat) YFBSB A69676 Bacillus subtilis 1423 -11528830 304180 phet phenylalanyl-trna synthetase beta subunit (db:genpept-bct1) (ec:6.1.1.20) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:130980) (re:133394) (di:complement) BSUB0015 Z99118 g2635328 Bacillus subtilis 1423 -11528830 220307 phet phenylalanyl-trna synthetase beta subunit (db:genpept-bct1) (ec:6.1.1.20) (de:b.subtilis genomic sequence 89009bp.) (nt:phenylalanyl-trna synthetase beta subunit) (le:36513) (re:38927) (di:direct) BSZ75208 Z75208 g1770031 Bacillus subtilis 1423 -11528830

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736848	738	22894	342	114

Description

6500724973 phenylalanyl-trna synthetase:alpha subunit:phenylalanyl-trna synthetase alpha chain:phenylalanine--trna ligase alpha chain:phers (gtcfc:10.6) (ec:6.1.1.20) (keggfc:5.15:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) pheS pheS Bacillus subtilis 1423 -11528831 100027 phes (ec:6.1.1.20) (de:-trna ligase alpha chain) (phers)) (db:swissprot) SYFA_BACSU P17921 BACILLUS SUBTILIS 1423 -11528831 7000686709 phes phenylalanine--trna ligase:alpha chain:phenylalanyl-trna synthetase alpha chain (cl:phenylalanine--trna ligase alpha chain) (ec:6.1.1.20) (db:pir1.dat) YFBSA H69675 Bacillus subtilis 1423 -11528831 220306 phes phenylalanyl-trna synthetase alpha subunit (db:genpept-bct1) (ec:6.1.1.20) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:133410) (re:134444) (di:complement) BSUB0015 Z99118 g2635329 Bacillus subtilis 1423 -11528831 304179 phes phenylalany-trna synthetase beta subunit (db:genpept-bct1) (ec:6.1.1.20) (de:b.subtilis genomic sequence 89009bp.) (nt:phenylalanyl-trna synthetase beta subunit) (le:35463) (re:36497) (di:direct) BSZ75208 Z75208 g1770030 Bacillus subtilis 1423 -11528831 5000688451 (de:(phes) (pn:phenylalanyl-trna synthetase alpha chain:phenylalanine--trna ligase alpha chain:phers:phenylalanyl-trna synthetase alpha chain :phenylalanine- trna ligase alpha chain:phers) (gtcfc:5.15:10.06) (ec:6.1.1.20) (syfa_b) pheS pheS Bacillus subtilis 1423 10117989

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736850	739	22895	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736897	740	22896	510	170

Description

6500724974 tyrosyl-trna synthetase:tyrosyl-trna synthetase 1:tyrosine--trna ligase:tyrrs (gtcfc:10.6) (ec:6.1.1.1) (keggfc:5.15:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) tyrS tyrS Bacillus subtilis 1423 -11528832 100237 tyrs (ec:6.1.1.1) (de:(tyrrs 1)) (db:swissprot) SYY1_BACSU P22326 BACILLUS SUBTILIS 1423 -11528832 125874 tyrs tyrosine--trna ligase:tyrs:major:tyrosyl-trna synthetase tyrs (cl:tyrosine--trna ligase) (ec:6.1.1.1) (db:pir1.dat) A42648 A42648 Bacillus subtilis 1423 -11528832 217009 tyrs tyrosine trna synthetase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:141251) (re:142519) (di:direct) AF008220 AF008220 g2293225 Bacillus subtilis 1423 -11528832 4000707358 tyrs transfer rna-tyr synthetase (sr:bacillus subtilis (individual_isolate br151) dna) (db:genpept-bct1) (de:bacillus subtilis tyrosine-transfer rna synthetase (tyrs) gene,complete cds.) (le:441) (re:1709) (di:direct) BACTYRSBR1 M77668 g143795 Bacillus subtilis 1423 -11528832 7500892647 tyrs tyrosyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:37908) (re:39176) (di:complement) BSUB0016 Z99119 g2635451 Bacillus subtilis 1423 -11528832 5000688460 (de:(tyrs) (pn:tyrosyl-trna synthetase 1:tyrosine--trna ligase:tyrrs:tyrosyl-trna synthetase 1 :tyrosine-trna ligase:tyrrs) (gtcfc:5.15:10.06) (ec:6.1.1.1) (syy1_bacsu) (keggfc:5.15:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus s) tyrS tyrS Bacillus subtilis 1423 10042091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736898	741	22897	495	165

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736902	742	22898	612	203

Description

GTC ORF with score 109 to: (or:Zea mays) (fn:post-transcriptional control of chloroplast) (db:genpept-pln2) (de:zea mays crp1 (crp1) mrna, nuclear gene encoding chloroplastprotein, crp1-hcf111 allele, complete cds.) (le:119) (re:2125) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736909	743	22899	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736927	744	22900	477	158

Description

6500724975 arog:aroa 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase / chorismate mutase-isozyme 3:phospho-2-dehydro-3-deoxyheptonate aldolase:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabino-heptulosonate 7-phosphate synthase / chorismate mutase (gtcfc:5.15) (keggfc:5.15) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) aroA aroA Bacillus subtilis 1423 -11528833 4000706913 aroa (ec:4.1.2.15:5.4.99.5) (de:heptulosonate 7-phosphate synthase) / chorismate mutase,) (db:swissprot) AROG_BACSU P39912 BACILLUS SUBTILIS 1423 -11528833 206270 aroa 2-dehydro-3-deoxyphosphoheptonate aldolase::3-deoxy-d-arabino-heptulosonate 7-phosphate synthase / chorism aroa:phospho-2-dehydro-3-deoxyheptonate aldolase (cl:2-dehydro-3-deoxyphosphoheptonate aldolase) (ec:4.1.2.15) (db:pir2.dat) S21418 S21418 Bacillus subtilis 1423 -11528833 219012 aroa daph synthase-chorismate mutase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:132601) (re:133677) (di:direct) AF008220 AF008220 g2293220 Bacillus subtilis 1423 -11528833 7500877185 aroa-arog chorismate mutase (db:genpept-bct1) (ec:4.1.2.15:5.4.99.5) (de:b.subtilis aroa-arog gene.) (nt:phospho-2-dehydro-3-deoxyheptonate aldolase) (le:667) (re:1743) (di:direct) BSAROAG X65945 g39813 Bacillus subtilis 1423 -11528833 5000688439 aroa chorismate mutase-isozyme 3 (fn:shikimate pathway) (db:genpept-bct1) (ec:4.1.2.15:5.4.99.5) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: arog;) (le:46749) (re:47825) (di:complement) BSUB0016 Z99119 g2635459 Bacillus subtilis 1423 -11528833 60213 aroa (ec:4.1.2.15:5.4.99.5) (de:heptulosonate 7-phosphate synthase) / chorismate mutase,) (db:swissprot) AROG_BACSU P39912 BACILLUS SUBTILIS 1423 -11528833 7000684632 aroa 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase / chorism aroa (db:pir) F69589 F69589 Bacillus subtilis 1423 -11528833

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736975	745	22901	492	163

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736993	746	22902	549	182

Description

GTC ORF with score 119 to: (sr:aspergillus parasiticus (strain su-1) (library: atcc 56775) dna) (db:genpept-pln1) (de:aspergillus parasticus (aflr) gene, complete cds.) (nt:zinc finger domain basepairs 501-585) (le:418) (re:1551) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736994	747	22903	495	165

Description

6500724976 ipa-9r:tyrs1:tyrt:tyrr:tyrz tyrosyl-trna synthetase:tyrosyl-trna synthetase 2:tyrosine--trna ligase:tyrrs (gtcfc:10.6) (ec:6.1.1.1) (keggfc:5.15:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) tyrZ tyrZ Bacillus subtilis 1423 -11528834 7000689201 tyrz tyrosine--trna ligase:tyrz:tyrosyl-trna synthetase minor tyrz (cl:tyrosine--trna ligase) (ec:6.1.1.1) (db:pir2.dat) S16426 S16426 Bacillus subtilis 1423 -11528834 7500954471 ipa-9r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:9166) (re:10407) (di:complement) BSGENR X73124 g413933 Bacillus subtilis 1423 -11528834 219246 tyrz tyrosyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-9r, tyrs1, tyrt) (le:147552) (re:148793) (di:direct) BSUB0020 Z99123 g2636381 Bacillus subtilis 1423 -11528834 170654 tyrz tyrosine--trna ligase:tyrz:tyrosyl-trna synthetase minor tyrz (cl:tyrosine--trna ligase) (ec:6.1.1.1) (db:pir) S16426 S16426 Bacillus subtilis 1423 -11528834

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501736995	748	22904	306	101

Description

6500724977 aroj:hish:hisc histidinol-phosphate aminotransferase / tyrosine/phenylalanine aminotransferase:histidinol-phosphate aminotransferase:imidazole acetol-phosphate transaminase (gtcfc:5.15) (ec:2.6.1.9) (keggfc:14.1) (bsorffc:3.1.4) (db:gtc-bacillus subtilis) hisC hisC Bacillus subtilis 1423 -11528835 7500883313 hisc:hish (ec:2.6.1.9) (de:phosphate transaminase)) (db:swissprot) HIS8_BACSU P17731 BACILLUS SUBTILIS 1423 -11528835 170036 hisc:hish histidinol-phosphate transaminase:tyrosine and phenylalanine aminotransferase hisc:histidinol-phosphate aminotransferase (cl:probable histidinol-phosphate transaminase) (ec:2.6.1.9) (db:pir2.dat) (mp:205 (degrees)) A26532 A26532 Bacillus subtilis 1423 -11528835 217040 hish hish (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:14250) (re:15332) (di:direct) BACVARGNS M80245 g143814 Bacillus subtilis 1423 -11528835 7500883314 hisc tyrosine/phenylalanine aminotransferase (fn:histidine biosynthesis) (db:genpept-bct1) (ec:2.6.1.9:2.6.1.5) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: aroj; histidinol-phosphate) (le:174116) (re:175198) (di:complement) BSUB0012 Z99115 g2634680 Bacillus subtilis 1423 -11528835 7000693098 hisc:hish histidinol-phosphate transaminase:tyrosine and phenylalanine aminotransferase hisc:histidinol-phosphate aminotransferase (ec:2.6.1.9) (db:pir) (mp:205 (degrees)) A26532 A26532 Bacillus subtilis 1423 -11528835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737034	749	22905	339	112

Description

6500724978 cobalamin-independent methionine synthase (gtcfc:5.16:5.4) (ec:2.1.1.14) (keggfc:5.4) (bsorffc:3.1.7) (db:gtc-bacillus subtilis) metC metC Bacillus subtilis 1423 -11528836 7000692379 metc cobalamin-independent methionine synthase metc (cl:cobalamin-independent methionine synthase) (db:pir2.dat) C69657 C69657 Bacillus subtilis 1423 -11528836 6000689774 metc metc (fn:involved in methionine metabolism) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:35445) (re:37733) (di:complement) BSAJ2571 AJ002571 g2632038 Bacillus subtilis 1423 -11528836 7500963541 metc cobalamin-independent methionine synthase (fn:methionine biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:188394) (re:190682) (di:complement) BSUB0007 Z99110 g2633672 Bacillus subtilis 1423 -11528836

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737048	750	22906	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737051	751	22907	285	94

Description

GTC ORF with score 129 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f319; 100 pct identical amino acid sequence and) (le:7415) (re:8374) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737054	752	22908	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737115	753	22909	408	136

Description

6500724979 bmr2d:bmtd:bltd spermine/spermidine acetyltransferase:transacetylase bltd (gtcfc:5.16:5.4) (ec:2.3.1.-) (keggfc:14.1) (bsorffc:3.1.7) (db:gtc-bacillus subtilis) bltD bltD Bacillus subtilis 1423 -11528837 7000694601 bltd spermine/spermidine acetyltransferase bltd (db:pir2.dat) B69595 B69595 Bacillus subtilis 1423 -11528837 215942 bltd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:811) (re:1269) (di:complement) BACJH642 D84432 g1303698 Bacillus subtilis 1423 -11528837 7500965198 bltd spermine/spermidine acetyltransferase (db:genpept-bct1) (ec:2.3.1.-) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: bmr2d, bmtd) (le:118163) (re:118621) (di:direct) BSUB0014 Z99117 g2635105 Bacillus subtilis 1423 -11528837

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737117	754	22910	633	210

Description

6500724980 mete:metk s-adenosylmethionine synthetase:methionine adenosyltransferase:adomet synthetase (gtcfc:5.16:5.4:6.4) (ec:2.5.1.6) (keggfc:5.4:6.4) (bsorffc:3.1.7) (db:gtc-bacillus subtilis) metK metK Bacillus subtilis 1423 -11528838 7502851552 metk:mete (ec:2.5.1.6) (de:adenosyltransferase) (adomet synthetase)) (db:swissprot) METK_BACSU P54419 BACILLUS SUBTILIS 1423 -11528838 7000694569 metk methionine adenosyltransferase (cl:methionine adenosyltransferase) (ec:2.5.1.6) (db:pir2.dat) D69657 D69657 Bacillus subtilis 1423 -11528838 4000714149 mete sam synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:50089) (re:51291) (di:direct) AF008220 AF008220 g2293164 Bacillus subtilis 1423 -11528838 7500954033 metk s-adenosylmethionine synthetase (db:genpept-bct1) (ec:2.5.1.6) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: mete) (le:129136) (re:130338) (di:complement) BSUB0016 Z99119 g2635539 Bacillus subtilis 1423 -11528838

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737122	755	22911	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737127	756	22912	786	261

Description

6500724981 alr:dal d-alanine racemase:alanine racemase (gtcfc:5.2:6.1:6.15) (ec:5.1.1.1) (keggfc:5.2:6.8) (bsorffc:3.2.5) (db:gtc-bacillus subtilis) dal dal Bacillus subtilis 1423 -11528839 7502851553 alr:dal (ec:5.1.1.1) (de:alanine racemase,) (db:swissprot) ALR_BACSU P10725 BACILLUS SUBTILIS 1423 -11528839 302719 alr alanine racemase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (ec:5.1.1.1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:50435) (re:51604) (di:direct) AB001488 AB001488 g1881274 Bacillus subtilis 1423 -11528839 7500954422 dal d-alanine racemase (db:genpept-bct1) (ec:5.1.1.1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: alr) (le:114179) (re:115348) (di:direct) BSUB0003 Z99106 g2632764 Bacillus subtilis 1423 -11528839 7000692903 dal d-alanine racemase dal (cl:alanine racemase) (db:pir) G69612 G69612 Bacillus subtilis 1423 -11528839

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737132	757	22913	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737135	758	22914	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737139	759	22915	294	97

Description

6500724982 hypothetical protein:similar to alanine racemase (gtcfc:5.2:6.15:14.1) (ec:5.1.1.1) (keggfc:5.2:6.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yncD yncD Bacillus subtilis 1423 -11528840 7502851554 yncd (ec:5.1.1.1) (de:putative alanine racemase,) (db:swissprot) ALR2_BACSU P94494 BACILLUS SUBTILIS 1423 -11528840 7000692162 yncd alanine racemase homolog yncd (cl:alanine racemase) (db:pir2.dat) F69888 F69888 Bacillus subtilis 1423 -11528840 220182 yncd yncd (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750128 Bacillus subtilis 1423 -11528840 7500963386 yncd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to alanine racemase) (le:115995) (re:117179) (di:complement) BSUB0010 Z99113 g2634148 Bacillus subtilis 1423 -11528840

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737140	760	22916	423	140

Description

GTC ORF with score 204 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c3h5.) (nt:spac3h5.11, len:393aa, similarity: some to a region) (le:30078:30336:31054:31279) (re:30282:31003:31205:31435) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737153	761	22917	570	189

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737157	762	22918	564	187

Description

6500724983 asparaginyl-trna synthetase:asparagine--trna ligase:asnrs (gtcfc:10.6) (ec:6.1.1.22) (keggfc:5.2:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) asnS asnS Bacillus subtilis 1423 -11528841 100133 asns (ec:6.1.1.22) (de:(asnrs)) (db:swissprot) SYN_BACSU P39772 BACILLUS SUBTILIS 1423 -11528841 7000686725 asns asparagine--trna ligase:asns:asparaginyl-trna synthetase asns (cl:lysine--trna ligase) (ec:6.1.1.22) (db:pir2.dat) B69591 B69591 Bacillus subtilis 1423 -11528841 217169 asns asparaginyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.22) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:41.1% of id... BACYPIA L47709 g1146247 Bacillus subtilis 1423 -11528841 7500892534 asns asparaginyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.22) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:149926) (re:151218) (di:complement) BSUB0012 Z99115 g2634654 Bacillus subtilis 1423 -11528841 5000688623 (de:(asns) (pn:asparaginyl-trna synthetase:asparagine--trna ligase:asnrs:asparaginyl-trna synthetase :asparagine-trna ligase:asnrs:fragment) (gtcfc:10.06) (ec:6.1.1.22) (syn_bacsu) (keggfc:5.2:10.1:10.2) (bsorffc:4.3.1) (db:gtc) asnS asnS Bacillus subtilis 1423 10041987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737245	763	22919	597	198

Description

6500724984 aspartate 1-decarboxylase:aspartate 1-decarboxylase precursor:aspartate alpha-decarboxylase (gtcfc:5.2:6.1:9.5) (ec:4.1.1.11) (keggfc:5.2:6.1) (bsorffc:3.4.9) (db:gtc-bacillus subtilis) panD panD Bacillus subtilis 1423 -11528842 88578 pand (ec:4.1.1.11) (de:decarboxylase)) (db:swissprot) PAND_BACSU P52999 BACILLUS SUBTILIS 1423 -11528842 7000686082 pand aspartate 1-decarboxylase pand (cl:aspartate 1-decarboxylase) (db:pir2.dat) A69672 A69672 Bacillus subtilis 1423 -11528842 217164 pand aspartate 1-decarboxylase (fn:pantothenic acid biosynthesis) (db:genpept-bct1) (ec:4.1.1.11) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc ge... BACYPIA L47709 g1146242 Bacillus subtilis 1423 -11528842 7500887648 pand aspartate 1-decarboxylase (fn:pantothenate biosynthesis) (db:genpept-bct1) (ec:4.1.1.11) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:156294) (re:156677) (di:complement) BSUB0012 Z99115 g2634659 Bacillus subtilis 1423 -11528842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737251	764	22920	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737263	765	22921	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737265	766	22922	810	270

Description

6500724985 alanyl-trna synthetase (gtcfc:10.6) (ec:6.1.1.7) (keggfc:5.2:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) alaS alaS Bacillus subtilis 1423 -11528843 7500892312 alas (ec:6.1.1.7) (de:alanyl-trna synthetase, (alanine--trna ligase) (alars)) (db:swissprot) SYA_BACSU O34526 BACILLUS SUBTILIS 1423 -11528843 7000692163 alas alanine--trna ligase:alas:alanyl-trna synthetase (cl:alanine--trna ligase) (ec:6.1.1.7) (db:pir2.dat) A69584 A69584 Bacillus subtilis 1423 -11528843 7500892314 alas alanyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.7) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:197994) (re:200630) (di:complement) BSUB0014 Z99117 g2635186 Bacillus subtilis 1423 -11528843 6000691241 alas alanyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.7) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:2314) (re:4950) (di:complement) BSUB0015 Z99118 g2635204 Bacillus subtilis 1423 -11528843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737266	767	22923	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737271	768	22924	654	217

Description

6500724986 aspartyl-trna synthetase (gtcfc:10.6) (ec:6.1.1.12) (keggfc:5.2:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) aspS aspS Bacillus subtilis 1423 -11528844 7500892349 asps (ec:6.1.1.12) (de:(asprs)) (db:swissprot) SYD_BACSU O32038 BACILLUS SUBTILIS 1423 -11528844 7000692242 asps aspartate--trna ligase:asps:aspartyl-trna synthetase (cl:lysine--trna ligase) (ec:6.1.1.12) (db:pir2.dat) D69591 D69591 Bacillus subtilis 1423 -11528844 7500892351 asps aspartyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.12) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:18878) (re:20656) (di:complement) BSUB0015 Z99118 g2635219 Bacillus subtilis 1423 -11528844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737272	769	22925	564	187

Description

6500724987 l-aspartate oxidase:quinolinate synthetase b (gtcfc:5.2:9.3:9.4) (ec:1.4.3.16) (keggfc:5.2:9.4) (bsorffc:3.4.2) (db:gtc-bacillus subtilis) (gtcfc:l-amino acid metabolism-alanine and aspartate metabolism:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6):metabolism of cofactor... nadB nadB Bacillus subtilis 1423 -11528845 85137 nadb (ec:1.4.3.16) (de:l-aspartate oxidase, (quinolinate synthetase b)) (db:swissprot) NADB_BACSU P38032 BACILLUS SUBTILIS 1423 -11528845 7000685904 nadb l-aspartate oxidase:nadb:nadb:quinolinate synthetase b (cl:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology) (ec:1.4.3.16) (db:pir2.dat) C47071 C47071 Bacillus subtilis 1423 -11528845 7500886229 nadb l-aspartate oxidase (fn:required for nad biosynthesis) (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis l-aspartate oxidase (nadb) and nifs genes,complete cds.) (le:1833) (re:3428) (di:direct) BACNADB M98822 g547611 Bacillus subtilis 1423 -11528845 216378 nadb l-aspartate oxidase (fn:required for nad biosynthesis (quinolinate) (db:genpept-bct1) (ec:1.4.3.16) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:52001) (re:53596) (di:complement) BSUB0015 Z99118 g2635252 Bacillus subtilis 1423 -11528845 170307 nadb l-aspartate oxidase:nadb:nadb:quinolinate synthetase b (cl:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology) (ec:1.4.3.16) (db:pir) C47071 C47071 Bacillus subtilis 1423 -11528845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737352	770	22926	645	214

Description

6500724988 aspartate-semialdehyde dehydrogenase:asa dehydrogenase (gtcfc:5.2:5.3:5.8) (ec:1.2.1.11) (keggfc:5.3:5.8) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) asd asd Bacillus subtilis 1423 -11528846 68414 asd (ec:1.2.1.11) (de:dehydrogenase)) (db:swissprot) DHAS_BACSU Q04797 BACILLUS SUBTILIS 1423 -11528846 7000685033 asd aspartate-semialdehyde dehydrogenase (cl:aspartate-semialdehyde dehydrogenase) (ec:1.2.1.11) (db:pir1.dat) F69590 F69590 Bacillus subtilis 1423 -11528846 215479 asd aspartate semialdehyde dehydrogenase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (ec:1.2.1.11) (de:bacillus subtilis protease, 3' end, dipicolinate synthase subunitsa and b (spovfa and spovfb), aspartate semialdehyde dehydrogenase(asd), aspartokinase i (dapg), dihydrodipico... BACDAP L08471 g142828 Bacillus subtilis 1423 -11528846 7500880235 asd aspartate-semialdehyde dehydrogenase (db:genpept-bct1) (ec:1.2.1.11) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:146962) (re:148002) (di:direct) BSUB0009 Z99112 g2634047 Bacillus subtilis 1423 -11528846

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737361	771	22927	651	216

Description

6500724989 lssd:dapg aspartokinase i:alpha and beta subunits:aspartokinase 1 alpha and beta subunits:aspartate kinase 1 (gtcfc:5.2:5.3:5.8) (ec:2.7.2.4) (keggfc:5.3:5.8) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) dapG dapG Bacillus subtilis 1423 -11528847 7500963438 dapg aspartokinase i alpha and beta subunits (db:genpept-bct1) (ec:2.7.2.4) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: lssd) (le:148094) (re:149308) (di:direct) BSUB0009 Z99112 g2634048 Bacillus subtilis 1423 -11528847 7000692240 dapg aspartokinase i alpha and beta subunits dapg (db:pir) B69613 B69613 Bacillus subtilis 1423 -11528847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737374	772	22928	606	201

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737439	773	22929	489	162

Description

6500724990 dihydrodipicolinate synthase:dhdps (gtcfc:5.2:5.8) (ec:4.2.1.52) (keggfc:5.8) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) dapA dapA Bacillus subtilis 1423 -11528848 67863 dapa (ec:4.2.1.52) (de:protein 81) (veg81)) (db:swissprot) DAPA_BACSU Q04796 BACILLUS SUBTILIS 1423 -11528848 7000684979 dapa dihydrodipicolinate synthase:dapa (cl:dihydrodipicolinate synthase) (ec:4.2.1.52) (db:pir2.dat) E46665 E46665 Bacillus subtilis 1423 -11528848 7500879989 dapa::gene dihydrodipicolinate synthase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (ec:4.2.1.52) (de:bacillus subtilis protease, 3' end, dipicolinate synthase subunitsa and b (spovfa and spovfb), aspartate semialdehyde dehydrogenase(asd), aspartokinase i (dapg), dihydrodipico... BACDAP L08471 g142830 Bacillus subtilis 1423 -11528848 215481 dapa dihydrodipicolinate synthase (fn:diaminopimelate/lysine biosynthesis) (db:genpept-bct1) (ec:4.2.1.52) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:149339) (re:150211) (di:direct) BSUB0009 Z99112 g2634049 Bacillus subtilis 1423 -11528848 169961 dapa dihydrodipicolinate synthase:dapa (ec:4.2.1.52) (db:pir) E46665 E46665 Bacillus subtilis 1423 -11528848

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737441	774	22930	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737442	775	22931	336	111

Description

6500724991 dihydrodipicolinate reductase (gtcfc:5.2:5.8) (ec:1.3.1.26) (keggfc:5.8) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) dapB dapB Bacillus subtilis 1423 -11528849 67870 dapb (ec:1.3.1.26) (de:dihydrodipicolinate reductase,) (db:swissprot) DAPB_BACSU P42976 BACILLUS SUBTILIS 1423 -11528849 7000684981 dapb dihydrodipicolinate reductase dapb (cl:dihydrodipicolinate reductase) (db:pir2.dat) A69613 A69613 Bacillus subtilis 1423 -11528849 217156 dapb dihydrodipicolinate reductase (fn:lysine biosynthesis) (db:genpept-bct1) (ec:1.3.1.26) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, comple... BACYPIA L47709 g1146234 Bacillus subtilis 1423 -11528849 7500879993 dapb dihydrodipicolinate reductase (fn:diaminopimelate/lysine biosynthesis) (db:genpept-bct1) (ec:1.3.1.26) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:163041) (re:163844) (di:complement) BSUB0012 Z99115 g2634667 Bacillus subtilis 1423 -11528849

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737443	776	22932	207	68

Description

5000688405 yxan:s14nr:ve7ar:asnh asparagine synthetase:glutamine-hydrolyzing:putative asparagine synthetase:glutamine-hydrolyzing (gtcfc:5.2) (ec:6.3.5.4) (keggfc:14.1) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) asnH asnH Bacillus subtilis 1423 -11528850 60374 asnh:s14nr:ve7ar (ec:6.3.5.4) (de:asparagine synthetase (glutamine-hydrolyzing),) (db:swissprot) ASNH_BACSU P42113 BACILLUS SUBTILIS 1423 -11528850 7000684645 asnh asparagine synthetase asnh (db:pir2.dat) A69591 A69591 Bacillus subtilis 1423 -11528850 215743 asnh probable asparagine synthetase (fn:glutamine-hydrolyzing) (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (ec:6.3.5.4) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:conserved universally; see swiss_prot acc#: p42113) (le:17911) (re:2... AB005554 AB005554 g904192 Bacillus subtilis 1423 -11528850 7500877253 asnh asparagine synthetase glutamine-hydrolyzing (db:genpept-bct1) (ec:6.3.5.4) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxan) (le:98439) (re:100682) (di:direct) BSUB0021 Z99124 g2636538 Bacillus subtilis 1423 -11528850 6500724992 yxan:s14nr:ve7ar asparagine synthetase:glutamine-hydrolyzing:putative asparagine synthetase:glutamine-hydrolyzing (gtcfc:5.2) (ec:6.3.5.4) (keggfc:14.1) (bsorffc:3.1.2) (db:gtc-bacillus subtilis) asnH asnH Bacillus subtilis 1423 -11528850

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737444	777	22933	489	162

Description

6500724993 leuc:leub 3-isopropylmalate dehydrogenase:beta-ipm dehydrogenase:imdh:3-ipm-dh (gtcfc:5.2:5.7) (ec:1.1.1.85) (keggfc:5.7) (bsorffc:3.1.5) (db:gtc-bacillus subtilis) leuB leuB Bacillus subtilis 1423 -11528851 220346 leub 3-isopropylmalate dehydrogenase (fn:leucine biosynthesis) (db:genpept-bct1) (ec:1.1.1.85) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: leuc) (le:94990) (re:96087) (di:complement) BSUB0015 Z99118 g2635292 Bacillus subtilis 1423 -11528851 304219 leub 3-isopropylmalate dehydrogenase (db:genpept-bct1) (ec:1.1.1.85) (de:b.subtilis genomic sequence 89009bp.) (nt:3-isopropylmalate dehydrogenase; formerly leuc) (le:73820) (re:74917) (di:direct) BSZ75208 Z75208 g1770070 Bacillus subtilis 1423 -11528851 7000692050 leub 3-isopropylmalate dehydrogenase:leub (cl:3-isopropylmalate dehydrogenase) (ec:1.1.1.85) (db:pir) A69650 A69650 Bacillus subtilis 1423 -11528851

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737445	778	22934	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737449	779	22935	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737451	780	22936	696	232

Description

GTC ORF with score 219 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:o309; 58 pct identical to 290 residues of the 319) (le:7062) (re:7991) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737459	781	22937	828	276

Description

6500724994 seryl-trna synthetase:serine--trna ligase:serrs (gtcfc:10.6) (ec:6.1.1.11) (keggfc:5.3:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) serS serS Bacillus subtilis 1423 -11528852 100173 sers (ec:6.1.1.11) (de:seryl-trna synthetase, (serine--trna ligase) (serrs)) (db:swissprot) SYS_BACSU P37464 BACILLUS SUBTILIS 1423 -11528852 7000686730 sers serine--trna ligase::seryl-trna synthetase (cl:serine--trna ligase) (ec:6.1.1.11) (db:pir2.dat) S66043 S66043 Bacillus subtilis 1423 -11528852 7500892576 sers seryl-trna synthetase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:84480) (re:85757) (di:direct) BAC180K D26185 g467403 Bacillus subtilis 1423 -11528852 215003 sers seryl-trna synthetase (db:genpept-bct1) (ec:6.1.1.11) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:20878) (re:22155) (di:direct) BSUB0001 Z99104 g2632280 Bacillus subtilis 1423 -11528852 206280 sers serine--trna ligase:sers:seryl-trna synthetase sers (cl:serine--trna ligase) (ec:6.1.1.11) (db:pir) S66043 S66043 Bacillus subtilis 1423 -11528852 5000688628 (de:(sers) (pn:seryl-trna synthetase:serine--trna ligase:serrs:seryl-trna synthetase :serine-trna ligase:serrs) (gtcfc:10.06) (ec:6.1.1.11) (sys_bacsu) (keggfc:5.3:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis)) serS serS Bacillus subtilis 1423 10042027

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737533	782	22938	327	108

Description

6500724995 hypothetical protein:similar to l-serine dehydratase (gtcfc:5.3:5.5:14.1) (ec:4.2.1.13) (keggfc:5.3:5.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylpA ylpA Bacillus subtilis 1423 -11528853 7000694154 ylpa l-serine dehydratase homolog ylpa (db:pir2.dat) G69879 G69879 Bacillus subtilis 1423 -11528853 5500687807 ylpa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to l-serine dehydratase) (le:59909) (re:60811) (di:direct) BSUB0009 Z99112 g2633958 Bacillus subtilis 1423 -11528853 7500964887 ylpa putative yhap protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:21681) (re:22583) (di:direct) BSY13937 Y13937 g2337815 Bacillus subtilis 1423 -11528853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737563	783	22939	756	251

Description

GTC ORF with score 163 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f25e2.) (nt:coded for by c. elegans cdna yk95g9.3; similar to) (le:8505:8654:8894) (re:8605:8851:9098) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737565	784	22940	240	80

Description

6500724996 threonine 3-dehydrogenase (gtcfc:5.3) (ec:1.1.1.103) (keggfc:5.3) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) tdh tdh Bacillus subtilis 1423 -11528854 7502851555 tdh (ec:1.1.1.103) (de:threonine 3-dehydrogenase,) (db:swissprot) TDH_BACSU O31776 BACILLUS SUBTILIS 1423 -11528854 7000694692 tdh l-threonine 3-dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.103) (db:pir1.dat) C69721 C69721 Bacillus subtilis 1423 -11528854 7500953166 tdh threonine 3-dehydrogenase (fn:threonine catabolism) (db:genpept-bct1) (ec:1.1.1.103) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:171409) (re:172452) (di:direct) BSUB0009 Z99112 g2634071 Bacillus subtilis 1423 -11528854

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737578	785	22941	420	139

Description

6500724997 2-amino-3-ketobutyrate coa ligase:glycine acetyl transferase (gtcfc:5.3) (ec:2.3.1.29) (keggfc:5.3) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) kbl kbl Bacillus subtilis 1423 -11528855 7000692035 kbl 2-amino-3-ketobutyrate coa ligase kbl (cl:5-aminolevulinate synthase) (db:pir2.dat) G69647 G69647 Bacillus subtilis 1423 -11528855 7500963287 kbl 2-amino-3-ketobutyrate coa ligase glycine (db:genpept-bct1) (ec:2.3.1.29) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:172465) (re:173643) (di:direct) BSUB0009 Z99112 g2634072 Bacillus subtilis 1423 -11528855

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737629	786	22942	267	88

Description

6500724998 hypothetical protein:similar to phosphoglycerate dehydrogenase (gtcfc:5.3:14.1) (ec:1.1.1.95) (keggfc:5.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaD yoaD Bacillus subtilis 1423 -11528856 7000694410 yoad phosphoglycerate dehydrogenase homolog yoad (db:pir2.dat) F69895 F69895 Bacillus subtilis 1423 -11528856 5500701868 yoad yoad (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis d-3-phosphoglycerate) (le:4036) (re:5070) (di:complement) AF027868 AF027868 g2619022 Bacillus subtilis 1423 -11528856 7500965071 yoad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to phosphoglycerate dehydrogenase) (le:23127) (re:24161) (di:complement) BSUB0011 Z99114 g2634250 Bacillus subtilis 1423 -11528856

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737641	787	22943	582	194

Description

GTC ORF with score 272 to: (sr:streptomyces hygroscopicus (strain:sf1293) dna) (db:genpept-bct2) (de:streptomyces hygroscopicus gene for carboxyphosphonoenolpyruvatephosphonomutase, complete cds.) (le:168) (re:1055) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737651	788	22944	327	109

Description

6500724999 threonine dehydratase:threonine dehydratase biosynthetic:threonine deaminase (gtcfc:5.3) (ec:4.2.1.16) (keggfc:5.3) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) ilvA ilvA Bacillus subtilis 1423 -11528857 7000694693 ilva threonine dehydratase ilva (cl:threonine dehydratase) (db:pir2.dat) A69644 A69644 Bacillus subtilis 1423 -11528857 217102 ilva threonine dehydratase (fn:isoleucine byosynthesis) (db:genpept-bct1) (ec:4.2.1.16) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (le:27414) (re:28682) (di:direct) BACYACA L77246 g1256645 Bacillus subtilis 1423 -11528857 7500954425 ilva threonine dehydratase (fn:isoleucine biosynthesis) (db:genpept-bct1) (ec:4.2.1.16) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:96470) (re:97738) (di:complement) BSUB0012 Z99115 g2634597 Bacillus subtilis 1423 -11528857

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737660	789	22945	492	164

Description

6500725000 phosphoglycerate dehydrogenase (gtcfc:5.3) (ec:1.1.1.95) (keggfc:5.3) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) serA serA Bacillus subtilis 1423 -11528858 7500891530 sera (ec:1.1.1.95) (de:d-3-phosphoglycerate dehydrogenase, (pgdh)) (db:swissprot) SERA_BACSU P35136 BACILLUS SUBTILIS 1423 -11528858 7000694411 sera phosphoglycerate dehydrogenase:sera (cl:bacillus phosphoglycerate dehydrogenase) (ec:1.1.1.95) (db:pir2.dat) C69705 C69705 Bacillus subtilis 1423 -11528858 7500891533 sera phosphoglycerate dehydrogenase (fn:serine biosynthesis) (db:genpept-bct1) (ec:1.1.1.95) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:15060) (re:16637) (di:direct) BSUB0013 Z99116 g2634742 Bacillus subtilis 1423 -11528858 216702 sera phosphoglycerate dehydrogenase (fn:serine biosynthesis) (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), y... BACSERA L47648 g1146196 Bacillus subtilis 1423 -11528858 7502851556 sera phosphoglycerate dehydrogenase (fn:serine biosynthesis) (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ... BACSERA L47648 g1146196 Bacillus subtilis 1423 -11528858

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737662	790	22946	228	75

Description

6500725001 hypothetical protein:probable d-serine dehydratase:d-serine deaminase (gtcfc:5.3:14.1) (ec:4.2.1.14) (keggfc:5.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjR yqjR Bacillus subtilis 1423 -11528859 98262 yqjr (ec:4.2.1.14) (de:probable d-serine dehydratase, (d-serine deaminase)) (db:swissprot) SDHD_BACSU P54555 BACILLUS SUBTILIS 1423 -11528859 7000686574 yqjr d-serine dehydratase homolog yqjr (cl:d-serine dehydratase) (db:pir2.dat) B69965 B69965 Bacillus subtilis 1423 -11528859 216213 yqjr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:248724) (re:250070) (di:direct) BACJH642 D84432 g1303969 Bacillus subtilis 1423 -11528859 7500891420 yqjr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to d-serine dehydratase) (le:73549) (re:74895) (di:complement) BSUB0013 Z99116 g2634812 Bacillus subtilis 1423 -11528859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737664	791	22947	396	131

Description

6500725002 hypothetical protein:probable glycine dehydrogenase:decarboxylating subunit 2:glycine decarboxylase:glycine cleavage system p-protein (gtcfc:5.3:14.1) (ec:1.4.4.2) (keggfc:5.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhK yqhK Bacillus subtilis 1423 -11528860 73441 yqhk (ec:1.4.4.2) (de:protein)) (db:swissprot) GCS2_BACSU P54377 BACILLUS SUBTILIS 1423 -11528860 7000685378 yqhk glycine dehydrogenase homolog yqhk (db:pir2.dat) B69959 B69959 Bacillus subtilis 1423 -11528860 216136 yqhk (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:172729) (re:174195) (di:direct) BACJH642 D84432 g1303892 Bacillus subtilis 1423 -11528860 217175 yqhk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to glycine dehydrogenase) (le:149426) (re:150892) (di:complement) BSUB0013 Z99116 g2634889 Bacillus subtilis 1423 -11528860

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737665	792	22948	399	133

Description

6500725003 hypothetical protein:probable glycine dehydrogenase:decarboxylating subunit 1:glycine decarboxylase:glycine cleavage system p-protein (gtcfc:5.3:14.1) (ec:1.4.4.2) (keggfc:5.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhJ yqhJ Bacillus subtilis 1423 -11528861 73439 yqhj (ec:1.4.4.2) (de:protein)) (db:swissprot) GCS1_BACSU P54376 BACILLUS SUBTILIS 1423 -11528861 7000685377 yqhj glycine dehydrogenase homolog yqhj (db:pir2.dat) A69959 A69959 Bacillus subtilis 1423 -11528861 216135 yqhj (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:171390) (re:172736) (di:direct) BACJH642 D84432 g1303891 Bacillus subtilis 1423 -11528861 217174 yqhj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to glycine dehydrogenase) (le:150885) (re:152231) (di:complement) BSUB0013 Z99116 g2634890 Bacillus subtilis 1423 -11528861

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737720	793	22949	510	169

Description

6500725004 ask:aeca:lysc aspartokinase ii alpha subunit:aa 1-:aspartokinase 2 alpha and beta subunits:aspartate kinase 2 (gtcfc:5.3:5.8) (ec:2.7.2.4) (keggfc:5.3:5.8) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) lysC lysC Bacillus subtilis 1423 -11528862 220323 lysc aspartokinase ii alpha subunit aa 1-408 and (fn:diaminopimelate/lysine biosynthesis) (db:genpept-bct1) (ec:2.7.2.4) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ask, aeca) (le:113493) (re:114719) (di:complement) BSUB0015 Z99118 g2635312 Bacillus subtilis 1423 -11528862 304196 lysca aspartokinase ii alpha subunit (db:genpept-bct1) (ec:2.7.2.4) (de:b.subtilis genomic sequence 89009bp.) (nt:aspartokinase ll alpha subunit; aminoethylcysteine) (le:55188) (re:56414) (di:direct) BSZ75208 Z75208 g1770047 Bacillus subtilis 1423 -11528862 7000692241 lysc aspartokinase ii alpha and beta subunits lysc (db:pir) A69654 A69654 Bacillus subtilis 1423 -11528862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737735	794	22950	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737741	795	22951	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737745	796	22952	402	133

Description

6500725005 thrsv:thrs threonyl-trna synthetase:threonyl-trna synthetase 1:threonine--trna ligase:thrrs (gtcfc:10.6) (ec:6.1.1.3) (keggfc:5.3:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) thrS thrS Bacillus subtilis 1423 -11528863 100183 thrs:thrsv (ec:6.1.1.3) (de:(thrrs)) (db:swissprot) SYT1_BACSU P18255 BACILLUS SUBTILIS 1423 -11528863 125887 thrs:thrsv threonine--trna ligase::major thrs:threonyl-trna synthetase (cl:threonine--trna ligase) (ec:6.1.1.3) (db:pir1.dat) (mp:250 (degrees)) YSBST1 B37770 Bacillus subtilis 1423 -11528863 216987 thrs threonine trna synthetase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:217934) (re:219865) (di:direct) AF008220 AF008220 g2293284 Bacillus subtilis 1423 -11528863 220275 (sr:b.subtilis (strain 168) vegetative form dna) (db:genpept-bct1) (de:b.subtilis threonyl-trna synthetase (thrsv) gene, complete cds.) (nt:(thrsv) (ec 6.1.1.3)) (le:365) (re:2296) (di:direct) BACTRNASB M36594 g143766 Bacillus subtilis 1423 -11528863 304148 thrs threonyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.3) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:163202) (re:165133) (di:complement) BSUB0015 Z99118 g2635360 Bacillus subtilis 1423 -11528863 4000707356 thrs threonyl-trna-synthetase (db:genpept-bct1) (ec:6.1.1.3) (de:b.subtilis genomic sequence 89009bp.) (nt:thrs (111-180); major threonyl-trna synthetase) (le:4774) (re:6705) (di:direct) BSZ75208 Z75208 g1769999 Bacillus subtilis 1423 -11528863 5000688629 (de:(thrs) (pn:threonyl-trna synthetase 1:threonine--trna ligase:thrrs:threonyl-trna synthetase 1 :threonine-trna ligase:thrrs) (gn:thrsv) (gtcfc:10.06) (ec:6.1.1.3) (syt1_bacsu) (keggfc:5.3:10.1:10.2) (bsorffc:4.3.1) (db:gtc-ba) thrS thrS Bacillus subtilis 1423 10042037

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737749	797	22953	615	204

Description

6500725006 thra:thrb homoserine kinase:hk (gtcfc:5.3) (ec:2.7.1.39) (keggfc:5.3) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) thrB thrB Bacillus subtilis 1423 -11528864 7000693110 thrb homoserine kinase (cl:homoserine kinase thrb) (ec:2.7.1.39) (db:pir2.dat) H69722 H69722 Bacillus subtilis 1423 -11528864 7500964057 thrb homoserine kinase (fn:threonine biosynthesis) (db:genpept-bct1) (ec:2.7.1.39) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: thra) (le:114902) (re:115831) (di:complement) BSUB0017 Z99120 g2635721 Bacillus subtilis 1423 -11528864

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737754	798	22954	495	165

Description

6500725007 thrb:thrc threonine synthase (gtcfc:5.3:9.3) (ec:4.2.99.2) (keggfc:5.3:9.3) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) (gtcfc:l-amino acid metabolism-glycine--serine and threonine metabolism:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) (keggfc:amino aci... thrC thrC Bacillus subtilis 1423 -11528865 7500893109 thrc (ec:4.2.99.2) (de:threonine synthase,) (db:swissprot) THRC_BACSU P04990 BACILLUS SUBTILIS 1423 -11528865 7000686797 thrc threonine synthase:thrc (cl:threonine dehydratase) (ec:4.2.99.2) (db:pir2.dat) A25364 A25364 Bacillus subtilis 1423 -11528865 219696 thrc threonine synthase (db:genpept-bct1) (ec:4.2.99.2) (de:b. subtilis thrb and thrc genes for homoserine kinase and threoninesynthase (ec 2.7.1.39 and ec 4.2.99.2, respectively).) (le:248) (re:1306) (di:direct) BSTHRBC X04603 g40211 Bacillus subtilis 1423 -11528865 7502851557 thrc threonine synthase (fn:threonine biosynthesis) (db:genpept-bct1) (ec:4.2.99.2) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: thrb) (le:115828) (re:116886) (di:complement) BSUB0017 Z99120 g2635722 Bacillus subtilis 1423 -11528865 101436 thrc (ec:4.2.99.2) (de:threonine synthase,) (db:swissprot) THRC_BACSU P04990 BACILLUS SUBTILIS 1423 -11528865 141865 thrc threonine synthase:thrc (cl:threonine dehydratase) (ec:4.2.99.2) (db:pir) A25364 A25364 Bacillus subtilis 1423 -11528865

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737757	799	22955	540	179

Description

6500725008 tdm:hom homoserine dehydrogenase:hdh (gtcfc:5.3:5.8) (ec:1.1.1.3) (keggfc:5.3:5.8) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) hom hom Bacillus subtilis 1423 -11528866 7000693108 hom homoserine dehydrogenase (cl:homoserine dehydrogenase:homoserine dehydrogenase homology) (ec:1.1.1.3) (db:pir1.dat) (mp:78 min) DEECHS A31973 Bacillus subtilis 1423 -11528866 7500964055 hom homoserine dehydrogenase (fn:threonine/methionine biosynthesis) (db:genpept-bct1) (ec:1.1.1.3) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:116886) (re:118187) (di:complement) BSUB0017 Z99120 g2635723 Bacillus subtilis 1423 -11528866

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737758	800	22956	279	92

Description

6500725009 thrs2:thrz threonyl-trna synthetase:threonyl-trna synthetase 2:threonine--trna ligase:thrrs (gtcfc:10.6) (ec:6.1.1.3) (keggfc:5.3:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) thrZ thrZ Bacillus subtilis 1423 -11528867 100190 thrz:thrs2 (ec:6.1.1.3) (de:(thrrs)) (db:swissprot) SYT2_BACSU P18256 BACILLUS SUBTILIS 1423 -11528867 125886 thrz:thrs2 threonine--trna ligase::minor thrz:threonyl-trna synthetase (cl:threonine--trna ligase) (ec:6.1.1.3) (db:pir1.dat) (mp:344 (degrees)) YSBST2 A37770 Bacillus subtilis 1423 -11528867 216986 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis threonyl-trna synthetase (thrs2) gene, complete cds.) (nt:threonyl-trna synthetase (thrs2) (ec 6.1.1.3)) (le:280) (re:2196) (di:direct) BACTRNASA M36593 g143764 Bacillus subtilis 1423 -11528867 7500892593 thrz threonyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.3) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: thrs2) (le:54908) (re:56824) (di:complement) BSUB0020 Z99123 g2636292 Bacillus subtilis 1423 -11528867 5000688630 (de:(thrz) (pn:threonyl-trna synthetase 2:threonine--trna ligase:thrrs:threonyl-trna synthetase 2 :threonine-trna ligase:thrrs) (gn:thrs2) (gtcfc:10.06) (ec:6.1.1.3) (syt2_bacsu) (keggfc:5.3:10.1:10.2) (bsorffc:4.3.1) (db:gtc-ba) thrZ thrZ Bacillus subtilis 1423 10042044

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737807	801	22957	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737816	802	22958	492	163

Description

6500725010 yhaf:serc phosphoserine aminotransferase (gtcfc:5.3) (ec:2.6.1.52) (keggfc:14.1) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) serC serC Bacillus subtilis 1423 -11528868 7500891555 serc (ec:2.6.1.52) (de:protein 234) (veg234)) (db:swissprot) SERC_BACSU P80862 BACILLUS SUBTILIS 1423 -11528868 7000694422 serc phosphoserine aminotransferase serc (cl:phosphoserine aminotransferase) (db:pir2.dat) D69705 D69705 Bacillus subtilis 1423 -11528868 7500891557 serc phosphoserine aminotransferase (fn:serine biosynthesis) (db:genpept-bct1) (ec:2.6.1.52) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yhaf) (le:75262) (re:76341) (di:complement) BSUB0006 Z99109 g2633338 Bacillus subtilis 1423 -11528868 4000714540 yhaf hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:similarity to phosphoserine aminotransferase from) (le:4572) (re:5651) (di:direct) BSY14077 Y14077 g2226117 Bacillus subtilis 1423 -11528868

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737823	803	22959	204	68

Description

6500725011 ketol-acid reductoisomerase:acetohydroxy-acid isomeroreductase:alpha-keto-beta-hydroxylacil reductoisomerase (gtcfc:5.3:5.7:9.5) (ec:1.1.1.86) (keggfc:5.7:9.5) (bsorffc:3.1.3:3.4.9) (db:gtc-bacillus subtilis) ilvC ilvC Bacillus subtilis 1423 -11528869 79245 ilvc (ec:1.1.1.86) (de:isomeroreductase) (alpha-keto-beta-hydroxylacil reductoisomerase)) (db:swissprot) ILVC_BACSU P37253 BACILLUS SUBTILIS 1423 -11528869 7000685623 ilvc ketol-acid reductoisomerase ilvc (cl:methanococcus ketol-acid reductoisomerase:ketol-acid reductoisomerase homology) (db:pir2.dat) C69644 C69644 Bacillus subtilis 1423 -11528869 215904 ilvc ketol-acid reductoisomerase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis ilvb, ilvn and ilvc genes, complete ilv-leuoperon.) (le:2979) (re:4007) (di:direct) BACILNB L03181 g143093 Bacillus subtilis 1423 -11528869 220344 ilvc ketol-acid reductoisomerase acetohydroxy-acid (fn:valine/isoleucine biosynthesis) (db:genpept-bct1) (ec:1.1.1.86) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:97651) (re:98679) (di:complement) BSUB0015 Z99118 g2635294 Bacillus subtilis 1423 -11528869 304217 ilvc ketol-acid reductoisomerase (db:genpept-bct1) (ec:1.1.1.86) (de:b.subtilis genomic sequence 89009bp.) (nt:ketol-acid reductoisomerase (acetohydroxy-acid) (le:71228) (re:72256) (di:direct) BSZ75208 Z75208 g1770068 Bacillus subtilis 1423 -11528869

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737824	804	22960	744	248

Description

6500725012 glycine betaine aldehyde dehydrogenase:betaine aldehyde dehydrogenase:badh (gtcfc:5.3) (ec:1.2.1.8) (keggfc:14.1) (bsorffc:3.1.3) (db:gtc-bacillus subtilis) gbsA gbsA Bacillus subtilis 1423 -11528870 5500685088 gbsa (ec:1.2.1.8) (de:betaine aldehyde dehydrogenase, (badh)) (db:swissprot) DHAB_BACSU P71016 BACILLUS SUBTILIS 1423 -11528870 7000685030 gbsa glycine betaine aldehyde dehydrogenase gbsa (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) A69629 A69629 Bacillus subtilis 1423 -11528870 220031 gbsa glycine betaine aldehyde dehydrogenase (fn:glycine betaine synthesis (osmoprotection)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:186392) (re:187864) (di:complement) BSUB0016 Z99119 g2635590 Bacillus subtilis 1423 -11528870 7500880230 gbsa (db:genpept-bct2) (de:bacillus subtilis gbsab operon, glycine betaine aldehydedehydrogenase gbsa, alcohol dehydrogenase gbsb genes, complete cds.) (nt:glycine betaine aldehyde dehydrogenase) (le:1263) (re:2735) (di:direct) BSU47861 U47861 g1524392 Bacillus subtilis 1423 -11528870

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737825	805	22961	528	175

Description

GTC ORF with score 675 to: (sr:schizosaccharomyces pombe (strain:jy333) dna, clone_lib:wildtyp) (db:genpept-pln1) (de:schizosaccharomyces pombe dna for elongation factor 2, completecds.) (nt:duplicated gene no.1 of 2) (le:268) (re:2796) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737826	806	22962	291	96

Description

6500725013 methionyl-trna synthetase:methionine--trna ligase:metrs (gtcfc:10.6) (ec:6.1.1.10) (keggfc:5.4:6.4:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) metS metS Bacillus subtilis 1423 -11528871 100120 mets (ec:6.1.1.10) (de:(metrs)) (db:swissprot) SYM_BACSU P37465 BACILLUS SUBTILIS 1423 -11528871 7000686723 mets methionine--trna ligase:mets:methionyl-trna synthetase mets (cl:methionine--trna ligase) (ec:6.1.1.10) (db:pir2.dat) S66067 S66067 Bacillus subtilis 1423 -11528871 7500892511 mets methionyl-trna synthetase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:109233) (re:111227) (di:direct) BAC180K D26185 g467427 Bacillus subtilis 1423 -11528871 215027 mets methionyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.10) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:45631) (re:47625) (di:direct) BSUB0001 Z99104 g2632305 Bacillus subtilis 1423 -11528871 206266 mets methionine--trna ligase:mets:methionyl-trna synthetase mets (ec:6.1.1.10) (db:pir) S66067 S66067 Bacillus subtilis 1423 -11528871 5000688627 (de:(mets) (pn:methionyl-trna synthetase:methionine--trna ligase:metrs:methionyl-trna synthetase :methionine-trna ligase:metrs) (gtcfc:10.06) (ec:6.1.1.10) (sym_bacsu) (keggfc:5.4:6.4:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus) metS metS Bacillus subtilis 1423 10041974

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737830	807	22963	864	288

Description

6500725014 ylol:fmt methionyl-trna formyltransferase (gtcfc:10.6) (ec:2.1.2.9) (keggfc:5.4:9.8:10.1) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) fmt fmt Bacillus subtilis 1423 -11528872 7000694212 fmt methionyl-trna formyltransferase:fmt (cl:methionyl-trna formyltransferase:phosphoribosylglycinamide formyltransferase homology) (ec:2.1.2.9) (db:pir2.dat) A69626 A69626 Bacillus subtilis 1423 -11528872 5500687796 fmt methionyl-trna formyltransferase (db:genpept-bct1) (ec:2.1.2.9) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylol) (le:47978) (re:48931) (di:direct) BSUB0009 Z99112 g2633945 Bacillus subtilis 1423 -11528872 7500964937 ylol putative fmt protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:9750) (re:10703) (di:direct) BSY13937 Y13937 g2337802 Bacillus subtilis 1423 -11528872

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737894	808	22964	510	169

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737897	809	22965	273	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737903	810	22966	339	112

Description

6500725015 snpa:spna:cyss cysteinyl-trna synthetase:cysteine--trna ligase:cysrs (gtcfc:10.6) (ec:6.1.1.16) (keggfc:5.5:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) cysS cysS Bacillus subtilis 1423 -11528873 215701 cyss:spna (ec:6.1.1.16) (de:(cysrs)) (db:swissprot) SYC_BACSU Q06752 BACILLUS SUBTILIS 1423 -11528873 7000686704 cyss cysteine--trna ligase:cyss:cysteinyl-trna synthetase cyss (cl:cysteine--trna ligase) (ec:6.1.1.16) (db:pir1.dat) C53402 C53402 Bacillus subtilis 1423 -11528873 7500892335 cyss cysteinyl-trna synthetase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:177049) (re:178449) (di:direct) BAC180K D26185 g467482 Bacillus subtilis 1423 -11528873 215082 cysteinyl-trna synthetase (sr:bacillus subtilis (strain 168t) dna) (db:genpept-bct1) (de:bacillus subtilis glutamyl-trna transferase (gltx), serineacetyltransferase (cyse), and cysteinyl-trna synthetase (cyss)genes, complete cds's.) (le:4109) (re:5509) (di:direct) BACGLUSYN L14580 g289284 Bacillus subtilis 1423 -11528873 5000688624 spna/cyss cysteine--trna ligase (db:genpept-bct1) (ec:6.1.1.16) (de:b.subtilis gene for cysteinyl-trna synthetase.) (le:321) (re:1721) (di:direct) BSCTS X73989 g499303 Bacillus subtilis 1423 -11528873 219113 cyss cysteinyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.16) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: snpa) (le:113447) (re:114847) (di:direct) BSUB0001 Z99104 g2632361 Bacillus subtilis 1423 -11528873 99994 cyss:spna (ec:6.1.1.16) (de:(cysrs)) (db:swissprot) SYC_BACSU Q06752 BACILLUS SUBTILIS 1423 -11528873 169944 cyss cysteine--trna ligase:cyss:cysteinyl-trna synthetase cyss (cl:cysteine--trna ligase) (ec:6.1.1.16) (db:pir) C53402 C53402 Bacillus subtilis 1423 -11528873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737917	811	22967	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737925	812	22968	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737995	813	22969	210	69

Description

GTC ORF with score 211 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501737996	814	22970	366	121

Description

GTC ORF with score 273 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738007	815	22971	672	224

Description

6500725016 hypothetical protein:similar to d-alanine aminotransferase (gtcfc:5.6:5.7:9.5:14.1) (ec:2.6.1.42) (keggfc:5.6:5.7:9.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheM yheM Bacillus subtilis 1423 -11528874 7500879960 dat (ec:2.6.1.21) (de:transaminase)) (db:swissprot) DAAA_BACSU O07597 BACILLUS SUBTILIS 1423 -11528874 7000692902 yhem d-alanine aminotransferase homolog yhem (cl:branched-chain-amino-acid aminotransferase) (db:pir2.dat) E69829 E69829 Bacillus subtilis 1423 -11528874 7500879962 yhem (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to d-alanine aminotransferase) (le:41974) (re:42822) (di:direct) BSUB0006 Z99109 g2633302 Bacillus subtilis 1423 -11528874 4000714628 yhem hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to d-amino acid aminotransferase from) (le:28622) (re:29470) (di:direct) BSY14082 Y14082 g2226223 Bacillus subtilis 1423 -11528874

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738012	816	22972	534	177

Description

6500725017 hypothetical protein:similar to 3-hydroxyisobutyrate dehydrogenase (gtcfc:5.6:14.1) (ec:1.1.1.31) (keggfc:5.6) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykwC ykwC Bacillus subtilis 1423 -11528875 7500950865 ykwc (de:hypothetical 30.7 kd protein in mcpc-kina intergenic region) (db:swissprot) YKWC_BACSU O34948 BACILLUS SUBTILIS 1423 -11528875 7000692048 ykwc 3-hydroxyisobutyrate dehydrogenase homolog ykwc (cl:3-hydroxyisobutyrate dehydrogenase:3-hydroxyisobutyrate dehydrogenase homology) (db:pir2.dat) B69870 B69870 Bacillus subtilis 1423 -11528875 6000689640 ykwc ykwc protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to 3-hydroxyisobutyrate dehydrogenase) (le:89) (re:955) (di:direct) BS16829KB AJ222587 g2632217 Bacillus subtilis 1423 -11528875 7500950868 ykwc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to 3-hydroxyisobutyrate dehydrogenase) (le:70345) (re:71211) (di:direct) BSUB0008 Z99111 g2633767 Bacillus subtilis 1423 -11528875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738075	817	22973	480	159

Description

6500725018 bfmb1b:bfmbab branched-chain alpha-keto acid dehydrogenase e1:2-oxoisovalerate dehydrogenase beta subunit:branched-chain alpha-keto acid dehydrogenase component beta chain:e1:bckdh e1-beta (gtcfc:5.6:12.1) (ec:1.2.4.4) (keggfc:5.6) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) bfmBAB bfmBAB Bacillus subtilis 1423 -11528876 87451 bfmbab:bfmb1b (ec:1.2.4.4) (de:(bckdh e1-beta)) (db:swissprot) ODBB_BACSU P37941 BACILLUS SUBTILIS 1423 -11528876 7000686031 bfmbab 3-methyl-2-oxobutanoate dehydrogenase lipoamide:e1 beta chain bfmbab:branched-chain alpha-oxo acid dehydrogenase e1 beta chain (cl:pyruvate dehydrogenase (lipoamide) beta chain) (ec:1.2.4.4) (db:pir2.dat) D69593 D69593 Bacillus subtilis 1423 -11528876 7500887090 branched chain alpha-keto acid dehydrogenase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis branched chain alpha-keto acid dehydrogenaseel-alpha, branched chain alpha-keto acid dehydrogenase e1-beta, andbranched chain alpha-keto acid dehydrogenase e2, complete cds.) (le:1222) ... BACBRANCH M97391 g142612 Bacillus subtilis 1423 -11528876 215302 bfmbab (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:220568) (re:221551) (di:direct) BACJH642 D84432 g1303943 Bacillus subtilis 1423 -11528876 216187 bfmbab branched-chain alpha-keto acid dehydrogenase e1 (db:genpept-bct1) (ec:1.2.4.4) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: bfmb1b) (le:102068) (re:103051) (di:complement) BSUB0013 Z99116 g2634838 Bacillus subtilis 1423 -11528876 136539 bfmbab 3-methyl-2-oxobutanoate dehydrogenase lipoamide:e1 beta chain bfmbab:branched-chain alpha-oxo acid dehydrogenase e1 beta chain (cl:pyruvate dehydrogenase (lipoamide) beta chain) (ec:1.2.4.4) (db:pir) D69593 D69593 Bacillus subtilis 1423 -11528876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738078	818	22974	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738088	819	22975	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738094	820	22976	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738095	821	22977	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738099	822	22978	867	289

Description

6500725019 bfmb1a:bfmbaa branched-chain alpha-keto acid dehydrogenase e1:2-oxoisovalerate dehydrogenase alpha subunit:branched-chain alpha-keto acid dehydrogenase component alpha chain:e1:bckdh e1-alpha (gtcfc:5.6:12.1) (ec:1.2.4.4) (keggfc:5.6) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) bfmBAA bfmBAA Bacillus subtilis 1423 -11528877 87445 bfmbaa:bfmb1a (ec:1.2.4.4) (de:(bckdh e1-alpha)) (db:swissprot) ODBA_BACSU P37940 BACILLUS SUBTILIS 1423 -11528877 7000686030 bfmbaa 3-methyl-2-oxobutanoate dehydrogenase lipoamide:e1 alpha chain bfmbaa:branched-chain alpha-oxo acid dehydrogenase e1 alpha chain (cl:pyruvate dehydrogenase (lipoamide) alpha chain:thiamine pyrophosphate-binding domain homology) (ec:1.2.4.4) (db:pir2.dat) C69593 C69593 Bacillus subtilis 1423 -11528877 7500887087 branched chain alpha-keto acid dehydrogenase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis branched chain alpha-keto acid dehydrogenasee1-alpha, branched chain alpha-keto acid dehydrogenase e1-beta, andbranched chain alpha-keto acid dehydrogenase e2, complete cds.) (le:216) (... BACBRANCH M97391 g142611 Bacillus subtilis 1423 -11528877 215301 bfmbaa (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:219562) (re:220554) (di:direct) BACJH642 D84432 g1303942 Bacillus subtilis 1423 -11528877 216186 bfmbaa branched-chain alpha-keto acid dehydrogenase e1 (db:genpept-bct1) (ec:1.2.4.4) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: bfmb1a) (le:103065) (re:104057) (di:complement) BSUB0013 Z99116 g2634839 Bacillus subtilis 1423 -11528877 136516 bfmbaa 3-methyl-2-oxobutanoate dehydrogenase lipoamide:e1 alpha chain bfmbaa:branched-chain alpha-oxo acid dehydrogenase e1 alpha chain (cl:pyruvate dehydrogenase (lipoamide) alpha chain:thiamine pyrophosphate-binding domain homology) (ec:1.2.4.4) (db:pir) C69593 C69593 Bacillus subtilis 1423 -11528877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738106	823	22979	591	196

Description

6500725020 hypothetical protein:leucine dehydrogenase:leudh (gtcfc:5.6:5.7:14.1) (ec:1.4.1.9) (keggfc:5.6:5.7) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiT yqiT Bacillus subtilis 1423 -11528878 68533 yqit (ec:1.4.1.9) (de:leucine dehydrogenase, (leudh)) (db:swissprot) DHLE_BACSU P54531 BACILLUS SUBTILIS 1423 -11528878 7000685043 yqit leucine dehydrogenase homolog yqit (cl:leucine dehydrogenase) (db:pir2.dat) B69962 B69962 Bacillus subtilis 1423 -11528878 216183 yqit (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:215890) (re:216984) (di:direct) BACJH642 D84432 g1303939 Bacillus subtilis 1423 -11528878 7500880259 yqit (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to leucine dehydrogenase) (le:106635) (re:107729) (di:complement) BSUB0013 Z99116 g2634842 Bacillus subtilis 1423 -11528878

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738121	824	22980	426	141

Description

6500725021 ipa-0r:ywaa hypothetical protein:putative branched-chain amino acid aminotransferase:bcat (gtcfc:5.6:5.7:9.5:14.1) (ec:2.6.1.42) (keggfc:5.6:5.7:9.5) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ywaA ywaA Bacillus subtilis 1423 -11528879 7000685625 ywaa branched-chain amino acid aminotransferase homolog ywaa (cl:branched-chain-amino-acid transaminase bat1) (db:pir2.dat) S57763 S57763 Bacillus subtilis 1423 -11528879 219053 ywaa unknown:highly similar to yeast twt1 protein (db:genpept-bct1) (de:b.subtilis cela, celb, celc, celd and ywaa genes.) (le:5632) (re:6723) (di:complement) BSCELABCD Z49992 g895752 Bacillus subtilis 1423 -11528879 7500963464 ywaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-0r; similar to) (le:157785) (re:158876) (di:direct) BSUB0020 Z99123 g2636390 Bacillus subtilis 1423 -11528879 79258 ilve_bacsu (de:putative branched-chain amino acid aminotransferase (ec 2.6.1.42).) P39576 P39576 Bacillus subtilis 1423 10021586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738194	825	22981	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738206	826	22982	213	70

Description

6500725022 isoleucyl-trna synthetase (gtcfc:10.6) (ec:6.1.1.5) (keggfc:5.7:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) ileS ileS Bacillus subtilis 1423 -11528880 7500892455 iles (ec:6.1.1.5) (de:(ilers)) (db:swissprot) SYI_BACSU Q45477 BACILLUS SUBTILIS 1423 -11528880 7000694136 iles isoleucine--trna ligase:iles:isoleucyl-trna synthetase (cl:isoleucine--trna ligase) (ec:6.1.1.5) (db:pir2.dat) H69643 H69643 Bacillus subtilis 1423 -11528880 7500892457 iles isoleucyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.5) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:14338) (re:17103) (di:direct) BSUB0009 Z99112 g2633916 Bacillus subtilis 1423 -11528880

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738207	827	22983	807	268

Description

6500725023 dihydroxy-acid dehydratase:dad (gtcfc:5.7:9.5) (ec:4.2.1.9) (keggfc:5.7:9.5) (bsorffc:3.4.9) (db:gtc-bacillus subtilis) ilvD ilvD Bacillus subtilis 1423 -11528881 7000685624 ilvd dihydroxy-acid dehydratase ilvd (cl:dihydroxy-acid dehydratase) (db:pir2.dat) D69644 D69644 Bacillus subtilis 1423 -11528881 7500954414 ilvd dihydroxy-acid dehydratase (fn:isoleucine byosynthesis) (db:genpept-bct1) (ec:4.2.1.9) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:51.0% identity with the escherichia coli) (le:19013) (re:20689) (di:direct) BACYACA L77246 g1256635 Bacillus subtilis 1423 -11528881 217092 ilvd dihydroxy-acid dehydratase (fn:valine/isoleucine biosynthesis) (db:genpept-bct1) (ec:4.2.1.9) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:104463) (re:106139) (di:complement) BSUB0012 Z99115 g2634607 Bacillus subtilis 1423 -11528881 79250 ilvd_bacsu (de:dihydroxy-acid dehydratase (ec 4.2.1.9) (dad).) P51785 P51785 Bacillus subtilis 1423 10021578

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738226	828	22984	402	134

Description

6500725024 valyl-trna synthetase:valine--trna ligase:valrs (gtcfc:10.6) (ec:6.1.1.9) (keggfc:5.7:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) valS valS Bacillus subtilis 1423 -11528882 220235 vals (ec:6.1.1.9) (de:valyl-trna synthetase, (valine--trna ligase) (valrs)) (db:swissprot) SYV_BACSU Q05873 BACILLUS SUBTILIS 1423 -11528882 7000686733 vals valine--trna ligase:vals:valyl-trna synthetase vals (cl:valine--trna ligase) (ec:6.1.1.9) (db:pir2.dat) S41420 S41420 Bacillus subtilis 1423 -11528882 7500892618 vals valyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.9) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:70795) (re:73437) (di:complement) BSUB0015 Z99118 g2635274 Bacillus subtilis 1423 -11528882 5000688631 vals valyl-trna synthetase (db:genpept-bct1) (de:b.subtilis vals gene.) (le:486) (re:3128) (di:direct) BSVALTRS X77239 g452309 Bacillus subtilis 1423 -11528882 100213 vals (ec:6.1.1.9) (de:valyl-trna synthetase, (valine--trna ligase) (valrs)) (db:swissprot) SYV_BACSU Q05873 BACILLUS SUBTILIS 1423 -11528882 142279 vals valine--trna ligase:vals:valyl-trna synthetase vals (cl:valine--trna ligase) (ec:6.1.1.9) (db:pir) S41420 S41420 Bacillus subtilis 1423 -11528882

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738238	829	22985	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738241	830	22986	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738314	831	22987	855	285

Description

6500725025 leucyl-trna synthetase:leucine--trna ligase:leurs (gtcfc:10.6) (ec:6.1.1.4) (keggfc:5.7:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) leuS leuS Bacillus subtilis 1423 -11528883 7500892490 leus (ec:6.1.1.4) (de:leucyl-trna synthetase, (leucine--trna ligase) (leurs)) (db:swissprot) SYL_BACSU P36430 BACILLUS SUBTILIS 1423 -11528883 7000694161 leus leucine--trna ligase::leucyl-trna synthetase (cl:leucine--trna ligase) (ec:6.1.1.4) (db:pir2.dat) D69650 D69650 Bacillus subtilis 1423 -11528883 4000714171 leus leucine trna synthetase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:74073) (re:76487) (di:direct) AF008220 AF008220 g2293181 Bacillus subtilis 1423 -11528883 7500892493 leus leucyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.4) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:103940) (re:106354) (di:complement) BSUB0016 Z99119 g2635516 Bacillus subtilis 1423 -11528883

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738366	832	22988	921	306

Description

6500725026 lysyl-trna synthetase:lysine--trna ligase:lysrs (gtcfc:10.6) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) lysS lysS Bacillus subtilis 1423 -11528884 100095 lyss (ec:6.1.1.6) (de:lysyl-trna synthetase, (lysine--trna ligase) (lysrs)) (db:swissprot) SYK_BACSU P37477 BACILLUS SUBTILIS 1423 -11528884 7000686719 lyss lysine--trna ligase:lyss:lysyl-trna synthetase lyss (cl:lysine--trna ligase) (ec:6.1.1.6) (db:pir2.dat) S66111 S66111 Bacillus subtilis 1423 -11528884 7500892470 lyss lysyl-trna thynthetase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:152326) (re:153825) (di:direct) BAC180K D26185 g467470 Bacillus subtilis 1423 -11528884 215070 lyss lysyl-trna synthetase (db:genpept-bct1) (ec:6.1.1.6) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:88724) (re:90223) (di:direct) BSUB0001 Z99104 g2632349 Bacillus subtilis 1423 -11528884 206265 lyss lysine--trna ligase:lyss:lysyl-trna synthetase lyss (cl:lysine--trna ligase) (ec:6.1.1.6) (db:pir) S66111 S66111 Bacillus subtilis 1423 -11528884 5000688626 (de:(lyss) (pn:lysyl-trna synthetase:lysine--trna ligase:lysrs:lysyl-trna synthetase :lysine-trna ligase:lysrs) (gtcfc:10.06) (ec:6.1.1.6) (syk_bacsu) (keggfc:5.8:10.1:10.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis)) lysS lysS Bacillus subtilis 1423 10041949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738442	833	22989	696	231

Description

6500725027 ydbq:murf udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-diaminopimelate-d-alanyl-d-alanyl ligase:udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-diaminopimelate-d-alanyl-d-alanyl ligase (gtcfc:5.8:11.4) (ec:6.3.2.15) (keggfc:5.8:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murF murF Bacillus subtilis 1423 -11528885 7500886140 murf (ec:6.3.2.15) (de:(d-alanyl-d-alanine-adding enzyme)) (db:swissprot) MURF_BACSU P96613 BACILLUS SUBTILIS 1423 -11528885 7000694891 murf udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-diaminopimelate-d-al murf (db:pir2.dat) F69662 F69662 Bacillus subtilis 1423 -11528885 302712 ydbq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable udp-n-acetylmuramoylalanyl-d-glutamyl-2,) (le:42447) (re:43820) (di:direct) AB001488 AB001488 g1881267 Bacillus subtilis 1423 -11528885 7500886143 murf udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-(fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:6.3.2.15) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ydbq) (le:106191) (re:107564) (di:direct) BSUB0003 Z99106 g2632757 Bacillus subtilis 1423 -11528885

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738444	834	22990	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738446	835	22991	381	126

Description

6500725028 hypothetical protein:similar to tetrahydrodipicolinate succinylase (gtcfc:5.8:14.1) (ec:2.3.1.117) (keggfc:5.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuQ ykuQ Bacillus subtilis 1423 -11528886 7000694671 ykuq tetrahydrodipicolinate succinylase homolog ykuq (db:pir2.dat) F69866 F69866 Bacillus subtilis 1423 -11528886 6000689672 ykuq ykuq protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to acetyltransferases) (le:23332) (re:24042) (di:direct) BS16829KB AJ222587 g2632238 Bacillus subtilis 1423 -11528886 7500965255 ykuq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to tetrahydrodipicolinate succinylase) (le:93588) (re:94298) (di:direct) BSUB0008 Z99111 g2633789 Bacillus subtilis 1423 -11528886

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738459	836	22992	624	208

Description

GTC ORF with score 113 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738465	837	22993	312	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738480	838	22994	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738482	839	22995	729	242

Description

6500725029 udp-n-acetylmuramoylalanyl-d-glutamate-2:6-diaminopimelate ligase:udp-n-acetylmuramoylalanyl-d-glutamate--2:6-diaminopimelate ligase:udp-n-acetylmuramyl-tripeptide synthetase (gtcfc:5.8:11.4) (ec:6.3.2.13) (keggfc:5.8:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murE murE Bacillus subtilis 1423 -11528887 7500886132 mure (ec:6.3.2.13) (de:(ec 6.3.2.13) (udp-n-acetylmuramyl-tripeptide synthetase)) (db:swissprot) MURE_BACSU Q03523 BACILLUS SUBTILIS 1423 -11528887 7000685887 mure udp-n-acetylmuramoylalanyl-d-glutamate--2:6-diaminopimelate ligase:mure (ec:6.3.2.13) (db:pir2.dat) (mp:133 (degrees)) B47691 B47691 Bacillus subtilis 1423 -11528887 5000688722 mure (fn:peptidoglycan precursor synthesis) (db:genpept-bct1) (ec:6.3.2.13) (de:b.subtilis genes spovd, mure, mray, murd.) (le:333) (re:1817) (di:direct) BSSPOG Z15056 g40162 Bacillus subtilis 1423 -11528887 219639 mure udp-n-acetylmuramoylananine-d-glutamate-2:6- (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:6.3.2.13) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:190939) (re:192423) (di:direct) BSUB0008 Z99111 g2633889 Bacillus subtilis 1423 -11528887 84711 mure (ec:6.3.2.13) (de:(ec 6.3.2.13) (udp-n-acetylmuramyl-tripeptide synthetase)) (db:swissprot) MURE_BACSU Q03523 BACILLUS SUBTILIS 1423 -11528887 170657 mure udp-n-acetylmuramoylalanyl-d-glutamate--2:6-diaminopimelate ligase:mure (ec:6.3.2.13) (db:pir) (mp:133 (degrees)) B47691 B47691 Bacillus subtilis 1423 -11528887

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738487	840	22996	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738559	841	22997	597	198

Description

6500725030 hypothetical protein:similar to xaa-his dipeptidase (gtcfc:5.8:14.1) (ec:3.5.1.18) (keggfc:5.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ytjP ytjP Bacillus subtilis 1423 -11528888 7000694902 ytjp xaa-his dipeptidase homolog ytjp (cl:peptidase v) (db:pir2.dat) B69994 B69994 Bacillus subtilis 1423 -11528888 4000714196 ytjp putative peptidase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:110303) (re:111694) (di:direct) AF008220 AF008220 g2293201 Bacillus subtilis 1423 -11528888 7500965435 ytjp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:similar to xaa-his dipeptidase) (le:68732) (re:70123) (di:complement) BSUB0016 Z99119 g2635482 Bacillus subtilis 1423 -11528888

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738565	842	22998	672	223

Description

6500725031 hypothetical protein:similar to diaminopimelate epimerase (gtcfc:5.8:14.1) (ec:5.1.1.7) (keggfc:5.8) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yutL yutL Bacillus subtilis 1423 -11528889 7502851558 dapf (ec:5.1.1.7) (de:diaminopimelate epimerase, (dap epimerase)) (db:swissprot) DAPF_BACSU O32114 BACILLUS SUBTILIS 1423 -11528889 7000692917 yutl diaminopimelate epimerase homolog yutl (cl:diaminopimelate epimerase) (db:pir2.dat) F70024 F70024 Bacillus subtilis 1423 -11528889 7500963936 yutl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:similar to diaminopimelate epimerase) (le:108097) (re:108951) (di:complement) BSUB0017 Z99120 g2635714 Bacillus subtilis 1423 -11528889

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738575	843	22999	276	91

Description

6500725032 ybds:ybxi hypothetical protein:similar to beta-lactamase (gtcfc:5.9:14.1) (ec:3.5.2.6) (keggfc:5.9) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybxI ybxI Bacillus subtilis 1423 -11528890 7000692265 ybxi beta-lactamase homolog ybxi:blar1 protein (cl:beta-lactamase oxa2:beta-lactamase oxa2 homology) (db:pir2.dat) B69752 B69752 Bacillus subtilis 1423 -11528890 7500963447 ybxi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ybds; similar to) (le:33888) (re:34691) (di:complement) BSUB0002 Z99105 g2632495 Bacillus subtilis 1423 -11528890 7500963448 ybds (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:31539) (re:32342) (di:complement) AB006424 AB006424 g3599631 Bacillus subtilis 1423 -11528890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738580	844	23000	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738581	845	23001	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738598	846	23002	435	144

Description

6500725033 beta-lactamase precursor:penicillinase (gtcfc:5.9:13.3) (ec:3.5.2.6) (keggfc:5.9) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) penP penP Bacillus subtilis 1423 -11528891 7000692266 penp beta-lactamase:penp:penicillinase (cl:beta-lactamase i) (ec:3.5.2.6) (db:pir2.dat) G69674 G69674 Bacillus subtilis 1423 -11528891 5500701885 penp penicillinase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (le:28526) (re:29446) (di:direct) AF027868 AF027868 g2619002 Bacillus subtilis 1423 -11528891 7500954316 penp beta-lactamase precursor (db:genpept-bct1) (ec:3.5.2.6) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:47617) (re:48537) (di:direct) BSUB0011 Z99114 g2634273 Bacillus subtilis 1423 -11528891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738599	847	23003	423	141

Description

6500725034 pantoate--beta-alanine ligase:pantothenate synthetase:pantoate activating enzyme (gtcfc:6.1:9.5) (ec:6.3.2.1) (keggfc:6.1:9.5) (bsorffc:3.4.9) (db:gtc-bacillus subtilis) panC panC Bacillus subtilis 1423 -11528892 88574 panc (ec:6.3.2.1) (de:(pantoate activating enzyme)) (db:swissprot) PANC_BACSU P52998 BACILLUS SUBTILIS 1423 -11528892 7000686079 panc pantothenate synthetase panc (cl:pantoate--beta-alanine ligase) (db:pir2.dat) H69671 H69671 Bacillus subtilis 1423 -11528892 217163 panc pantothenate synthetase (fn:pantothenic acid biosynthesis) (db:genpept-bct1) (ec:6.3.2.1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gen... BACYPIA L47709 g1146241 Bacillus subtilis 1423 -11528892 7500887644 panc pantothenate synthetase (fn:pantothenate biosynthesis) (db:genpept-bct1) (ec:6.3.2.1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:156679) (re:157539) (di:complement) BSUB0012 Z99115 g2634660 Bacillus subtilis 1423 -11528892

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738602	848	23004	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738605	849	23005	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738606	850	23006	1086	362

Description

6500725035 d-alanyl-d-alanine carboxypeptidase:penicillin-binding protein 5:d-alanyl-d-alanine carboxypeptidase precursor:dd-peptidase:dd-carboxypeptidase:cpase:pbp5 (gtcfc:6.1:11.4) (ec:3.4.16.4) (keggfc:14.1) (bsorffc:3.2.5:5.2.1) (db:gtc-bacillus subtilis) dacA dacA Bacillus subtilis 1423 -11528893 67825 daca (ec:3.4.16.4) (de:peptidase) (dd-carboxypeptidase) (cpase) (pbp5)) (db:swissprot) DACA_BACSU P08750 BACILLUS SUBTILIS 1423 -11528893 7000684974 daca serine-type d-ala-d-ala carboxypeptidase:daca:daca:penicillin binding protein 5 (cl:penicillin-binding protein 5) (ec:3.4.16.4) (db:pir2.dat) S66040 S66040 Bacillus subtilis 1423 -11528893 7500879964 daca d-alanine carboxypeptidase pbp-5 (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:81134) (re:82465) (di:direct) BAC180K D26185 g467400 Bacillus subtilis 1423 -11528893 215000 daca d-alanyl-d-alanine carboxypeptidase (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:3.4.16.4) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:17532) (re:18863) (di:direct) BSUB0001 Z99104 g2632277 Bacillus subtilis 1423 -11528893 206166 daca serine-type d-ala-d-ala carboxypeptidase:daca:daca:penicillin binding protein 5 (cl:penicillin-binding protein 5) (ec:3.4.16.4) (db:pir) S66040 S66040 Bacillus subtilis 1423 -11528893 5000688686 (de:(daca) (pn:d-alanyl-d-alanine carboxypeptidase precursor:dd-peptidase:dd-carboxypeptidase:cpase:pbp5:d-alanyl-d-alanine carboxypeptidase precursor :dd- peptidase:dd-carboxypeptidase:cpase:pbp5) (gtcfc:11.02) (ec:3.4.16.4) (d) dacA dacA Bacillus subtilis 1423 10010422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738690	851	23007	516	171

Description

6500725036 ddl:ddla d-alanyl-d-alanine ligase a:d-alanine--d-alanine ligase:d-alanylalanine synthetase (gtcfc:6.1:6.15:8.1:11.4) (ec:6.3.2.4) (keggfc:6.8:7.3:8.1) (bsorffc:3.2.5) (db:gtc-bacillus subtilis) ddlA ddlA Bacillus subtilis 1423 -11528894 5500685077 ddla:ddl (ec:6.3.2.4) (de:d-alanine--d-alanine ligase, (d-alanylalanine synthetase)) (db:swissprot) DDL_BACSU P96612 BACILLUS SUBTILIS 1423 -11528894 7000684997 ddla d-alanyl-d-alanine ligase a ddla (cl:d-alanine--d-alanine ligase) (db:pir2.dat) D69613 D69613 Bacillus subtilis 1423 -11528894 302711 ddla probable d-alanine--d-alanine ligase a (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (ec:6.3.2.4) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:41311) (re:42375) (di:direct) AB001488 AB001488 g1881266 Bacillus subtilis 1423 -11528894 7500880108 ddla d-alanyl-d-alanine ligase a (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:6.3.2.4) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:105055) (re:106119) (di:direct) BSUB0003 Z99106 g2632756 Bacillus subtilis 1423 -11528894

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738700	852	23008	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738709	853	23009	765	255

Description

6500725037 d-alanyl-d-alanine carboxypeptidase:penicillin-binding protein 5 (gtcfc:6.1:11.4) (ec:3.4.16.4) (keggfc:14.1) (bsorffc:3.2.5:5.2.1) (db:gtc-bacillus subtilis) dacB dacB Bacillus subtilis 1423 -11528895 67828 dacb (ec:3.4.16.4) (de:(pbp-5*)) (db:swissprot) DACB_BACSU P35150 BACILLUS SUBTILIS 1423 -11528895 7000684975 dacb serine-type d-ala-d-ala carboxypeptidase:dacb precursor:penicillin-binding protein 5* dacb (ec:3.4.16.4) (db:pir2.dat) S45552 S45552 Bacillus subtilis 1423 -11528895 7500879967 dacb penicillin-binding protein (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:15078) (re:16226) (di:direct) BACDIA L09228 g410134 Bacillus subtilis 1423 -11528895 215513 dacb d-alanyl-d-alanine carboxypeptidase (fn:required for spore cortex synthesis) (db:genpept-bct1) (ec:3.4.16.4) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:27357) (re:28505) (di:complement) BSUB0013 Z99116 g2634754 Bacillus subtilis 1423 -11528895 170427 dacb serine-type d-ala-d-ala carboxypeptidase:dacb precursor:penicillin-binding protein 5* dacb (ec:3.4.16.4) (db:pir) S45552 S45552 Bacillus subtilis 1423 -11528895 5000688687 (de:(dacb) (pn:penicillin-binding protein 5 precursor:d-alanyl-d-alanine carboxypeptidase:dd-peptidase:dd-carboxypeptidase:pbp-5 :penicillin-binding protein 5" precursor:d-alanyl-d-alanine carboxypeptidase :dd-peptidase:dd-carboxypeptid) dacB dacB Bacillus subtilis 1423 10010425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738712	854	23010	279	92

Description

6500725038 penicilin binding protein:penicillin-binding protein dacf precursor:d-alanyl-d-alanine carboxypeptidase:dd-peptidase:dd-carboxypeptidase (gtcfc:6.1:11.4) (ec:3.4.16.4) (keggfc:14.1) (bsorffc:3.2.5:5.2.1) (db:gtc-bacillus subtilis) dacF dacF Bacillus subtilis 1423 -11528896 216241 dacf (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:273387) (re:274556) (di:direct) BACJH642 D84432 g1303997 Bacillus subtilis 1423 -11528896 7500965043 dacf d-alanyl-d-alanine carboxypeptidase penicilin (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:3.4.16.4) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:49063) (re:50232) (di:complement) BSUB0013 Z99116 g2634783 Bacillus subtilis 1423 -11528896 7000694353 dacf penicillin-binding protein d-alanyl-d-alanine carboxypeptidas dacf (db:pir) F69612 F69612 Bacillus subtilis 1423 -11528896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738713	855	23011	204	67

Description

6500725039 pac:ggt gamma-glutamyltranspeptidase:gamma-glutamyltranspeptidase precursor (gtcfc:6.16:6.4:6.5:8.2:10.11) (ec:2.3.2.2) (keggfc:6.4:6.5:6.9:8.6) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) ggt ggt Bacillus subtilis 1423 -11528897 73582 ggt (ec:2.3.2.2) (de:gamma-glutamyltranspeptidase precursor,) (db:swissprot) GGT_BACSU P54422 BACILLUS SUBTILIS 1423 -11528897 7000685385 ggt gamma-glutamyltransferase:precursor:gamma glutamyl transpeptidase (cl:gamma-glutamyltransferase) (ec:2.3.2.2) (db:pir2.dat) F69631 F69631 Bacillus subtilis 1423 -11528897 220044 ggt gamma-glutamyltranspeptidase (fn:glutathione metabolism) (db:genpept-bct1) (ec:2.3.2.2) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: pac) (le:222733) (re:224496) (di:direct) BSUB0010 Z99113 g2634224 Bacillus subtilis 1423 -11528897 6000684748 ggt gamma-glutamyltranspeptidase (fn:glutathione metabolism) (db:genpept-bct1) (ec:2.3.2.2) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: pac) (le:3763) (re:5526) (di:direct) BSUB0011 Z99114 g2634235 Bacillus subtilis 1423 -11528897 7500882326 ggt gamma-glutamyltranspeptidase (sr:bacillus subtilis strain=jh642) (db:genpept-bct2) (de:bacillus subtilis gamma-glutamyltranspeptidase (ggt) gene, completecds.) (le:250) (re:2013) (di:direct) BSU49358 U49358 g1491813 Bacillus subtilis 1423 -11528897 5000688473 (de:(ggt) (pn:gamma-glutamyltranspeptidase precursor) (gtcfc:6.16) (ec:2.3.2.2) (ggt_bacsu) (keggfc:6.4:6.5:6.9) (db:gtc-bacillus subtilis)) ggt ggt Bacillus subtilis 1423 10016116

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738714	856	23012	873	290

Description

6500725040 glutathione peroxidase:glutathione peroxidase homolog bsaa (gtcfc:6.16) (keggfc:14.2) (bsorffc:3.3.5) (db:gtc-bacillus subtilis) bsaA bsaA Bacillus subtilis 1423 -11528898 62048 bsaa (de:glutathione peroxidase homolog bsaa) (db:swissprot) BSAA_BACSU P52035 BACILLUS SUBTILIS 1423 -11528898 7000684731 bsaa glutathione peroxidase bsaa (cl:glutathione peroxidase) (db:pir2.dat) E69596 E69596 Bacillus subtilis 1423 -11528898 217089 bsaa stress-associated protein (fn:stress responce) (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:alternate gene name ypgp; 51% identity to citrus) (le:16416) (re:16898) (di:direct) BACYACA L77246 g1256632 Bacillus subtilis 1423 -11528898 7500877944 bsaa glutathione peroxidase (fn:stress response) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:108254) (re:108736) (di:complement) BSUB0012 Z99115 g2634610 Bacillus subtilis 1423 -11528898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738716	857	23013	471	156

Description

GTC ORF with score 105 to: (or:Escherichia coli) (sr:escherichia coli (strain k-12) (clone: plc(2-5,5-8,5-14).) dna) (db:genpept-bct1) (de:e.coli agmatine ureohydrolase (speb) gene, complete cds.) (nt:orf1; putative) (le:271) (re:1287) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738718	858	23014	492	163

Description

6500725041 udp-n-acetylmuramoylalanine d-glutamate ligase:udp-n-acetylmuramoylalanine--d-glutamate ligase:udp-n-acetylmuranoyl-l-alanyl-d-glutamate synthetase (gtcfc:6.7:11.4) (ec:6.3.2.9) (keggfc:6.6:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murD murD Bacillus subtilis 1423 -11528899 7500886118 murd (ec:6.3.2.9) (de:adding enzyme)) (db:swissprot) MURD_BACSU Q03522 BACILLUS SUBTILIS 1423 -11528899 7000685886 murd udp-n-acetylmuramoylalanine--d-glutamate ligase:murd (ec:6.3.2.9) (db:pir2.dat) (mp:133 (degrees)) D47691 D47691 Bacillus subtilis 1423 -11528899 5000688470 murd (fn:peptidoglycan precursor synthesis) (db:genpept-bct1) (ec:6.3.2.9) (de:b.subtilis genes spovd, mure, mray, murd.) (le:2905) (re:4260) (di:direct) BSSPOG Z15056 g580932 Bacillus subtilis 1423 -11528899 219641 murd udp-n-acetylmuramoylalanine d-glutamate ligase (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:6.3.2.9) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:193511) (re:194866) (di:direct) BSUB0008 Z99111 g2633891 Bacillus subtilis 1423 -11528899 84708 murd (ec:6.3.2.9) (de:adding enzyme)) (db:swissprot) MURD_BACSU Q03522 BACILLUS SUBTILIS 1423 -11528899 170656 murd udp-n-acetylmuramoylalanine--d-glutamate ligase:murd (ec:6.3.2.9) (db:pir) (mp:133 (degrees)) D47691 D47691 Bacillus subtilis 1423 -11528899

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738732	859	23015	1215	405

Description

6500725042 ytxf:murc udp-n-acetyl muramate-alanine ligase (gtcfc:6.7:11.4) (ec:6.3.2.8) (keggfc:6.6:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murC murC Bacillus subtilis 1423 -11528900 7500886099 murc (ec:6.3.2.8) (de:acetylmuranoyl-l-alanine synthetase)) (db:swissprot) MURC_BACSU P40778 BACILLUS SUBTILIS 1423 -11528900 7000694890 murc udp-n-acetylmuramate--alanine ligase:murc (ec:6.3.2.8) (db:pir2.dat) C69662 C69662 Bacillus subtilis 1423 -11528900 4000714213 murc putative udp-n-acetylmuramate-alanine ligase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:129638) (re:130936) (di:direct) AF008220 AF008220 g2293216 Bacillus subtilis 1423 -11528900 7500886102 murc udp-n-acetyl muramate-alanine ligase (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:6.3.2.8) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ytxf) (le:49490) (re:50788) (di:complement) BSUB0016 Z99119 g2635463 Bacillus subtilis 1423 -11528900

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738736	860	23016	576	192

Description

6500725043 tms26:tms:tms-26:gcad udp-n-acetylglucosamine pyrophosphorylase:n-acetylglucosamine-1-phosphate uridyltransferase:tms protein (gtcfc:7.1:11.4) (ec:2.7.7.23) (keggfc:4.4) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) gcaD gcaD Bacillus subtilis 1423 -11528901 7000692333 gcad:tms26 udp-n-acetylglucosamine pyrophosphorylase gcad:cell division protein tms26:tms protein (cl:n-acetylglucosamine-1-phosphate uridyltransferase) (db:pir2.dat) S66080 S66080 Bacillus subtilis 1423 -11528901 7500965428 tms26 temperature sensitive cell division (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:119952) (re:121322) (di:direct) BAC180K D26185 g467439 Bacillus subtilis 1423 -11528901 215039 gcad udp-n-acetylglucosamine pyrophosphorylase (fn:peptidoglycan and lipopolysaccharide) (db:genpept-bct1) (ec:2.7.7.23) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: tms, tms26) (le:56350) (re:57720) (di:direct) BSUB0001 Z99104 g2632317 Bacillus subtilis 1423 -11528901 206161 gcad:tms26 udp-n-acetylglucosamine pyrophosphorylase gcad:cell division protein tms26 (db:pir) S66080 S66080 Bacillus subtilis 1423 -11528901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738811	861	23017	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738812	862	23018	861	287

Description

6500725044 hypothetical protein:similar to glucosamine-6-phosphate isomerase (gtcfc:7.1:14.1) (ec:5.3.1.10) (keggfc:4.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfT ybfT Bacillus subtilis 1423 -11528902 7500896729 ybft (de:hypothetical 27.3 kd protein in gltp-cwlj intergenic region) (db:swissprot) YBFT_BACSU O31458 BACILLUS SUBTILIS 1423 -11528902 7000693029 ybft glucosamine-6-phosphate isomerase homolog ybft (cl:glucosamine-6-phosphate isomerase) (db:pir2.dat) E69750 E69750 Bacillus subtilis 1423 -11528902 7500896731 ybft (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glucosamine-6-phosphate isomerase) (le:62162) (re:62911) (di:complement) BSUB0002 Z99105 g2632522 Bacillus subtilis 1423 -11528902 7500896732 ybft (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:59813) (re:60562) (di:complement) AB006424 AB006424 g3599658 Bacillus subtilis 1423 -11528902

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738836	863	23019	684	227

Description

6500725045 ylxc:murb udp-n-acetylenolpyruvoylglucosamine reductase:udp-n-acetylmuramate dehydrogenase (gtcfc:7.1:11.4) (ec:1.1.1.158) (keggfc:4.4) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murB murB Bacillus subtilis 1423 -11528903 84700 murb (ec:1.1.1.158) (de:acetylmuramate dehydrogenase)) (db:swissprot) MURB_BACSU P18579 BACILLUS SUBTILIS 1423 -11528903 170455 murb udp-n-acetylenolpyruvoylglucosamine reductase murb:hypothetical protein murg 3 region (db:pir2.dat) A43727 S26500 Bacillus subtilis 1423 -11528903 7500886096 (sr:bacillus subtilis (clone: lambda-bs1) dna) (db:genpept-bct1) (de:bacillus subtilis (clone lambda-bs1) cell division and sporulationprotein (dds) gene, complete cds.) (nt:orf2) (le:479) (re:1390) (di:direct) BACDDSA M31827 g142833 Bacillus subtilis 1423 -11528903 215484 murb udp-n-acetylenolpyruvoylglucosamine reductase (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:1.1.1.158) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ylxc) (le:197268) (re:198179) (di:direct) BSUB0008 Z99111 g2633894 Bacillus subtilis 1423 -11528903 7000685885 murb udp-n-acetylenolpyruvoylglucosamine reductase murb:hypothetical protein murg 3 region (db:pir) A43727 PC1128 Bacillus subtilis 1423 -11528903 5000688499 (de:(murb) (pn:udp-n-acetylenolpyruvoylglucosamine reductase:udp-n-acetylmuramate dehydrogenase) (gtcfc:7.01) (ec:1.1.1.158) (murb_bacsu) (keggfc:4.4) (db:gtc-bacillus subtilis)) murB murB Bacillus subtilis 1423 10026891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738843	864	23020	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738852	865	23021	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738912	866	23022	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738922	867	23023	834	278

Description

6500725046 n-acetylglucosamine-6-phosphate deacetylase (gtcfc:7.1:11.4) (ec:3.5.1.25) (keggfc:4.4) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) nagA nagA Bacillus subtilis 1423 -11528904 7500886253 naga (ec:3.5.1.25) (de:deacetylase)) (db:swissprot) NAGA_BACSU O34450 BACILLUS SUBTILIS 1423 -11528904 7000694275 naga n-acetylglucosamine-6-phosphate deacetylase naga (db:pir2.dat) A69664 A69664 Bacillus subtilis 1423 -11528904 7500886255 naga n-acetylglucosamine-6-phosphate deacetylase (fn:n-acetyl glucosamine utilization) (db:genpept-bct1) (ec:3.5.1.25) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:194866) (re:196056) (di:direct) BSUB0018 Z99121 g2636014 Bacillus subtilis 1423 -11528904 5500701762 naga n-acetylglucosamine 6-p deacetylase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:31777) (re:32967) (di:complement) AF017113 AF017113 g2618856 Bacillus subtilis 1423 -11528904

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738924	868	23024	465	154

Description

GTC ORF with score 114 to: (sr:epstein-barr virus type 2 misp japanese isolate) (db:genpept-vrl) (de:nuclear antigen-3b {exons berf2a and berf2b} (epstein-barr virus-2ebv-2, misp, japanese isolate, genomic, 3840 nt).) (le:142:577) (re:498:3780) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738927	869	23025	396	132

Description

6500725047 n-acetylglucosamine-6-phosphate isomerase (gtcfc:7.1:11.4) (ec:5.3.1.10) (keggfc:4.4) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) nagB nagB Bacillus subtilis 1423 -11528905 7500886264 nagb (ec:5.3.1.10) (de:phosphate deaminase) (gnpda)) (db:swissprot) NAGB_BACSU O35000 BACILLUS SUBTILIS 1423 -11528905 7000694276 nagb n-acetylglucosamine-6-phosphate isomerase nagb (cl:glucosamine-6-phosphate isomerase) (db:pir2.dat) B69664 B69664 Bacillus subtilis 1423 -11528905 7500886266 nagb n-acetylglucosamine-6-phosphate isomerase (fn:n-acetyl glucosamine utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:196053) (re:196781) (di:direct) BSUB0018 Z99121 g2636015 Bacillus subtilis 1423 -11528905 5500701761 nagb glucosamine-6-p isomerase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (nt:glucosamine-6-p deaminase) (le:31052) (re:31780) (di:complement) AF017113 AF017113 g2618855 Bacillus subtilis 1423 -11528905

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738928	870	23026	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738930	871	23027	591	197

Description

6500725048 hypothetical protein:putative udp-n-acetylglucosamine 2-epimerase:udp-glcnac-2-epimerase (gtcfc:7.1:14.1) (ec:5.1.3.14) (keggfc:4.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yvyH yvyH Bacillus subtilis 1423 -11528906 219381 yvyh (ec:5.1.3.14) (de:glcnac-2-epimerase)) (db:swissprot) YVYH_BACSU P39131 BACILLUS SUBTILIS 1423 -11528906 7000688633 yvyh udp-n-acetylglucosamine 2-epimerase homolog yvyh (db:pir2.dat) D70049 D70049 Bacillus subtilis 1423 -11528906 5000688504 orfx unknown (db:genpept-bct1) (de:b.subtilis lytr, orfx, and gtab genes.) (nt:similar to escherichia coli o389 gene product,) (le:193) (re:1335) (di:complement) BSLYTGTA Z22516 g405622 Bacillus subtilis 1423 -11528906 7500952870 yvyh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to udp-n-acetylglucosamine 2-epimerase) (le:66211) (re:67353) (di:complement) BSUB0019 Z99122 g2636092 Bacillus subtilis 1423 -11528906 116617 yvyh (ec:5.1.3.14) (de:glcnac-2-epimerase)) (db:swissprot) YVYH_BACSU P39131 BACILLUS SUBTILIS 1423 -11528906

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501738932	872	23028	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739018	873	23029	216	72

Description

6500725049 udp-n-acetylglucosamine 1-carboxyvinyltransferase (gtcfc:7.1:11.4) (ec:2.5.1.7) (keggfc:4.4) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murA murA Bacillus subtilis 1423 -11528907 7000694889 mura udp-n-acetylglucosamine 1-carboxyvinyltransferase mura (cl:udp-n-acetylglucosamine 1-carboxyvinyltransferase murz) (db:pir2.dat) A69662 A69662 Bacillus subtilis 1423 -11528907 219026 mura udp-n-acetylglucosamine (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:1943) (re:3253) (di:direct) BSATPC Z81356 g1648861 Bacillus subtilis 1423 -11528907 304079 mura udp-n-acetylglucosamine (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:2.5.1.7) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:179914) (re:181224) (di:complement) BSUB0019 Z99122 g2636201 Bacillus subtilis 1423 -11528907

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739019	874	23030	1053	351

Description

6500725050 lssf:rev-4:mura:murz udp-n-acetylglucosamine 1-carboxyvinyltransferase:probable udp-n-acetylglucosamine 1-carboxyvinyltransferase:enoylpyruvate transferase:udp-n-acetylglucosamine enolpyruvyl transferase:ept (gtcfc:7.1:11.4) (ec:2.5.1.7) (keggfc:4.4) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murZ murZ Bacillus subtilis 1423 -11528908 304116 mura:murz (ec:2.5.1.7) (de:enolpyruvyl transferase) (ept)) (db:swissprot) MURA_BACSU P19670 BACILLUS SUBTILIS 1423 -11528908 170655 murz udp-n-acetylglucosamine 1-carboxyvinyltransferase:murz (cl:udp-n-acetylglucosamine 1-carboxyvinyltransferase murz) (ec:2.5.1.7) (db:pir2.dat) G32354 S55428 Bacillus subtilis 1423 -11528908 5000688498 murz udp-n-acetylglucosamine (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:14403) (re:15692) (di:direct) BSDNA320D Z49782 g853767 Bacillus subtilis 1423 -11528908 7500886090 murz udp-n-acetylglucosamine (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:2.5.1.7) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: murz, lssf, rev-4) (le:208051) (re:209340) (di:complement) BSUB0019 Z99122 g2636235 Bacillus subtilis 1423 -11528908 6000684913 murz udp-n-acetylglucosamine (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:2.5.1.7) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: murz, lssf, rev-4) (le:6741) (re:8030) (di:complement) BSUB0020 Z99123 g2636247 Bacillus subtilis 1423 -11528908 84694 mura:murz (ec:2.5.1.7) (de:enolpyruvyl transferase) (ept)) (db:swissprot) MURA_BACSU P19670 BACILLUS SUBTILIS 1423 -11528908 7000685883 murz udp-n-acetylglucosamine 1-carboxyvinyltransferase:murz (ec:2.5.1.7) (db:pir) G32354 G32354 Bacillus subtilis 1423 -11528908 219144 murz udp-n-acetylglucosamine (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:2.5.1.7) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: murz, lssf, rev-4) (le:6741) (re:8030) (di:complement) BSUB0020 Z99123 g2636247 Bacillus subtilis 1423 -11528908

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739026	875	23031	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739035	876	23032	798	266

Description

6500725051 hypothetical protein:similar to dolichol phosphate mannose synthase (gtcfc:7.1:11.3:14.1) (ec:2.4.1.83) (keggfc:7.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykcC ykcC Bacillus subtilis 1423 -11528909 7500938421 ykcc (de:hypothetical 37.4 kd protein in spoiisa-htra intergenic region) (db:swissprot) YKCC_BACSU O34319 BACILLUS SUBTILIS 1423 -11528909 7000692954 ykcc dolichol phosphate mannose synthase homolog ykcc (cl:stress response protein csbb) (db:pir2.dat) E69855 E69855 Bacillus subtilis 1423 -11528909 6000689732 ykcc ykcc (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:putative dolichol phosphate mannose synthetase) (le:8574) (re:9545) (di:direct) BSAJ2571 AJ002571 g2632010 Bacillus subtilis 1423 -11528909 7500938424 ykcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to dolichol phosphate mannose synthase) (le:161523) (re:162494) (di:direct) BSUB0007 Z99110 g2633643 Bacillus subtilis 1423 -11528909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739047	877	23033	807	269

Description

5000688506 rodd:gtaa:gtad:tage udp-glucose polyglycerol phosphate glucosyltransferase:probable poly:glycerol-phosphate alpha-glucosyltransferase:teichoic acid biosynthesis protein e (gtcfc:7.1:11.3:11.4) (ec:2.4.1.52) (keggfc:7.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagE tagE Bacillus subtilis 1423 -11528910 7500892734 tage:rodd:gtaa (ec:2.4.1.52) (de:(ec 2.4.1.52) (teichoic acid biosynthesis protein e)) (db:swissprot) TAGE_BACSU P13484 BACILLUS SUBTILIS 1423 -11528910 7000686747 tage:rodd poly glycerol-phosphate alpha-glucosyltransferase:tage:probable rodd protein:udp-glucose--polyglycerol phosphate glucosyltransferase tage (ec:2.4.1.52) (db:pir2.dat) (mp:310 degrees) S06048 S06048 Bacillus subtilis 1423 -11528910 219599 (db:genpept-bct1) (de:bacillus subtilis rodc operon.) (nt:rodd (gtaa) polypeptide (aa 1-673)) (le:157) (re:2178) (di:direct) BSRODC X15200 g580920 Bacillus subtilis 1423 -11528910 6500725052 tage udp-glucose:polyglycerol phosphate (fn:teichoic acid biosynthesis) (db:genpept-bct1) (ec:2.4.1.52) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: rodd, gtaa, gtad) (le:80369) (re:82390) (di:complement) BSUB0019 Z99122 g2636099 Bacillus subtilis 1423 -11528910 100419 tage:rodd:gtaa (ec:2.4.1.52) (de:(ec 2.4.1.52) (teichoic acid biosynthesis protein e)) (db:swissprot) TAGE_BACSU P13484 BACILLUS SUBTILIS 1423 -11528910 170460 tage:rodd poly glycerol-phosphate alpha-glucosyltransferase:tage:probable rodd protein:udp-glucose--polyglycerol phosphate glucosyltransferase tage (ec:2.4.1.52) (db:pir) (mp:310 degrees) S06048 S06048 Bacillus subtilis 1423 -11528910

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739105	878	23034	282	93

Description

GTC ORF with score 282 to: (fn:activates signaling pathway for fungal growth) (sr:emericella nidulans strain=fgsc4) (db:genpept-pln2) (de:emericella nidulans fada (fada) gene, complete cds.) (nt:a heterotrimeric g protein alpha subunit (i);) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739115	879	23035	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739122	880	23036	435	145

Description

6500725053 hypothetical protein:similar to cdp-glucose 4:6-dehydratase (gtcfc:7.2:14.1) (ec:4.2.1.45) (keggfc:7.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnG yfnG Bacillus subtilis 1423 -11528911 7000692332 yfng cdp-glucose 4:6-dehydratase homolog yfng (cl:udpglucose 4-epimerase homology) (db:pir2.dat) B69815 B69815 Bacillus subtilis 1423 -11528911 1500696649 yfng (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to cdp-glucose 4,6-dehydratase) (le:198111) (re:199016) (di:direct) BSUB0004 Z99107 g2633041 Bacillus subtilis 1423 -11528911 7500963500 yfng (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:14175) (re:15080) (di:complement) D86418 D86418 g2116765 Bacillus subtilis 1423 -11528911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739125	881	23037	603	201

Description

6500725054 phoaiii:phob alkaline phosphatase iii:alkaline phosphatase iii precursor:apase iii (gtcfc:8.1:9.13:9.6:13.10) (ec:3.1.3.1) (keggfc:8.1:9.7:9.12) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of complex lipids-glycerolipid metabolism:metabolism of cofactors and vitamins-other cofactors:metabolism of cofactors and vitami... phoB phoB Bacillus subtilis 1423 -11528912 7000692175 phob:phoaiii alkaline phosphatase:iii precursor:alkaline phosphatase b phob (cl:alkaline phosphatase) (ec:3.1.3.1) (db:pir2.dat) C69676 C69676 Bacillus subtilis 1423 -11528912 1500693332 phob alkaline phosphatase iii (db:genpept-bct1) (ec:3.1.3.1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: phoaiii) (le:19113) (re:20501) (di:complement) BSUB0004 Z99107 g2632887 Bacillus subtilis 1423 -11528912 7500954200 phob (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis alkaline phosphatase iiia; p19405) (le:6115) (re:7503) (di:complement) D88802 D88802 g1945090 Bacillus subtilis 1423 -11528912

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739139	882	23038	315	104

Description

6500725055 phoaiv:phoa alkaline phosphatase a:alkaline phosphatase iv precursor:apase iv (gtcfc:8.1:9.13:9.6:13.10) (ec:3.1.3.1) (keggfc:8.1:9.7:9.12) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of complex lipids-glycerolipid metabolism:metabolism of cofactors and vitamins-other cofactors:metabolism of cofactors and vitami... phoA phoA Bacillus subtilis 1423 -11528913 90708 phoa:phoaiv (ec:3.1.3.1) (de:alkaline phosphatase iv precursor, (apase iv)) (db:swissprot) PPB4_BACSU P19406 BACILLUS SUBTILIS 1423 -11528913 7000686160 phoa:phoaiv alkaline phosphatase:iv precursor:alkaline phosphatase a phoa:alkaline phosphomonoesterase:glycerophosphatase:phosphomonoesterase (cl:alkaline phosphatase) (ec:3.1.3.1) (db:pir2.dat) (mp:73 min) B69676 B69676 Bacillus subtilis 1423 -11528913 219758 phoa alkaline phosphatase a (db:genpept-bct1) (de:bacillus subtilis jh642 alkaline phosphatase a (phoa) gene,complete cds.) (nt:gene name was formerly phoaiv) (le:509) (re:1894) (di:direct) BSU02550 U02550 g470383 Bacillus subtilis 1423 -11528913 4000707259 phoa alkaline phosphatase a (db:genpept-bct1) (ec:3.1.3.1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: phoaiv) (le:17035) (re:18420) (di:complement) BSUB0006 Z99109 g2633276 Bacillus subtilis 1423 -11528913 7500888336 phoaiv alkaline phosphatase (fn:catalytic activity: an orthophosphoric) (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:see subtilist bg10183, embl u02550 and swiss prot) (le:3683) (re:5068) (di:complement) BSY14082 Y14082 g2226197 Bacillus subtilis 1423 -11528913 5000688531 (de:(phoa) (pn:alkaline phosphatase iv precursor:alkaline phosphatase iv precursor :apase iv) (gn:phoaiv) (gtcfc:9.06:9.13) (ec:3.1.3.1) (ppb4_bacsu) (keggfc:8.1:9.7:9.12) (bsorffc:2.3.0) (db:gtc-bacillus subtilis)) phoA phoA Bacillus subtilis 1423 10032823

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739143	883	23039	276	91

Description

GTC ORF with score 131 to: (fn:involved in transcriptional activation) (sr:saccharomyces cerevisiae (strain ybp1) dna) (db:genpept-pln1) (de:yeast putative transcriptional activator (ada2) gene, complete cds.) (le:308) (re:1612) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739219	884	23040	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739230	885	23041	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739236	886	23042	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739240	887	23043	363	120

Description

6500725056 hypothetical protein:similar to glycerophosphodiester phosphodiesterase (gtcfc:8.1:8.4:14.1) (ec:3.1.4.46) (keggfc:8.1:8.4) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdW yhdW Bacillus subtilis 1423 -11528914 7000693060 yhdw glycerophosphodiester phosphodiesterase homolog yhdw (db:pir2.dat) E69827 E69827 Bacillus subtilis 1423 -11528914 4000714623 yhdw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to glycerophosphodiester phosphodiesterase) (le:37668) (re:38399) (di:complement) BSUB0006 Z99109 g2633297 Bacillus subtilis 1423 -11528914 7500964032 yhdw hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to glycerol diester phosphodiesterase) (le:24316) (re:25047) (di:complement) BSY14082 Y14082 g2226218 Bacillus subtilis 1423 -11528914

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739250	888	23044	300	100

Description

6500725057 iol:idh:e83g:iolg myo-inositol 2-dehydrogenase (gtcfc:8.2) (ec:1.1.1.18) (keggfc:14.1) (bsorffc:7.7.1) (db:gtc-bacillus subtilis) iolG iolG Bacillus subtilis 1423 -11528915 83697 idh:iolg:e83g (ec:1.1.1.18) (de:myo-inositol 2-dehydrogenase,) (db:swissprot) MI2D_BACSU P26935 BACILLUS SUBTILIS 1423 -11528915 7000685848 iolg:idh myo-inositol 2-dehydrogenase:iolg:inositol dehydrogenase (ec:1.1.1.18) (db:pir2.dat) JH0511 JH0511 Bacillus subtilis 1423 -11528915 7500885624 idh inositol dehydrogenase (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis inositol dehydrogenase (idh) gene.) (le:527) (re:1561) (di:direct) BACIDH M76431 g143086 Bacillus subtilis 1423 -11528915 303048 e83g::idh myo-inositol dehydrogenase (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (le:7360) (re:8394) (di:direct) BACIOLO D14399 g709987 Bacillus subtilis 1423 -11528915 215916 iolg myo-inositol 2-dehydrogenase (fn:myo-inositol catabolism) (db:genpept-bct1) (ec:1.1.1.18) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: iol, idh) (le:75295) (re:76329) (di:complement) BSUB0021 Z99124 g2636516 Bacillus subtilis 1423 -11528915 170358 iolg:idh myo-inositol 2-dehydrogenase:iolg:inositol dehydrogenase (ec:1.1.1.18) (db:pir) JH0511 JH0511 Bacillus subtilis 1423 -11528915 215899 e83g::idh myo-inositol dehydrogenase (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (le:7360) (re:8394) (di:direct) BACIOLO D14399 g709987 Bacillus subtilis 1423 -11528915 5000688480 (de:(idh) (pn:myo-inositol 2-dehydrogenase) (gn:iolg:e83g) (gtcfc:7.01) (ec:1.1.1.18) (mi2d_bacsu) (keggfc:11.1) (bsorffc:2.1.0) (db:gtc-bacillus subtilis)) idh idh Bacillus subtilis 1423 10025911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739252	889	23045	456	151

Description

5000688780 yxdf:e83f:iolf inositol transport protein:hypothetical metabolite transport protein in idh 5region (gtcfc:8.2:12.2) (keggfc:14.2) (bsorffc:1.1.2:7.7.1) (db:gtc-bacillus subtilis) iolF iolF Bacillus subtilis 1423 -11528916 116792 yxdf:e83f (de:hypothetical metabolite transport protein in idh 5'region) (db:swissprot) YXDF_BACSU P42417 BACILLUS SUBTILIS 1423 -11528916 7000688730 iolf inositol transport protein iolf (db:pir2.dat) F69645 F69645 Bacillus subtilis 1423 -11528916 215915 e83f hypothetical protein (sr:bacillus subtilis (strain:bgsc 1a1 (168 trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis 15 kb chromosome segment contains the iol operon.) (nt:homologous to quinolone resistant protein nora;) (le:6018) (re:7337) (di:direct) BACIOLO D14399 g709986 Bacillus subtilis 1423 -11528916 303047 iolf inositol transport protein (fn:myo-inositol catabolism) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxdf) (le:76352) (re:77671) (di:complement) BSUB0021 Z99124 g2636517 Bacillus subtilis 1423 -11528916 6500725058 yxdf:e83f inositol transport protein:hypothetical metabolite transport protein in idh 5region (gtcfc:8.2:12.2) (keggfc:14.2) (bsorffc:1.1.2:7.7.1) (db:gtc-bacillus subtilis) iolF iolF Bacillus subtilis 1423 -11528916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739267	890	23046	762	254

Description

GTC ORF with score 216 to: (db:genpept) (de:aureobasidium pullulans cosmid ppsr-22 hydroxylase, multidrugresistance-like protein (apmdr1), and peptide synthetase genes,complete cds.) (le:13308:13350:13743:13878) (re:19541:19541:19541:19541) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739268	891	23047	555	184

Description

GTC ORF with score 256 to: (db:genpept) (de:aureobasidium pullulans cosmid ppsr-22 hydroxylase, multidrugresistance-like protein (apmdr1), and peptide synthetase genes,complete cds.) (le:13308:13350:13743:13878) (re:19541:19541:19541:19541) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739347	892	23048	954	317

Description

5000688363 mmsa:yxda:e83a:iola methylmalonate-semialdehyde dehydrogenase:probable methylmalonate-semialdehyde dehydrogenase:acylating:mmsdh (gtcfc:8.2) (ec:1.2.1.27) (keggfc:14.1) (bsorffc:7.7.1) (db:gtc-bacillus subtilis) iolA iolA Bacillus subtilis 1423 -11528917 83922 mmsa:iola:e83a (ec:1.2.1.27) (de:(ec 1.2.1.27) (mmsdh)) (db:swissprot) MMSA_BACSU P42412 BACILLUS SUBTILIS 1423 -11528917 7000685857 iola methylmalonate-semialdehyde dehydrogenase iola (db:pir2.dat) A69645 A69645 Bacillus subtilis 1423 -11528917 215758 iola (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:highly similar to methylmalonate-semialdehyde) (le:34696) (re:36159) (di:direct) AB005554 AB005554 g904207 Bacillus subtilis 1423 -11528917 7500885696 iola methylmalonate-semialdehyde dehydrogenase (fn:myo-inositol catabolism) (db:genpept-bct1) (ec:1.2.1.27) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: mmsa, yxda) (le:82433) (re:83896) (di:complement) BSUB0021 Z99124 g2636522 Bacillus subtilis 1423 -11528917 6500725059 mmsa:yxda:e83a methylmalonate-semialdehyde dehydrogenase:probable methylmalonate-semialdehyde dehydrogenase:acylating:mmsdh (gtcfc:8.2) (ec:1.2.1.27) (keggfc:14.1) (bsorffc:7.7.1) (db:gtc-bacillus subtilis) iolA iolA Bacillus subtilis 1423 -11528917

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739350	893	23049	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739354	894	23050	738	246

Description

GTC ORF with score 294 to: (sr:baker's yeast) (db:genpept-pln2) (de:skt5 (skt5)=protoplast regeneration and killer toxin resistancegene (saccharomyces cerevisiae, genomic mutant, 2177 nt).) (nt:protoplast regeneration and killer toxin resistance) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739431	895	23051	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739438	896	23052	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739443	897	23053	777	258

Description

6500725060 thic:thia hypothetical protein:thiamin biosynthesis protein (gtcfc:9.1) (keggfc:14.2) (bsorffc:3.4.3) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-thiamine metabolism (vitamin b1)) thiA thiA Bacillus subtilis 1423 -11528918 7500893044 thic:thia (de:thiamin biosynthesis protein thic) (db:swissprot) THIC_BACSU P45740 BACILLUS SUBTILIS 1423 -11528918 7000692285 thia biosynthesis of the pyrimidine moiety of thiamin thia (db:pir2.dat) D69722 D69722 Bacillus subtilis 1423 -11528918 7500893046 thia (fn:biosynthesis of the pyrimidine moiety of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:152583) (re:154355) (di:direct) BSUB0005 Z99108 g2633202 Bacillus subtilis 1423 -11528918 220384 thia 65.9 kd protein (fn:involved in the biosynthesis of the pyrimidine) (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:19433) (re:21205) (di:direct) BSZ82044 Z82044 g1673401 Bacillus subtilis 1423 -11528918

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739451	898	23054	204	67

Description

6500725061 uroporphyrinogen iii decarboxylase:uroporphyrinogen decarboxylase:upd (gtcfc:9.10) (ec:4.1.1.37) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemE hemE Bacillus subtilis 1423 -11528919 68141 heme (ec:4.1.1.37) (de:uroporphyrinogen decarboxylase, (upd)) (db:swissprot) DCUP_BACSU P32395 BACILLUS SUBTILIS 1423 -11528919 7000684994 heme uroporphyrinogen decarboxylase:heme:uroporphyrinogen iii decarboxylase heme (cl:uroporphyrinogen decarboxylase) (ec:4.1.1.37) (db:pir2.dat) B47045 B47045 Bacillus subtilis 1423 -11528919 7500880097 heme uroporphyrinogen decarboxylase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (ec:4.1.1.37) (de:bacillus subtilis penicillin binding protein 1a (pona) gene;uroporphyrinogen decarboxylase (heme) gene; ferrochelatase (hemh)gene complete cds, (hemy) gene, complete cds; orfa... BACHEMEHY M97208 g143043 Bacillus subtilis 1423 -11528919 215830 heme uroporphyrinogen iii decarboxylase (fn:porphyrin biosynthesis) (db:genpept-bct1) (ec:4.1.1.37) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:86090) (re:87151) (di:direct) BSUB0006 Z99109 g2633348 Bacillus subtilis 1423 -11528919 4000707031 heme uroporphyrinogen iii decarboxylase (db:genpept-bct2) (ec:4.1.1.37) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p32395; dcup_bacsu.) (le:5949) (re:7010) (di:direct) BSY14083 Y14083 g2226230 Bacillus subtilis 1423 -11528919 170661 heme uroporphyrinogen decarboxylase:heme:uroporphyrinogen iii decarboxylase heme (ec:4.1.1.37) (db:pir) B47045 B47045 Bacillus subtilis 1423 -11528919 5000688547 (de:(heme) (pn:uroporphyrinogen decarboxylase:uroporphyrinogen decarboxylase :upd) (gtcfc:9.10) (ec:4.1.1.37) (dcup_bacsu) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis)) hemE hemE Bacillus subtilis 1423 10010734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739452	899	23055	234	78

Description

GTC ORF with score 131 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739467	900	23056	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739474	901	23057	864	287

Description

6500725062 hemf:hemh ferrochelatase:protoheme ferro-lyase:heme synthetase (gtcfc:9.10) (ec:4.99.1.1) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemH hemH Bacillus subtilis 1423 -11528920 76775 hemh:hemf (ec:4.99.1.1) (de:synthetase)) (db:swissprot) HEMZ_BACSU P32396 BACILLUS SUBTILIS 1423 -11528920 7000685516 hemh ferrochelatase:hemh (ec:4.99.1.1) (db:pir2.dat) C47045 C47045 Bacillus subtilis 1423 -11528920 7500883206 hemh ferrochelatase (fn:iron is inserted into protoporphyrin ix giving) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (ec:4.99.1.1) (de:bacillus subtilis penicillin binding protein 1a (pona) gene;uroporphyrinogen decarboxylase (heme) gene; ferrochelatase (hem... BACHEMEHY M97208 g143044 Bacillus subtilis 1423 -11528920 215831 hemh ferrochelatase (fn:incorporation of iron into protoporphyrin ix) (db:genpept-bct1) (ec:4.99.1.1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: hemf) (le:87223) (re:88155) (di:direct) BSUB0006 Z99109 g2633349 Bacillus subtilis 1423 -11528920 4000707120 hemh ferrochelatase ec 4.99.1.1:incorporation of (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p32396; hemz_bacsu.) (le:7082) (re:8014) (di:direct) BSY14083 Y14083 g2226231 Bacillus subtilis 1423 -11528920 206169 hemh ferrochelatase:hemh (ec:4.99.1.1) (db:pir) C47045 C47045 Bacillus subtilis 1423 -11528920 5000688549 (de:(hemh) (pn:ferrochelatase:ferrochelatase :protoheme ferro-lyase:heme synthetase) (gn:hemf) (gtcfc:9.10) (ec:4.99.1.1) (hemz_bacsu) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis)) hemH hemH Bacillus subtilis 1423 10019138

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739545	902	23058	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739546	903	23059	219	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739550	904	23060	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739564	905	23061	657	218

Description

5000688548 hemg:hemy protoporphyrinogen ix and coproporphyrinogen iii oxidase:protoporphyrinogen oxidase:ppo (gtcfc:9.10) (ec:1.3.3.4) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemY hemY Bacillus subtilis 1423 -11528921 76730 hemy:hemg (ec:1.3.3.4) (de:protoporphyrinogen oxidase, (ppo)) (db:swissprot) PPOX_BACSU P32397 BACILLUS SUBTILIS 1423 -11528921 7000685512 hemy coproporphyrinogen iii oxidase / protoporphyrinogen ix oxidase hemy (db:pir2.dat) D47045 D47045 Bacillus subtilis 1423 -11528921 7500883182 hemy (fn:involved in a late step of protoheme ix) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis penicillin binding protein 1a (pona) gene;uroporphyrinogen decarboxylase (heme) gene; ferrochelatase (hemh)gene complete cds, ... BACHEMEHY M97208 g143045 Bacillus subtilis 1423 -11528921 215832 hemy protoporphyrinogen ix and coproporphyrinogen iii (fn:late steps of protoheme ix synthesis (porphyrin) (db:genpept-bct1) (ec:1.3.3.4) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: hemg) (le:88170) (re:89582) (di:direct) BSUB0006 Z99109 g2633350 Bacillus subtilis 1423 -11528921 4000707119 hemy protoporphyrinogen ix oxidase (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p32397; hemg_bacsu.) (le:8029) (re:9441) (di:direct) BSY14083 Y14083 g2226232 Bacillus subtilis 1423 -11528921 169940 hemy coproporphyrinogen iii oxidase / protoporphyrinogen ix oxidase hemy (db:pir) D47045 D47045 Bacillus subtilis 1423 -11528921 6500725063 hemg protoporphyrinogen ix and coproporphyrinogen iii oxidase:protoporphyrinogen oxidase:ppo (gtcfc:9.10) (ec:1.3.3.4) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemY hemY Bacillus subtilis 1423 -11528921

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739679	906	23062	423	140

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739682	907	23063	870	290

Description

6500725064 hypothetical protein:similar to uroporphyrin-iii c-methyltransferase (gtcfc:9.10:14.1) (ec:2.1.1.107) (keggfc:9.10) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylnD ylnD Bacillus subtilis 1423 -11528922 7000694895 ylnd uroporphyrin-iii c-methyltransferase homolog ylnd (cl:s-adenosyl-l-methionine uroporphyrinogen methyltransferase) (db:pir2.dat) D69877 D69877 Bacillus subtilis 1423 -11528922 5500687778 ylnd putative s-adenosyl l-methionine (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (le:4227) (re:5000) (di:direct) BSPYREYLO AJ000974 g2462960 Bacillus subtilis 1423 -11528922 7500965432 ylnd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to uroporphyrin-iii c-methyltransferase) (le:35040) (re:35813) (di:direct) BSUB0009 Z99112 g2633934 Bacillus subtilis 1423 -11528922

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739696	908	23064	201	66

Description

6500725065 delta-aminolevulinic acid dehydratase:porphobilinogen synthase:alad:aladh (gtcfc:9.10) (ec:4.2.1.24) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemB hemB Bacillus subtilis 1423 -11528923 76479 hemb (ec:4.2.1.24) (de:synthase) (alad) (aladh)) (db:swissprot) HEM2_BACSU P30950 BACILLUS SUBTILIS 1423 -11528923 7000685506 hemb porphobilinogen synthase:hemb:delta-aminolevulinic acid dehydratase hemb (cl:porphobilinogen synthase) (ec:4.2.1.24) (db:pir2.dat) C42728 C42728 Bacillus subtilis 1423 -11528923 7500883144 hemb aminolevulinic acid dehydratase (fn:porphobilinogen synthesis) (sr:b.subtilis dna) (db:genpept-bct1) (ec:4.2.1.24) (de:bacillus subtilis hemaxcdbl gene cluster.) (le:4189) (re:5163) (di:direct) BACHEMAXC M57676 g143039 Bacillus subtilis 1423 -11528923 215827 hemb delta-aminolevulinic acid dehydratase (fn:porphyrin biosynthesis) (db:genpept-bct1) (ec:4.2.1.24) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:78172) (re:79146) (di:complement) BSUB0015 Z99118 g2635278 Bacillus subtilis 1423 -11528923 141925 hemb porphobilinogen synthase:hemb:delta-aminolevulinic acid dehydratase hemb (cl:porphobilinogen synthase) (ec:4.2.1.24) (db:pir) C42728 C42728 Bacillus subtilis 1423 -11528923 5000688544 (de:(hemb) (pn:delta-aminolevulinic acid dehydratase:alad:aladh:delta-aminolevulinic acid dehydratase :porphobilinogen synthase:alad:aladh) (gtcfc:9.10) (ec:4.2.1.24) (hem2_bacsu) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus) hemB hemB Bacillus subtilis 1423 10018842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739701	909	23065	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739704	910	23066	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739712	911	23067	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739804	912	23068	969	323

Description

6500725066 uroporphyrinogen iii cosynthase:uroporphyrinogen-iii synthase:uros:uroporphyrinogen-iii cosynthetase:hydroxymethylbilane hydrolyase:cyclizing (gtcfc:9.10) (ec:4.2.1.75) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemD hemD Bacillus subtilis 1423 -11528924 76510 hemd (ec:4.2.1.75) (de:iii cosynthetase) (hydroxymethylbilane hydrolyase (cyclizing))) (db:swissprot) HEM4_BACSU P21248 BACILLUS SUBTILIS 1423 -11528924 7000685509 hemd uroporphyrinogen-iii synthase:hemd:uroporphyrinogen iii cosynthase hemd (ec:4.2.1.75) (db:pir2.dat) B42728 B42728 Bacillus subtilis 1423 -11528924 7500883159 hemd uroporphyrinogen iii synthase (sr:b.subtilis dna) (db:genpept-bct1) (ec:4.2.1.24) (de:bacillus subtilis hemaxcdbl gene cluster.) (le:3404) (re:4192) (di:direct) BACHEMAXC M57676 g143038 Bacillus subtilis 1423 -11528924 215826 hemd uroporphyrinogen iii cosynthase (fn:cyclisation of hydroxymethylbilane (porphyrin) (db:genpept-bct1) (ec:4.2.1.75) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:79143) (re:79931) (di:complement) BSUB0015 Z99118 g2635279 Bacillus subtilis 1423 -11528924 170663 hemd uroporphyrinogen-iii synthase:hemd:uroporphyrinogen iii cosynthase hemd (ec:4.2.1.75) (db:pir) B42728 B42728 Bacillus subtilis 1423 -11528924 5000688546 (de:(hemd) (pn:uroporphyrinogen-iii synthase:uros:uroporphyrinogen-iii cosynthetase:uroporphyrinogen-iii synthase :uros:uroporphyrinogen- iii cosynthetase:hydroxymethylbilane hydrolyase:cyclizing) (gtcfc:9.10) (ec:4.2.1.75) (hem4) hemD hemD Bacillus subtilis 1423 10018873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739814	913	23069	195	64

Description

6500725067 porphobilinogen deaminase:pbg:hydroxymethylbilane synthase:hmbs:pre-uroporphyrinogen synthase (gtcfc:9.10) (ec:4.3.1.8) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemC hemC Bacillus subtilis 1423 -11528925 76497 hemc (ec:4.3.1.8) (de:synthase) (hmbs) (pre-uroporphyrinogen synthase)) (db:swissprot) HEM3_BACSU P16616 BACILLUS SUBTILIS 1423 -11528925 125703 hemc hydroxymethylbilane synthase::porphobilinogen deaminase hemc:pre-uroporphyrinogen synthase (cl:hydroxymethylbilane synthase) (ec:4.3.1.8) (db:pir1.dat) IBBS C35252 Bacillus subtilis 1423 -11528925 215825 hemc porphobilinogen deaminase (fn:hydroxymethylbilane synthesis from) (sr:b.subtilis dna) (db:genpept-bct1) (ec:4.3.1.8) (de:bacillus subtilis hemaxcdbl gene cluster.) (le:2470) (re:3414) (di:direct) BACHEMAXC M57676 g143037 Bacillus subtilis 1423 -11528925 7500883152 hemc porphobilinogen deaminase hydroxymethylbilane (fn:hydroxymethylbilane synthesis from) (db:genpept-bct1) (ec:4.3.1.8) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:79921) (re:80865) (di:complement) BSUB0015 Z99118 g2635280 Bacillus subtilis 1423 -11528925 5000688545 (de:(hemc) (pn:porphobilinogen deaminase:pbg:hmbs:porphobilinogen deaminase :pbg:hydroxymethylbilane synthase:hmbs:pre-uroporphyrinogen synthase) (gtcfc:9.10) (ec:4.3.1.8) (hem3_bacsu) (keggfc:9.10) (bsorffc:3.4.7) (db:gtc-baci) hemC hemC Bacillus subtilis 1423 10018860

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739815	914	23070	192	63

Description

6500725068 heme-containing membrane protein:cytochrome aa3 controlling protein (gtcfc:9.10) (keggfc:14.2) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) ctaA ctaA Bacillus subtilis 1423 -11528926 66712 ctaa (de:cytochrome aa3 controlling protein) (db:swissprot) CTAA_BACSU P12946 BACILLUS SUBTILIS 1423 -11528926 7000684934 ctaa cytochrome caa3 oxidase ctaa (cl:cytochrome caa3 oxidase ctaa) (db:pir2.dat) A33960 A33960 Bacillus subtilis 1423 -11528926 7500879521 ctaa (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis (py79, w168), (clone pa1503) cytochrome aa3controlling protein (ctaa) gene, complete cds.) (nt:cytochrome aa3 controlling protein) (le:136) (re:1056) (di:... BACCOXCA M23915 g142717 Bacillus subtilis 1423 -11528926 215393 ctaa ctaa protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:3166) (re:4086) (di:complement) BS16823KB Z98682 g2339990 Bacillus subtilis 1423 -11528926 5500684523 ctaa heme-containing membrane protein (fn:required for biosynthesis of cytochrome caa3) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:162649) (re:163569) (di:complement) BSUB0008 Z99111 g2633858 Bacillus subtilis 1423 -11528926 169942 ctaa cytochrome caa3 oxidase ctaa (db:pir) A33960 A33960 Bacillus subtilis 1423 -11528926

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739816	915	23071	666	222

Description

6500725069 yqer:hemn coproporphyrinogen iii oxidase:probable oxygen-independent coproporphyrinogen iii oxidase:coproporphyrinogenase:coprogen oxidase (gtcfc:9.10) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemN hemN Bacillus subtilis 1423 -11528927 7000692880 hemn coproporphyrinogen iii oxidase hemn (cl:oxygen-independent coproporphyrinogen oxidase) (db:pir2.dat) B69640 B69640 Bacillus subtilis 1423 -11528927 216049 yqer (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:88757) (re:89857) (di:direct) BACJH642 D84432 g1303805 Bacillus subtilis 1423 -11528927 7500953843 hemn coproporphyrinogen iii oxidase (fn:porphyrin biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqer) (le:29573) (re:30673) (di:complement) BSUB0014 Z99117 g2634996 Bacillus subtilis 1423 -11528927

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739823	916	23072	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739828	917	23073	249	83

Description

GTC ORF with score 113 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1086.) (nt:similar to saccharomyces cerevisiae orf yor091w,) (le:<1) (re:870) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739834	918	23074	1080	360

Description

5000688552 membrane-bound protein:hemx protein (gtcfc:9.10) (keggfc:14.2) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemX hemX Bacillus subtilis 1423 -11528928 76768 hemx (de:hemx protein) (db:swissprot) HEMX_BACSU P16645 BACILLUS SUBTILIS 1423 -11528928 7000685515 hemx hema concentration negative effector hemx (db:pir2.dat) B35252 B35252 Bacillus subtilis 1423 -11528928 7500883201 hemx (sr:b.subtilis dna) (db:genpept-bct1) (de:bacillus subtilis hemaxcdbl gene cluster.) (nt:unidentified gene product) (le:1607) (re:2437) (di:direct) BACHEMAXC M57676 g143036 Bacillus subtilis 1423 -11528928 215824 hemx membrane-bound protein (fn:negative effector of the concentration of hema) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:80898) (re:81728) (di:complement) BSUB0015 Z99118 g2635281 Bacillus subtilis 1423 -11528928 304231 hemx membrane-bound protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:membrane bound protein dispensable for heme) (le:88179) (re:89009) (di:direct) BSZ75208 Z75208 g1770082 Bacillus subtilis 1423 -11528928 170077 hemx hema concentration negative effector hemx (db:pir) B35252 B35252 Bacillus subtilis 1423 -11528928 220358 hemx membrane-bound protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:membrane bound protein dispensable for heme) (le:88179) (re:89009) (di:direct) BSZ75208 Z75208 g1770082 Bacillus subtilis 1423 -11528928 6500725070 membrane-bound protein:hemx protein (gtcfc:9.10) (keggfc:14.2) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) hemX hemX Bacillus subtilis 1423 -11528928

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739842	919	23075	675	225

Description

GTC ORF with score 655 to: (fn:converts indole-3-acetaldehyde to) (db:genpept-pln2) (ec:1.2.1.3) (de:ustilago maydis cytosolic indole-3-acetaldehyde dehydrogenase(iad1) gene, complete cds.) (nt:cytosolic protein; belongs to the aldehyde) (le:55) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739851	920	23076	483	160

Description

6500725071 glutamyl-trna reductase:glutr (gtcfc:10.6) (ec:1.2.1.-) (keggfc:14.1) (bsorffc:3.4.7:4.3.1) (db:gtc-bacillus subtilis) hemA hemA Bacillus subtilis 1423 -11528929 76453 hema (ec:1.2.1.-) (de:glutamyl-trna reductase, (glutr)) (db:swissprot) HEM1_BACSU P16618 BACILLUS SUBTILIS 1423 -11528929 7000685503 hema glutamyl-trna reductase:hema:hema protein (cl:glutamyl-trna reductase) (ec:1.2.1.-) (db:pir2.dat) A35252 A35252 Bacillus subtilis 1423 -11528929 7500883133 hema nad p h:glutamyl-transfer rna reductase (sr:b.subtilis dna) (db:genpept-bct1) (de:bacillus subtilis hemaxcdbl gene cluster.) (nt:the product of this hema gene is not an) (le:232) (re:1599) (di:direct) BACHEMAXC M57676 g143035 Bacillus subtilis 1423 -11528929 215823 hema glutamyl-trna reductase (fn:porphyrin biosynthesis) (db:genpept-bct1) (ec:1.2.1.-) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:81736) (re:83103) (di:complement) BSUB0015 Z99118 g2635282 Bacillus subtilis 1423 -11528929 304230 hema nad p h:glutamyl-transfer rna reductase (db:genpept-bct1) (ec:2.3.1.37) (de:b.subtilis genomic sequence 89009bp.) (nt:nad(p)h:glutamyl-t-rna reductase of the c-5 pathway) (le:86804) (re:88171) (di:direct) BSZ75208 Z75208 g1770081 Bacillus subtilis 1423 -11528929 137939 hema glutamyl-trna reductase:hema:hema protein (cl:glutamyl-trna reductase) (ec:1.2.1.-) (db:pir) A35252 A35252 Bacillus subtilis 1423 -11528929 220357 hema nad p h:glutamyl-transfer rna reductase (db:genpept-bct1) (ec:2.3.1.37) (de:b.subtilis genomic sequence 89009bp.) (nt:nad(p)h:glutamyl-t-rna reductase of the c-5 pathway) (le:86804) (re:88171) (di:direct) BSZ75208 Z75208 g1770081 Bacillus subtilis 1423 -11528929 5000688431 (de:(hema) (pn:glutamyl-trna reductase:glutr:glutamyl-trna reductase :glutr) (gtcfc:5.13:5.14:9.10) (ec:1.2.1.-) (hem1_bacsu) (keggfc:5.13:5.14:9.10) (bsorffc:3.4.7) (db:gtc-bacillus subtilis)) hemA hemA Bacillus subtilis 1423 10018816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739913	921	23077	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739917	922	23078	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739932	923	23079	564	187

Description

6500725072 hypothetical protein:possible protoporphyrinogen oxidase (gtcfc:9.10) (ec:1.3.3.-) (keggfc:14.1) (bsorffc:3.4.7) (db:gtc-bacillus subtilis) ywkE ywkE Bacillus subtilis 1423 -11528930 304126 ywke (de:hemk protein homolog) (db:swissprot) HEMK_BACSU P45873 BACILLUS SUBTILIS 1423 -11528930 7000685513 ywke protoporphyrinogen oxidase homolog ywke (db:pir2.dat) S55438 S55438 Bacillus subtilis 1423 -11528930 5000688553 ywke (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:product similar to e.coli prfa2 protein) (le:24695) (re:25561) (di:direct) BSDNA320D Z49782 g853777 Bacillus subtilis 1423 -11528930 7500883184 ywke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:similar to protoporphyrinogen oxidase) (le:198182) (re:199048) (di:complement) BSUB0019 Z99122 g2636225 Bacillus subtilis 1423 -11528930 76734 ywke (de:hemk protein homolog) (db:swissprot) HEMK_BACSU P45873 BACILLUS SUBTILIS 1423 -11528930 170682 ywke protoporphyrinogen oxidase homolog ywke (db:pir) S55438 S55438 Bacillus subtilis 1423 -11528930 219154 ywke (db:genpept-bct2) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:product similar to e.coli prfa2 protein) (le:24695) (re:25561) (di:direct) BSDNA320D Z49782 g853777 Bacillus subtilis 1423 -11528930

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739941	924	23080	546	182

Description

6500725073 molybdopterin-guanine dinucleotide biosynthesis protein a (gtcfc:9.11) (keggfc:14.2) (bsorffc:3.4.8) (db:gtc-bacillus subtilis) mobA mobA Bacillus subtilis 1423 -11528931 7000694233 moba molybdopterin-guanine dinucleotide biosynthesis moba (db:pir2.dat) C69659 C69659 Bacillus subtilis 1423 -11528931 7500964959 moba moba (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to h. influenza moba, swiss-prot accession) (le:608) (re:1207) (di:direct) AF012285 AF012285 g3282110 Bacillus subtilis 1423 -11528931 7500964958 moba molybdopterin-guanine dinucleotide biosynthesis (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:100120) (re:100719) (di:direct) BSUB0008 Z99111 g2633797 Bacillus subtilis 1423 -11528931

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739945	925	23081	180	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501739951	926	23082	645	214

Description

GTC ORF with score 196 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f52d1.) (nt:similar to family 31 of the glycosyl hydrolases;) (le:21170:21361:22026:22790) (re:21241:21458:22259:23128) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740013	927	23083	681	226

Description

6500725074 molybdopterin biosynthesis protein (gtcfc:9.11) (keggfc:14.2) (bsorffc:3.4.8) (db:gtc-bacillus subtilis) moeB moeB Bacillus subtilis 1423 -11528932 7000694228 moeb molybdopterin biosynthesis protein moeb (db:pir2.dat) F69659 F69659 Bacillus subtilis 1423 -11528932 7500964952 moeb molybdopterin biosynthesis protein moeb (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:member of the moeb/hesa/thif family; similar to) (le:1258) (re:2277) (di:direct) AF012285 AF012285 g3282111 Bacillus subtilis 1423 -11528932 7500964951 moeb molybdopterin biosynthesis protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:100770) (re:101789) (di:direct) BSUB0008 Z99111 g2633798 Bacillus subtilis 1423 -11528932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740017	928	23084	345	114

Description

6500725075 molybdopterin biosynthesis protein (gtcfc:9.11) (keggfc:14.2) (bsorffc:3.4.8) (db:gtc-bacillus subtilis) moeA moeA Bacillus subtilis 1423 -11528933 7000694227 moea molybdopterin biosynthesis protein moea (cl:molybdenum cofactor biosynthesis protein moea-2) (db:pir2.dat) E69659 E69659 Bacillus subtilis 1423 -11528933 7500964950 moea molybdopterin biosynthesis protein moea (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to moea from h. influenza, swiss-prot) (le:2295) (re:3587) (di:direct) AF012285 AF012285 g3282112 Bacillus subtilis 1423 -11528933 7500964949 moea molybdopterin biosynthesis protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:101807) (re:103099) (di:direct) BSUB0008 Z99111 g2633799 Bacillus subtilis 1423 -11528933

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740035	929	23085	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740052	930	23086	432	143

Description

6500725076 molybdopterin-guanine dinucleotide biosynthesis protein b (gtcfc:9.11) (keggfc:14.2) (bsorffc:3.4.8) (db:gtc-bacillus subtilis) mobB mobB Bacillus subtilis 1423 -11528934 7000694234 mobb molybdopterin-guanine dinucleotide biosynthesis mobb (db:pir2.dat) D69659 D69659 Bacillus subtilis 1423 -11528934 7500964961 mobb molybdopterin-guanine dinucleotide biosynthesis (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:mobb; similar to mobb from h. influenza, swiss-prot) (le:3548) (re:4069) (di:direct) AF012285 AF012285 g3282113 Bacillus subtilis 1423 -11528934 7500964960 mobb molybdopterin-guanine dinucleotide biosynthesis (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:103060) (re:103581) (di:direct) BSUB0008 Z99111 g2633800 Bacillus subtilis 1423 -11528934

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740053	931	23087	630	209

Description

6500725077 molybdopterin converting factor:subunit 2 (gtcfc:9.11) (keggfc:14.2) (bsorffc:3.4.8) (db:gtc-bacillus subtilis) moaE moaE Bacillus subtilis 1423 -11528935 7000694230 moae molybdopterin converting factor subunit 2 moae (cl:molybdopterin-converting factor chain 2) (db:pir2.dat) B69659 B69659 Bacillus subtilis 1423 -11528935 7500964956 moae molybdopterin converting factor:subunit 2 (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:moae; similar to moae from e. coli, swiss-prot) (le:4069) (re:4542) (di:direct) AF012285 AF012285 g3282114 Bacillus subtilis 1423 -11528935 7500964955 moae molybdopterin converting factor subunit 2 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:103581) (re:104054) (di:direct) BSUB0008 Z99111 g2633801 Bacillus subtilis 1423 -11528935

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740117	932	23088	540	179

Description

6500725078 molybdopterin converting factor:subunit 1 (gtcfc:9.11) (keggfc:14.2) (bsorffc:3.4.8) (db:gtc-bacillus subtilis) moaD moaD Bacillus subtilis 1423 -11528936 7000694229 moad molybdopterin converting factor subunit 1 moad (cl:molybdopterin-converting factor chain 1) (db:pir2.dat) A69659 A69659 Bacillus subtilis 1423 -11528936 7500964954 moad molybdopterin converting factor:subunit 1 (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:moad; similar to moad from e. coli, swiss-prot) (le:4535) (re:4768) (di:direct) AF012285 AF012285 g3282115 Bacillus subtilis 1423 -11528936 7500964953 moad molybdopterin converting factor subunit 1 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:104047) (re:104280) (di:direct) BSUB0008 Z99111 g2633802 Bacillus subtilis 1423 -11528936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740137	933	23089	750	250

Description

6500725079 molybdopterin precursor biosynthesis protein b (gtcfc:9.11) (keggfc:14.2) (bsorffc:3.4.8) (db:gtc-bacillus subtilis) moaB moaB Bacillus subtilis 1423 -11528937 7000694232 moab molybdopterin precursor biosynthesis moab (cl:molybdenum cofactor biosynthesis protein b moab) (db:pir2.dat) H69658 H69658 Bacillus subtilis 1423 -11528937 4000714232 moab putative molibdenum cofactor biosynthesis (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:164099) (re:164611) (di:direct) AF008220 AF008220 g2293241 Bacillus subtilis 1423 -11528937 7500964957 moab molybdopterin precursor biosynthesis protein b (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:15816) (re:16328) (di:complement) BSUB0016 Z99119 g2635430 Bacillus subtilis 1423 -11528937

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740141	934	23090	504	167

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740150	935	23091	468	155

Description

6500725080 bfcc:petd:qcrc menaquinol:cytochrome c oxidoreductase:cytochrome b/c subunit:menaquinol-cytochrome c reductase cytochrome b/c subunit (gtcfc:9.12) (keggfc:14.2) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) qcrC qcrC Bacillus subtilis 1423 -11528938 92703 qcrc:bfcc (de:menaquinol-cytochrome c reductase cytochrome b/c subunit) (db:swissprot) QCRC_BACSU P46913 BACILLUS SUBTILIS 1423 -11528938 7000686258 qcrc menaquinol:cytochrome c oxidoreductase cytochrome b/c subunit qcrc (db:pir2.dat) D69687 D69687 Bacillus subtilis 1423 -11528938 217151 qcrc cytochrome b (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:29.1% of identical aminoa... BACYPIA L47709 g1146229 Bacillus subtilis 1423 -11528938 219877 qcrc cytochrome c (db:genpept-bct1) (de:bacillus subtilis menaquinol:cytochrome c reductase complex (qcr),rieske iron-sulfur protein (qcra), cytochrome b (qcrb), cytochromec (qcrc) genes, complete cds.) (nt:qcrc) (le:1608) (re:2375) (di:direct) BSU25535 U25535 g942583 Bacillus subtilis 1423 -11528938 7500889203 qcrc menaquinol:cytochrome c oxidoreductase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: bfcc, petd) (le:166812) (re:167579) (di:complement) BSUB0012 Z99115 g2634672 Bacillus subtilis 1423 -11528938 5000689101 (de:(qcrc) (pn:menaquinol-cytochrome c reductase cytochrome b) (gn:bfcc) (gtcfc:13.07) (ec:) (qcrc_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) qcrC qcrC Bacillus subtilis 1423 10034731

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740152	936	23092	288	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740263	937	23093	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740264	938	23094	585	194

Description

6500725081 bfcb:petb:qcrb menaquinol:cytochrome c oxidoreductase:cytochrome b subunit:menaquinol-cytochrome c reductase cytochrome b subunit (gtcfc:9.12) (keggfc:14.2) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) qcrB qcrB Bacillus subtilis 1423 -11528939 92702 qcrb:bfcb (de:menaquinol-cytochrome c reductase cytochrome b subunit) (db:swissprot) QCRB_BACSU P46912 BACILLUS SUBTILIS 1423 -11528939 7000686257 qcrb cytochrome b6 homolog qcrb:menaquinol--cytochrome c oxidoreductase cytochrome b6 subunit (cl:cytochrome b6:cytochrome b6 homology) (db:pir2.dat) C69687 C69687 Bacillus subtilis 1423 -11528939 217150 qcrb cytochrome b (fn:cytochrome reductase) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt... BACYPIA L47709 g1146228 Bacillus subtilis 1423 -11528939 219876 qcrb cytochrome b (db:genpept-bct1) (de:bacillus subtilis menaquinol:cytochrome c reductase complex (qcr),rieske iron-sulfur protein (qcra), cytochrome b (qcrb), cytochromec (qcrc) genes, complete cds.) (nt:qcrb) (le:899) (re:1573) (di:direct) BSU25535 U25535 g942582 Bacillus subtilis 1423 -11528939 7500889202 qcrb menaquinol:cytochrome c oxidoreductase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: bfcb, petb) (le:167614) (re:168288) (di:complement) BSUB0012 Z99115 g2634673 Bacillus subtilis 1423 -11528939 5000689100 (de:(qcrb) (pn:menaquinol-cytochrome c reductase cytochrome b subunit) (gn:bfcb) (gtcfc:13.07) (ec:) (qcrb_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) qcrB qcrB Bacillus subtilis 1423 10034730

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740276	939	23095	417	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740285	940	23096	504	168

Description

GTC ORF with score 92 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f32b5.) (nt:weak similarity to rat and mouse sperm outer dense) (le:9192:10590:11183) (re:9337:10833:11357) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740288	941	23097	381	126

Description

GTC ORF with score 189 to: (sr:pseudomonas sp. plasmid:phn671 dna, clone:phpb12) (db:genpept-bct1) (de:pseudomonas sp. plasmid phn671 hydantoinase and n-carbamyl-l-aminoacid amidohydrolase genes, complete cds.) (le:5031) (re:6275) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740291	942	23098	939	312

Description

6500725082 o-succinylbenzoic acid-coa ligase (gtcfc:9.12) (ec:6.2.1.26) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) menE menE Bacillus subtilis 1423 -11528940 7000694331 mene o-succinylbenzoate--coa ligase::menaquinone biosynthesis enzyme mene:o-succinylbenzoate-coenzyme a synthase:osb-coa synthase (cl:acetate--coa ligase homology) (ec:6.2.1.26) (db:pir2.dat) H69656 H69656 Bacillus subtilis 1423 -11528940 4000714125 mene osb-coa synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:30307) (re:31767) (di:direct) AF008220 AF008220 g2293149 Bacillus subtilis 1423 -11528940 7500965026 mene o-succinylbenzoic acid-coa ligase (fn:menaquinone biosynthesis) (db:genpept-bct1) (ec:6.2.1.26) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:148660) (re:150120) (di:complement) BSUB0016 Z99119 g2635563 Bacillus subtilis 1423 -11528940

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740303	943	23099	624	207

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740304	944	23100	225	74

Description

6500725083 dihydroxynapthoic acid synthetase (gtcfc:9.12) (ec:4.1.3.36) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) menB menB Bacillus subtilis 1423 -11528941 7000692921 menb naphthoate synthase:menb:dhna synthase:dihydroxynaphthoate synthase:dihydroxynapthoic acid synthetase menb:menaquinone biosynthesis enzyme/enoyl coa hydratase homolog (cl:naphthoate synthase:enoyl-coa hydratase homology) (ec:4.1.3.36) (db:pir2.dat) F69656 F69656 Bacillus subtilis 1423 -11528941 4000714124 menb dihydroxynaphthoate synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:29401) (re:30216) (di:direct) AF008220 AF008220 g2293148 Bacillus subtilis 1423 -11528941 7500963939 menb dihydroxynapthoic acid synthetase (fn:menaquinone biosynthesis) (db:genpept-bct1) (ec:4.1.3.36) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:150211) (re:151026) (di:complement) BSUB0016 Z99119 g2635564 Bacillus subtilis 1423 -11528941

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740402	945	23101	741	247

Description

6500725084 2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2:4-cyclohexadiene-1-carboxylate synthase (gtcfc:9.12) (ec:4.1.1.71) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) menD menD Bacillus subtilis 1423 -11528942 7000692040 mend 2-succinyl-6-hydroxy-2:4-cyclohexadiene-1-carboxylate synthase::mencf protein:mend protein (ec:6.4.-.-) (db:pir2.dat) G69656 G69656 Bacillus subtilis 1423 -11528942 4000714122 mend shchc synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:26812) (re:28554) (di:direct) AF008220 AF008220 g2293146 Bacillus subtilis 1423 -11528942 7500963292 mend 2-oxoglutarate decarboxylase and (fn:menaquinone biosynthesis) (db:genpept-bct1) (ec:4.1.1.71) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:151873) (re:153615) (di:complement) BSUB0016 Z99119 g2635566 Bacillus subtilis 1423 -11528942

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740458	946	23102	771	257

Description

6500725085 icsm:entc:menf menaquinone-specific isochorismate synthase (gtcfc:9.12) (ec:5.4.99.6) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) menF menF Bacillus subtilis 1423 -11528943 83450 menf:icsm (ec:5.4.99.6) (de:menaquinone-specific isochorismate synthase,) (db:swissprot) MENF_BACSU P23973 BACILLUS SUBTILIS 1423 -11528943 7000685823 menf probable isochorismate synthase:menaquinone-specific menf (cl:isochorismate synthase) (ec:5.4.99.6) (db:pir2.dat) A69657 A69657 Bacillus subtilis 1423 -11528943 216327 menf isochorismate synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:25400) (re:26815) (di:direct) AF008220 AF008220 g2293145 Bacillus subtilis 1423 -11528943 4000707199 menf menaquinone-specific isochorismate synthase (fn:menaquinone biosynthesis) (db:genpept-bct1) (ec:5.4.99.6) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: icsm, entc) (le:153612) (re:155027) (di:complement) BSUB0016 Z99119 g2635567 Bacillus subtilis 1423 -11528943 7500885495 menf isochorismate synthase (sr:bacillus subtilis (strain rb1) dna) (db:genpept-bct2) (de:bacillus subtilis menaquinone operon: menf, mend, menb and menegenes, complete cds.) (nt:based on similarity to e. coli entc, a. hydrophila) (le:143) (re:1558) (di:direct) BACMENAQOP M74538 g1185288 Bacillus subtilis 1423 -11528943 5000688561 (de:(menf) (pn:menaquinone-specific isochorismate synthase) (gn:icsm) (gtcfc:9.12) (ec:5.4.99.6) (menf_bacsu) (keggfc:9.13) (db:gtc-bacillus subtilis)) menF menF Bacillus subtilis 1423 10025664

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740540	947	23103	639	212

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740546	948	23104	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740550	949	23105	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740659	950	23106	375	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740671	951	23107	333	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740674	952	23108	1020	339

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740701	953	23109	513	170

Description

GTC ORF with score 508 to: (sr:thale cress) (db:genpept-pln2) (ec:2.1.1.14) (de:arabidopsis thaliana cobalamin-independent methionine synthase(atcims) mrna, complete cds.) (nt:5-methyltetrahydropteroyltriglutamate-homocysteine) (le:9) (re:2306) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740702	954	23110	453	150

Description

6500725086 hypothetical protein:involved in siderophore 2:3-dihydroxybenzoate:dhb synthesis (gtcfc:9.12) (keggfc:14.2) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) dhbF dhbF Bacillus subtilis 1423 -11528944 7502851559 dhbf (de:probable serine activating enzyme) (db:swissprot) DHBF_BACSU P45745 BACILLUS SUBTILIS 1423 -11528944 7000694113 dhbf enterobactin synthetase component dhbf:enterochelin synthetase component f (cl:enterobactin synthetase component f:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir1.dat) E69615 E69615 Bacillus subtilis 1423 -11528944 7500964868 dhbf (fn:involved in siderophore 2,3-dihydroxybenzoate) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:85876) (re:89712) (di:complement) BSUB0017 Z99120 g2635693 Bacillus subtilis 1423 -11528944

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740706	955	23111	558	186

Description

6500725087 isochorismatase:2:3 dihydro-2:3 dihydroxybenzoate synthase (gtcfc:9.12) (ec:3.3.2.1) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) dhbB dhbB Bacillus subtilis 1423 -11528945 68446 dhbb (ec:3.3.2.1) (de:synthase) (superoxide-inducible protein 1) (soi1)) (db:swissprot) DHBB_BACSU P45743 BACILLUS SUBTILIS 1423 -11528945 7000685038 dhbb isochorismatase:dhbb (cl:isochorismatase) (ec:3.3.2.1) (db:pir2.dat) B69615 B69615 Bacillus subtilis 1423 -11528945 219890 dhbb isochorismatase (fn:siderophore 2,3-dihydroxybenzoate (dhb)) (db:genpept-bct1) (ec:3.3.2.1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:89732) (re:90670) (di:complement) BSUB0017 Z99120 g2635694 Bacillus subtilis 1423 -11528945 7500880245 dhbb isochorismatase (db:genpept-bct2) (de:bacillus subtilis 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase(dhba), isochorismate synthase (dhbc), 2,3-dihydroxybenzoate-ampligase (dhbe), and isochorismatase (dhbb) genes, complete cds, and(dhbf) gene, partial cds.) (nt:base... BSU26444 U26444 g837333 Bacillus subtilis 1423 -11528945 5000688556 (de:(dhbb) (pn:isochorismatase:isochorismatase :2,3 dihydro-2,3 dihydroxybenzoate synthase) (gtcfc:9.12) (ec:3.3.2.1) (dhbb_bacsu) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis)) dhbB dhbB Bacillus subtilis 1423 10011038

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740755	956	23112	879	292

Description

GTC ORF with score 359 to: (sr:baker"s yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmids 9481, 9509, 9926,9461, and lambda 3641.) (nt:involved in spore wall maturation; ydr402c;) (le:34974) (re:36443) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740762	957	23113	189	62

Description

GTC ORF with score 196 to: (db:genpept-pln1) (de:rp59=ribosomal protein...l46=ribosomal protein (kluyveromycesmarxianus, genomic, 3 genes, 1573 nt, segment 2 of 3).) (nt:ribosomal protein; this sequence comes from fig.) (le:347) (re:739) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740763	958	23114	348	115

Description

6500725088 ente:dhbe enterobactin synthetase component e:2:3-dihydroxybenzoate-amp ligase:dihydroxybenzoic acid-activating enzyme (gtcfc:9.12) (ec:6.3.2.-) (keggfc:14.1) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) dhbE dhbE Bacillus subtilis 1423 -11528946 68450 dhbe:ente (ec:6.3.2.-) (de:activating enzyme)) (db:swissprot) DHBE_BACSU P40871 BACILLUS SUBTILIS 1423 -11528946 7000685040 dhbe 2:3-dihydroxybenzoate--carrier protein ligase, dhbe:2,3-dihydroxybenzoate--amp ligase (misnomer):dihydroxybenzoic acid-activating enzyme component e:ente protein homolog:enterobactin synthetase component e:enterochelin synthetase component e) (cl:4-coumarate--coa ligase:acetate--coa ligase ... D69615 D69615 Bacillus subtilis 1423 -11528946 219889 dhbe 2:3-dihydroxybenzoate-amp ligase enterobactin (fn:siderophore 2,3-dihydroxybenzoate (dhb)) (db:genpept-bct1) (ec:6.3.2.-) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: ente) (le:90698) (re:92317) (di:complement) BSUB0017 Z99120 g2635695 Bacillus subtilis 1423 -11528946 7500880247 dhbe 2:3-dihydroxybenzoate-amp ligase (db:genpept-bct2) (de:bacillus subtilis 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase(dhba), isochorismate synthase (dhbc), 2,3-dihydroxybenzoate-ampligase (dhbe), and isochorismatase (dhbb) genes, complete cds, and(dhbf) gene, partial cds.) (nt:base... BSU26444 U26444 g837332 Bacillus subtilis 1423 -11528946

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740780	959	23115	516	171

Description

6500725089 isochorismate synthase:isochorismate synthase dhbc (gtcfc:9.12) (ec:5.4.99.6) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) dhbC dhbC Bacillus subtilis 1423 -11528947 68447 dhbc (ec:5.4.99.6) (de:isochorismate synthase dhbc,) (db:swissprot) DHBC_BACSU P45744 BACILLUS SUBTILIS 1423 -11528947 7000685039 dhbc isochorismate synthase dhbc (cl:isochorismate synthase) (db:pir2.dat) C69615 C69615 Bacillus subtilis 1423 -11528947 219888 dhbc isochorismate synthase (fn:siderophore 2,3-dihydroxybenzoate (dhb)) (db:genpept-bct1) (ec:5.4.99.6) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:92346) (re:93542) (di:complement) BSUB0017 Z99120 g2635696 Bacillus subtilis 1423 -11528947 7500880246 dhbc isochorismate synthase (db:genpept-bct2) (de:bacillus subtilis 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase(dhba), isochorismate synthase (dhbc), 2,3-dihydroxybenzoate-ampligase (dhbe), and isochorismatase (dhbb) genes, complete cds, and(dhbf) gene, partial cds.) (nt:base... BSU26444 U26444 g837331 Bacillus subtilis 1423 -11528947 5000688557 (de:(dhbc) (pn:isochorismate synthase dhbc) (gtcfc:9.12) (ec:5.4.99.6) (dhbc_bacsu) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis)) dhbC dhbC Bacillus subtilis 1423 10011039

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740873	960	23116	978	326

Description

6500725090 enta:dhba 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase (gtcfc:9.12) (ec:1.3.1.28) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) dhbA dhbA Bacillus subtilis 1423 -11528948 68445 dhba:enta (ec:1.3.1.28) (de:(cold shock protein csi14)) (db:swissprot) DHBA_BACSU P39071 BACILLUS SUBTILIS 1423 -11528948 7000685037 dhba 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.3.1.28) (db:pir1.dat) A69615 A69615 Bacillus subtilis 1423 -11528948 219887 dhba 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase (fn:siderophore 2,3-dihydroxybenzoate (dhb)) (db:genpept-bct1) (ec:1.3.1.28) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: enta) (le:93568) (re:94353) (di:complement) BSUB0017 Z99120 g2635697 Bacillus subtilis 1423 -11528948 7500880244 dhba 2:3-dihydro-2:3-dihydroxybenzoate dehydrogenase (db:genpept-bct2) (de:bacillus subtilis 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase(dhba), isochorismate synthase (dhbc), 2,3-dihydroxybenzoate-ampligase (dhbe), and isochorismatase (dhbb) genes, complete cds, and(dhbf) gene, partial cds.) (nt:base... BSU26444 U26444 g837330 Bacillus subtilis 1423 -11528948 5000688555 (de:(dhba) (pn:2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase) (gn:enta) (gtcfc:9.12) (ec:1.3.1.28) (dhba_bacsu) (keggfc:9.13) (bsorffc:3.4.6) (db:gtc-bacillus subtilis)) dhbA dhbA Bacillus subtilis 1423 10011037

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740883	961	23117	633	210

Description

6500725091 yxkl:cydb cytochrome bd ubiquinol oxidase:subunit ii:cytochrome d ubiquinol oxidase subunit ii (gtcfc:9.12) (ec:1.10.3.-) (keggfc:14.1) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) cydB cydB Bacillus subtilis 1423 -11528949 5500685059 cydb (ec:1.10.3.-) (de:cytochrome d ubiquinol oxidase subunit ii,) (db:swissprot) CYDB_BACSU P94365 BACILLUS SUBTILIS 1423 -11528949 7000684957 cydb cytochrome bd ubiquinol oxidase subunit ii cydb (cl:cytochrome d ubiquinol oxidase) (db:pir2.dat) B69611 B69611 Bacillus subtilis 1423 -11528949 222877 cydb cytochrome bd ubiquinol oxidase subunit ii (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxkl) (le:177183) (re:178199) (di:complement) BSUB0020 Z99123 g2636410 Bacillus subtilis 1423 -11528949 301544 cydb (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to cytochrome d ubiquinol oxidase) (le:46266) (re:47282) (di:direct) D83026 D83026 g1783251 Bacillus subtilis 1423 -11528949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740907	962	23118	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740909	963	23119	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740917	964	23120	411	136

Description

GTC ORF with score 92 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t27e13 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:24166:24378:24540:24710) (re:24290:24429:24619:24862) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740920	965	23121	198	66

Description

6500725092 yxkk:cyda cytochrome bd ubiquinol oxidase:subunit i:cytochrome d ubiquinol oxidase subunit i (gtcfc:9.12) (ec:1.10.3.-) (keggfc:14.1) (bsorffc:3.4.6) (db:gtc-bacillus subtilis) cydA cydA Bacillus subtilis 1423 -11528950 5500685058 cyda (ec:1.10.3.-) (de:cytochrome d ubiquinol oxidase subunit i,) (db:swissprot) CYDA_BACSU P94364 BACILLUS SUBTILIS 1423 -11528950 7000684956 cyda cytochrome bd ubiquinol oxidase subunit i cyda (cl:cytochrome d complex terminal oxidase chain i) (db:pir2.dat) A69611 A69611 Bacillus subtilis 1423 -11528950 222876 cyda cytochrome bd ubiquinol oxidase subunit i (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxkk) (le:178183) (re:179589) (di:complement) BSUB0020 Z99123 g2636411 Bacillus subtilis 1423 -11528950 301543 cyda (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to cytochrome d ubiquinol oxidase) (le:44876) (re:46282) (di:direct) D83026 D83026 g1783250 Bacillus subtilis 1423 -11528950

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740993	966	23122	507	168

Description

6500725093 thioredoxin-like protein (gtcfc:9.13) (keggfc:14.2) (bsorffc:3.4.5) (db:gtc-bacillus subtilis) tlp tlp Bacillus subtilis 1423 -11528951 7000694691 tlp thioredoxin-like protein tlp (db:pir2.dat) C69724 C69724 Bacillus subtilis 1423 -11528951 7500965273 tlpa tlpa (fn:thioredoxin like protein) (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:12123) (re:12374) (di:direct) BC170DEGR Z73234 g1405455 Bacillus subtilis 1423 -11528951 217886 tlp thioredoxin-like protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:148502) (re:148753) (di:direct) BSUB0010 Z99113 g2634186 Bacillus subtilis 1423 -11528951

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501740999	967	23123	474	157

Description

6500725094 trx:trxa thioredoxin:trx (gtcfc:9.13) (keggfc:14.2) (bsorffc:3.4.5) (db:gtc-bacillus subtilis) trxA trxA Bacillus subtilis 1423 -11528952 122367 trxa thioredoxin (cl:thioredoxin:thioredoxin homology) (db:pir1.dat) (mp:70 min) B37192 B37192 Bacillus subtilis 1423 -11528952 215191 trx thioredoxin (sr:bacillus subtilis (strain 168) (tissue library: atcc 6633) dna) (db:genpept-bct1) (de:bacillus subtilis thioredoxin (trx), uvrb and aspartokinase iigenes, complete cds.) (nt:putative) (le:11) (re:325) (di:direct) BACAPKII J03294 g142520 Bacillus subtilis 1423 -11528952 220320 trxa thioredoxin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: trx) (le:116996) (re:117310) (di:complement) BSUB0015 Z99118 g2635315 Bacillus subtilis 1423 -11528952 304193 trxa thioredoxin (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:thioredoxin;putative) (le:52597) (re:52911) (di:direct) BSZ75208 Z75208 g1770044 Bacillus subtilis 1423 -11528952

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741020	968	23124	276	91

Description

6500725095 yvch:trxb thioredoxin reductase (gtcfc:9.13) (ec:1.6.4.5) (keggfc:14.1) (bsorffc:3.4.5) (db:gtc-bacillus subtilis) trxB trxB Bacillus subtilis 1423 -11528953 7000694690 trxb thioredoxin reductase nadph (cl:thioredoxin reductase:thioredoxin reductase homology) (ec:1.6.4.5) (db:pir1.dat) A69727 A69727 Bacillus subtilis 1423 -11528953 1500694014 trxb thioredoxin reductase (db:genpept-bct1) (ec:1.6.4.5) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvch) (le:172717) (re:173667) (di:complement) BSUB0018 Z99121 g2635992 Bacillus subtilis 1423 -11528953 7500953867 yvch hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable thioredoxin reductase) (le:8004) (re:8954) (di:direct) BSZ94043 Z94043 g1945648 Bacillus subtilis 1423 -11528953

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741028	969	23125	393	130

Description

GTC ORF with score 251 to: (sr:grape powdery mildew) (db:genpept-pln2) (ec:1.14.14.1) (de:uncinula necator eburicol c14-alpha-demethylase (cyp51) gene,complete cds.) (nt:unspecific monooxygenase; cytochrome p450 sterol) (le:203:504:755) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741129	970	23126	627	208

Description

6500725096 putative chalcone synthase:naringenin-chalcone synthase (gtcfc:9.13:14.3) (ec:2.3.1.74) (keggfc:9.14) (bsorffc:8.3.1) (db:gtc-bacillus subtilis) bcsA bcsA Bacillus subtilis 1423 -11528954 61520 bcsa (ec:2.3.1.74) (de:synthase)) (db:swissprot) BCSA_BACSU P54157 BACILLUS SUBTILIS 1423 -11528954 7000684691 bcsa naringenin-chalcone synthase bcsa (db:pir2.dat) A69593 A69593 Bacillus subtilis 1423 -11528954 217076 bcsa naringenin-chalcone synthase (db:genpept-bct1) (ec:2.3.1.74) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:25.6% of identity to the lycopersicon esculentum) (le:3397) (re:4494) (di:direct) BACYACA L77246 g1256619 Bacillus subtilis 1423 -11528954 7500877732 bcsa naringenin-chalcone synthase (fn:phenylalanine metabolism) (db:genpept-bct1) (ec:2.3.1.74) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:120658) (re:121755) (di:complement) BSUB0012 Z99115 g2634624 Bacillus subtilis 1423 -11528954 5000688429 (de:(bcsa) (pn:putative chalcone synthase:naringenin-chalcone synthase) (gtcfc:5.13) (ec:2.3.1.74) (bcsa_bacsu) (keggfc:5.13) (db:gtc-bacillus subtilis)) bcsA bcsA Bacillus subtilis 1423 10004229

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501741130	971	23127	756	251

Description

6500725097 riboflavin kinase / fad synthase:riboflavin kinase:flavokinase / fmn adenylyltransferase:fad pyrophosphorylase:fad synthetase (gtcfc:9.2) (keggfc:9.2) (bsorffc:3.4.4) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) ribC ribC Bacillus subtilis 1423 -11528955 7000694511 ribc riboflavin kinase / fad synthase ribc (cl:conserved hypothetical protein hi0963) (db:pir2.dat) D69692 D69692 Bacillus subtilis 1423 -11528955 219590 ribc fmn adenylyltransferase (db:genpept-bct1) (de:b.subtilis ribc, rpso and pnpa genes.) (nt:riboflavin kinase) (le:88) (re:1038) (di:direct) BSRIBRPS Z80835 g1592690 Bacillus subtilis 1423 -11528955 304138 ribc fad synthase (fn:riboflavin biosynthesis) (db:genpept-bct1) (ec:2.7.1.26:2.7.7.2) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:riboflavin kinase) (le:138805) (re:139755) (di:direct) BSUB0009 Z99112 g2634039 Bacillus subtilis 1423 -11528955

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501741148	972	23128	459	152

Description

6500725098 riboflavin synthase:beta subunit:6:7-dimethyl-8-ribityllumazine synthase:dmrl synthase:lumazine synthase:riboflavin synthase beta chain (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (bsorffc:3.4.4) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) ribH ribH Bacillus subtilis 1423 -11528956 215507 ribh (ec:2.5.1.9) (de:(lumazine synthase) (riboflavin synthase beta chain)) (db:swissprot) RISB_BACSU P11998 BACILLUS SUBTILIS 1423 -11528956 170509 ribh riboflavin synthase:complex beta chain ribh (ec:2.5.1.9) (db:pir2.dat) A26708 S45546 Bacillus subtilis 1423 -11528956 7500889814 ribh (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:11253) (re:11717) (di:direct) BACDIA L09228 g410128 Bacillus subtilis 1423 -11528956 219580 (db:genpept-bct1) (de:b.subtilis riboflavin biosynthesis operon ribg, ribb, riba, ribh,and ribt genes.) (nt:ribh protein product (aa 1-154)) (le:4199) (re:4663) (di:direct) BSRIB X51510 g40088 Bacillus subtilis 1423 -11528956 7502851560 ribh riboflavin synthase beta subunit (fn:riboflavin biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:31866) (re:32330) (di:complement) BSUB0013 Z99116 g2634760 Bacillus subtilis 1423 -11528956 94484 ribh (ec:2.5.1.9) (de:(lumazine synthase) (riboflavin synthase beta chain)) (db:swissprot) RISB_BACSU P11998 BACILLUS SUBTILIS 1423 -11528956 7000686342 ribh riboflavin synthase:complex beta chain ribh (ec:2.5.1.9) (db:pir) A26708 A26708 Bacillus subtilis 1423 -11528956

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741170	973	23129	810	270

Description

6500725099 gtp cyclohydrolase ii and 3:4-dihydroxy-2-butanone 4-phosphate synthase:gtp cyclohydrolase ii / 3:4-dihydroxy-2-butanone 4-phosphate synthase:dhbp synthase (gtcfc:9.2) (ec:3.5.4.25) (keggfc:9.2) (bsorffc:3.4.4) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) ribA ribA Bacillus subtilis 1423 -11528957 215506 riba (ec:3.5.4.25) (de:phosphate synthase (dhbp synthase)) (db:swissprot) GCH2_BACSU P17620 BACILLUS SUBTILIS 1423 -11528957 7000685373 riba gtp cyclohydrolase ii:3:4-dihydroxy-2-butanone 4-phosphate synthase:riba:riba protein (cl:riba bifunctional protein:3, 4-dihydroxy-2-butanone 4-phosphate synthase homology:cyclohydrolase homology) (ec:3.5.4.25:5.4.99.-) (db:pir2.dat) S45545 S45545 Bacillus subtilis 1423 -11528957 7500882252 riba (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:10024) (re:11220) (di:direct) BACDIA L09228 g410127 Bacillus subtilis 1423 -11528957 219579 (db:genpept-bct1) (de:b.subtilis riboflavin biosynthesis operon ribg, ribb, riba, ribh,and ribt genes.) (nt:riba protein product (aa 1-398)) (le:2970) (re:4166) (di:direct) BSRIB X51510 g40087 Bacillus subtilis 1423 -11528957 7502851561 riba gtp cyclohydrolase ii and (fn:riboflavin biosynthesis) (db:genpept-bct1) (ec:3.5.4.25) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:32363) (re:33559) (di:complement) BSUB0013 Z99116 g2634761 Bacillus subtilis 1423 -11528957 73405 riba (ec:3.5.4.25) (de:phosphate synthase (dhbp synthase)) (db:swissprot) GCH2_BACSU P17620 BACILLUS SUBTILIS 1423 -11528957 170507 riba gtp cyclohydrolase ii:3:4-dihydroxy-2-butanone 4-phosphate synthase:riba:riba protein (cl:riba bifunctional protein:3, 4-dihydroxy-2-butanone 4-phosphate synthase homology:cyclohydrolase homology) (ec:3.5.4.25:5.4.99.-) (db:pir) S45545 S45545 Bacillus subtilis 1423 -11528957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741188	974	23130	414	137

Description

6500725100 ribe:ribb riboflavin synthase:alpha subunit:riboflavin synthase alpha chain (gtcfc:9.2) (ec:2.5.1.9) (keggfc:9.2) (bsorffc:3.4.4) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) ribB ribB Bacillus subtilis 1423 -11528958 219578 ribe:ribb (ec:2.5.1.9) (de:riboflavin synthase alpha chain,) (db:swissprot) RISA_BACSU P16440 BACILLUS SUBTILIS 1423 -11528958 123460 ribb riboflavin synthase:alpha chain (cl:riboflavin synthase alpha chain) (ec:2.5.1.9) (db:pir1.dat) A35711 S45544 Bacillus subtilis 1423 -11528958 215505 ribb (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:9362) (re:10009) (di:direct) BACDIA L09228 g410126 Bacillus subtilis 1423 -11528958 7500889812 (db:genpept-bct1) (de:b.subtilis riboflavin biosynthesis operon ribg, ribb, riba, ribh,and ribt genes.) (nt:ribb protein product (aa 1-215)) (le:2308) (re:2955) (di:direct) BSRIB X51510 g40086 Bacillus subtilis 1423 -11528958 7502851562 ribb riboflavin synthase alpha subunit (fn:riboflavin biosynthesis) (db:genpept-bct1) (ec:2.5.1.9) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:33574) (re:34221) (di:complement) BSUB0013 Z99116 g2634762 Bacillus subtilis 1423 -11528958 94477 ribe:ribb (ec:2.5.1.9) (de:riboflavin synthase alpha chain,) (db:swissprot) RISA_BACSU P16440 BACILLUS SUBTILIS 1423 -11528958

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741191	975	23131	615	204

Description

6500725101 ribd:ribt reductase:ribt protein (gtcfc:9.2) (keggfc:14.2) (bsorffc:3.4.4) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) ribT ribT Bacillus subtilis 1423 -11528959 215508 ribt (de:ribt protein) (db:swissprot) RIBT_BACSU P17622 BACILLUS SUBTILIS 1423 -11528959 7000686331 ribt reductase ribt:ribtd protein (db:pir2.dat) S45547 S45547 Bacillus subtilis 1423 -11528959 7500889778 ribtd (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:11830) (re:12204) (di:direct) BACDIA L09228 g410129 Bacillus subtilis 1423 -11528959 5000688524 (db:genpept-bct1) (de:b.subtilis riboflavin biosynthesis operon ribg, ribb, riba, ribh,and ribt genes.) (nt:ribt protein product (aa 1-124)) (le:4776) (re:5150) (di:direct) BSRIB X51510 g40089 Bacillus subtilis 1423 -11528959 219581 ribt reductase (fn:riboflavin biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ribd) (le:31379) (re:31753) (di:complement) BSUB0013 Z99116 g2634759 Bacillus subtilis 1423 -11528959 94346 ribt (de:ribt protein) (db:swissprot) RIBT_BACSU P17622 BACILLUS SUBTILIS 1423 -11528959 170516 ribt reductase ribt:ribtd protein (db:pir) S45547 S45547 Bacillus subtilis 1423 -11528959

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741197	976	23132	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741273	977	23133	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741282	978	23134	429	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741286	979	23135	459	153

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741303	980	23136	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741304	981	23137	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741306	982	23138	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741317	983	23139	390	129

Description

6500725102 riboflavin-specific deaminase (gtcfc:9.2) (ec:3.5.4.-) (keggfc:14.1) (bsorffc:3.4.4) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-riboflavin metabolism (vitamin b2)) ribG ribG Bacillus subtilis 1423 -11528960 94344 ribg (ec:3.5.4.-) (de:riboflavin-specific deaminase,) (db:swissprot) RIBG_BACSU P17618 BACILLUS SUBTILIS 1423 -11528960 170508 ribg riboflavin-specific deaminase ribg (db:pir2.dat) PN0100 S45543 Bacillus subtilis 1423 -11528960 7500889776 ribg (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:8266) (re:9351) (di:direct) BACDIA L09228 g410125 Bacillus subtilis 1423 -11528960 215504 (db:genpept-bct1) (de:b.subtilis riboflavin biosynthesis operon ribg, ribb, riba, ribh,and ribt genes.) (nt:ribg protein product (aa 1-361)) (le:1212) (re:2297) (di:direct) BSRIB X51510 g40085 Bacillus subtilis 1423 -11528960 219577 ribg riboflavin-specific deaminase (fn:riboflavin biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:34232) (re:35317) (di:complement) BSUB0013 Z99116 g2634763 Bacillus subtilis 1423 -11528960 7000686329 ribg riboflavin-specific deaminase ribg (db:pir) PN0100 PN0100 Bacillus subtilis 1423 -11528960 5000688523 (de:(ribg) (pn:riboflavin-specific deaminase:riboflavin biosynthesis protein ribg) (gtcfc:9.02) (ec:3.5.4.-) (ribg_bacsu) (keggfc:11.1) (bsorffc:3.4.4) (db:gtc-bacillus subtilis)) ribG ribG Bacillus subtilis 1423 10036324

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501741327	984	23140	573	190

Description

6500725103 yrxb:nadc nicotinate-nucleotide pyrophosphorylase (gtcfc:9.3:9.4) (ec:2.4.2.19) (keggfc:9.4) (bsorffc:3.4.2) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6):metabolism of cofactors and vitamins-nicotinate (niacin) and nicotinamide metabolism (n... nadC nadC Bacillus subtilis 1423 -11528961 7500886234 nadc (ec:2.4.2.19) (de:(decarboxylating)) (qaprtase) (general stress protein 70) (gsp70)) (db:swissprot) NADC_BACSU P39666 BACILLUS SUBTILIS 1423 -11528961 7000694316 nadc nicotinate-nucleotide pyrophosphorylase nadc (cl:nicotinate-nucleotide pyrophosphorylase (carboxylating)) (db:pir2.dat) G69663 G69663 Bacillus subtilis 1423 -11528961 7500886236 nadc nicotinate-nucleotide pyrophosphorylase (fn:required for nad biosynthesis (nad/nadp) (db:genpept-bct1) (ec:2.4.2.19) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: yrxb) (le:51178) (re:52047) (di:complement) BSUB0015 Z99118 g2635251 Bacillus subtilis 1423 -11528961

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501741328	985	23141	372	123

Description

6500725104 3-methyl-2-oxobutanoate hydroxymethyltransferase:ketopantoate hydroxymethyltransferase (gtcfc:9.5:9.6) (ec:2.1.2.11) (keggfc:9.5:9.8) (bsorffc:3.4.9) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-pantothenate and coa biosynthesis:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) panB panB Bacillus subtilis 1423 -11528962 88568 panb (ec:2.1.2.11) (de:(ketopantoate hydroxymethyltransferase)) (db:swissprot) PANB_BACSU P52996 BACILLUS SUBTILIS 1423 -11528962 7000686077 panb ketopantoate hydroxymethyltransferase panb (cl:3-methyl-2-oxobutanoate hydroxymethyltransferase) (db:pir2.dat) G69671 G69671 Bacillus subtilis 1423 -11528962 217162 panb ketopantoate hydroxymethyltransferase (fn:pantothenic acid biosynthesis) (db:genpept-bct1) (ec:2.1.2.11) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc ge... BACYPIA L47709 g1146240 Bacillus subtilis 1423 -11528962 7500887640 panb ketopantoate hydroxymethyltransferase (fn:pantothenate biosynthesis) (db:genpept-bct1) (ec:2.1.2.11) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:157541) (re:158374) (di:complement) BSUB0012 Z99115 g2634661 Bacillus subtilis 1423 -11528962 5000688537 (de:(panb) (pn:3-methyl-2-oxobutanoate hydroxymethyltransferase:ketopantoate hydroxymethyltransferase) (gtcfc:9.06) (ec:2.1.2.11) (panb_bacsu) (keggfc:9.5:9.8) (db:gtc-bacillus subtilis)) panB panB Bacillus subtilis 1423 10030695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741432	986	23142	954	318

Description

6500725105 dethiobiotin synthetase:dethiobiotin synthase:dtb synthetase:dtbs (gtcfc:9.6) (ec:6.3.3.3) (keggfc:9.6) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) bioD bioD Bacillus subtilis 1423 -11528963 61731 biod (ec:6.3.3.3) (de:synthetase) (dtbs)) (db:swissprot) BIOD_BACSU P53558 BACILLUS SUBTILIS 1423 -11528963 7000684709 biod dethiobiotin synthetase biod (db:pir2.dat) E69594 E69594 Bacillus subtilis 1423 -11528963 220064 biod desthiobiotin synthetase (fn:biotin pathway) (db:genpept-bct1) (de:bacillus subtilis biotin biosynthetic operon genes, complete andpartial cds.) (le:5390) (re:6085) (di:direct) BSU51868 U51868 g1277028 Bacillus subtilis 1423 -11528963 7500877828 biod dethiobiotin synthetase (fn:biotin biosynthesis) (db:genpept-bct1) (ec:6.3.3.3) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:92803) (re:93498) (di:complement) BSUB0016 Z99119 g2635505 Bacillus subtilis 1423 -11528963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741438	987	23143	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741440	988	23144	762	254

Description

GTC ORF with score 318 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f2i9 genomic sequence,complete sequence.) (nt:unknown protein) (le:47876:48026:48227:48637) (re:47930:48147:48287:48705) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741446	989	23145	864	288

Description

6500725106 8-amino-7-oxononanoate synthase:7-keto-8-amino-pelargonic acid synthetase:7-kap synthetase:l-alanine--pimelyl coa ligase (gtcfc:9.6) (ec:2.3.1.47) (keggfc:9.6) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) bioF bioF Bacillus subtilis 1423 -11528964 61738 biof (ec:2.3.1.47) (de:ligase)) (db:swissprot) BIOF_BACSU P53556 BACILLUS SUBTILIS 1423 -11528964 7000684710 biof 8-amino-7-oxononanoate synthase biof (cl:5-aminolevulinate synthase) (db:pir2.dat) F69594 F69594 Bacillus subtilis 1423 -11528964 220063 biof kapa synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:85763) (re:86932) (di:direct) AF008220 AF008220 g2293185 Bacillus subtilis 1423 -11528964 4000706926 biof l-alanine -pimelyl coa ligase (fn:biotin pathway) (db:genpept-bct1) (de:bacillus subtilis biotin biosynthetic operon genes, complete andpartial cds.) (le:4224) (re:5393) (di:direct) BSU51868 U51868 g1277027 Bacillus subtilis 1423 -11528964 7500877830 biof 8-amino-7-oxononanoate synthase (fn:biotin biosynthesis) (db:genpept-bct1) (ec:2.3.1.47) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:93495) (re:94664) (di:complement) BSUB0016 Z99119 g2635506 Bacillus subtilis 1423 -11528964

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741469	990	23146	777	259

Description

6500725107 adenosylmethionine-8-amino-7-oxononanoate aminotransferase:7:8-diamino-pelargonic acid aminotransferase:dapa aminotransferase (gtcfc:9.6:10.7) (ec:2.6.1.62) (keggfc:9.6) (bsorffc:3.4.1:4.3.3) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-protein translation and modification) bioA bioA Bacillus subtilis 1423 -11528965 61705 bioa (ec:2.6.1.62) (de:aminotransferase)) (db:swissprot) BIOA_BACSU P53555 BACILLUS SUBTILIS 1423 -11528965 7000684705 bioa adenosylmethionine-8-amino-7-oxononanoate aminotransferase bioa (cl:beta-alanine--pyruvate transaminase) (db:pir2.dat) C69594 C69594 Bacillus subtilis 1423 -11528965 220062 bioa dapa aminotransferase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:84427) (re:85773) (di:direct) AF008220 AF008220 g2293184 Bacillus subtilis 1423 -11528965 4000706922 bioa dapa aminotransferase (fn:biotin pathway) (db:genpept-bct1) (de:bacillus subtilis biotin biosynthetic operon genes, complete andpartial cds.) (le:2888) (re:4234) (di:direct) BSU51868 U51868 g1277026 Bacillus subtilis 1423 -11528965 7500877799 bioa adenosylmethionine-8-amino-7-oxononanoate (fn:biotin biosynthesis) (db:genpept-bct1) (ec:2.6.1.62) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:94654) (re:96000) (di:complement) BSUB0016 Z99119 g2635507 Bacillus subtilis 1423 -11528965

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741472	991	23147	375	125

Description

6500725108 6-carboxyhexanoate-coa ligase (gtcfc:9.6) (ec:6.2.1.14) (keggfc:9.6) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) bioW bioW Bacillus subtilis 1423 -11528966 7000692069 biow 6-carboxyhexanoate-coa ligase biow (cl:6-carboxyhexanoate--coa ligase biow) (db:pir2.dat) H69594 H69594 Bacillus subtilis 1423 -11528966 4000714178 biow pimelyl-coa synthetase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:83703) (re:84437) (di:direct) AF008220 AF008220 g2293183 Bacillus subtilis 1423 -11528966 7500963313 biow 6-carboxyhexanoate-coa ligase (fn:biotin biosynthesis) (db:genpept-bct1) (ec:6.2.1.14) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:95990) (re:96724) (di:complement) BSUB0016 Z99119 g2635508 Bacillus subtilis 1423 -11528966

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741475	992	23148	624	207

Description

6500725109 dihydropteroate synthase:dhps:dihydropteroate pyrophosphorylase (gtcfc:9.6) (ec:2.5.1.15) (keggfc:9.7) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) sul sul Bacillus subtilis 1423 -11528967 7000689078 sul dihydropteroate synthase::dihydropteroate pyrophosphorylase (cl:dihydropteroate synthase:dihydropteroate synthase homology) (ec:2.5.1.15) (db:pir1.dat) G69719 G69719 Bacillus subtilis 1423 -11528967 7500954034 sul dihydropteroate pyrophosphorylase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:149336) (re:150193) (di:direct) BAC180K D26185 g467466 Bacillus subtilis 1423 -11528967 215066 sul dihydropteroate synthase (fn:dihydrofolate biosynthesis) (db:genpept-bct1) (ec:2.5.1.15) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:85734) (re:86591) (di:direct) BSUB0001 Z99104 g2632344 Bacillus subtilis 1423 -11528967 206167 sul dihydropteroate synthase:sul:dihydropteroate pyrophosphorylase (cl:dihydropteroate synthase:dihydropteroate synthase homology) (ec:2.5.1.15) (db:pir) G69719 G69719 Bacillus subtilis 1423 -11528967

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741481	993	23149	513	170

Description

6500725110 7:8-dihydro-6-hydroxymethylpterin pyrophosphokinase:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase:7:8-dihydro-6-hydroxymethylpterin-pyrophosphokinase:hppk:6-hydroxymethyl-7:8-dihydropterin pyrophosphokinase:pppk (gtcfc:9.6) (ec:2.7.6.3) (keggfc:9.7) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) folK folK Bacillus subtilis 1423 -11528968 77549 folk (ec:2.7.6.3) (de:(hppk) (6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase) (pppk)) (db:swissprot) HPPK_BACSU P29252 BACILLUS SUBTILIS 1423 -11528968 7000685555 folk 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase::6-hydroxymethyl-7:8-dihydropterin pyrophosphokinase:7:8-dihydro-6-hydroxymethylpterin pyrophosphokinase (cl:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase homology) (ec:2.7.6.3) (db:pir2.dat) S66109 S66109 Bacillus subtilis 1423 -11528968 7500883497 folk 7:8-dihydro-6-hydroxymethylpterin-pyrophosphokin (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:150545) (re:151048) (di:direct) BAC180K D26185 g467468 Bacillus subtilis 1423 -11528968 215068 folk 7:8-dihydro-6-hydroxymethylpterin (fn:dihydrofolate biosynthesis) (db:genpept-bct1) (ec:2.7.6.3) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:86943) (re:87446) (di:direct) BSUB0001 Z99104 g2632346 Bacillus subtilis 1423 -11528968 206153 folk 7:8-dihydro-6-hydroxymethylpterin pyrophosphokinase folk (cl:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase homology) (db:pir) S66109 S66109 Bacillus subtilis 1423 -11528968 5000688529 (de:(folk) (pn:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase:hppk:6- hydroxymethyl-7,8-dihydropterin pyrophosphokinase:pppk:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase :7,8-dihydro-6-hydroxy) folK folK Bacillus subtilis 1423 10019909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741483	994	23150	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741491	995	23151	327	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741550	996	23152	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741561	997	23153	507	168

Description

6500725111 tmp:dfra dihydrofolate reductase (gtcfc:9.6) (ec:1.5.1.3) (keggfc:9.7:9.8) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) dfrA dfrA Bacillus subtilis 1423 -11528969 69433 dfra (ec:1.5.1.3) (de:dihydrofolate reductase,) (db:swissprot) DYR_BACSU P11045 BACILLUS SUBTILIS 1423 -11528969 217098 dfra dihydrofolate reductase (db:genpept-bct1) (ec:1.5.1.3) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (le:24342) (re:24848) (di:direct) BACYACA L77246 g1256641 Bacillus subtilis 1423 -11528969 7500880744 dfra dihydrofolate reductase (fn:glycine/purine/dna precursor synthesis,) (db:genpept-bct1) (ec:1.5.1.3) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: tmp) (le:100304) (re:100810) (di:complement) BSUB0012 Z99115 g2634601 Bacillus subtilis 1423 -11528969 7000685115 dfra dihydrofolate reductase dfra (cl:type i dihydrofolate reductase:type i dihydrofolate reductase homology) (db:pir) F69614 F69614 Bacillus subtilis 1423 -11528969 5000688526 (de:(dfra) (pn:dihydrofolate reductase) (gtcfc:9.06) (ec:1.5.1.3) (dyr_bacsu) (keggfc:9.7:9.8) (bsorffc:3.4.1) (db:gtc-bacillus subtilis)) dfrA dfrA Bacillus subtilis 1423 10012015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741579	998	23154	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741599	999	23155	450	149

Description

6500725112 gtp cyclohydrolase i:gtp-ch-i (gtcfc:9.6) (ec:3.5.4.16) (keggfc:9.7) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) mtrA mtrA Bacillus subtilis 1423 -11528970 73385 mtra (ec:3.5.4.16) (de:gtp cyclohydrolase i, (gtp-ch-i)) (db:swissprot) GCH1_BACSU P19465 BACILLUS SUBTILIS 1423 -11528970 7000685372 mtra gtp cyclohydrolase i:mtra (cl:gtp cyclohydrolase i) (ec:3.5.4.16) (db:pir2.dat) A38256 A38256 Bacillus subtilis 1423 -11528970 7500882242 mtra regulatory protein (sr:b.subtilis (strain w168) cell line bg2087 dna, clone 7a) (db:genpept-bct1) (de:b.subtilis regulatory protein (mtra and mtrb) genes, complete cds.) (le:396) (re:968) (di:direct) BACMTRAA M37320 g143231 Bacillus subtilis 1423 -11528970 216368 mtra mtra (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:396) (re:968) (di:direct) BACVARGNS M80245 g143799 Bacillus subtilis 1423 -11528970 217025 mtra gtp cyclohydrolase i (fn:tetrahydrofolate biosynthesis) (db:genpept-bct1) (ec:3.5.4.16) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:188480) (re:189052) (di:complement) BSUB0012 Z99115 g2634696 Bacillus subtilis 1423 -11528970 140973 mtra gtp cyclohydrolase i:mtra (cl:gtp cyclohydrolase i) (ec:3.5.4.16) (db:pir) A38256 A38256 Bacillus subtilis 1423 -11528970 5000688530 (de:(mtra) (pn:gtp-ch-i:gtp cyclohydrolase i) (gtcfc:9.06) (ec:3.5.4.16) (gch1_bacsu) (keggfc:9.7) (bsorffc:3.4.1) (db:gtc-bacillus subtilis)) mtrA mtrA Bacillus subtilis 1423 10015919

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741658	1000	23156	264	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741660	1001	23157	588	195

Description

6500725113 folyl-polyglutamate synthetase:folylpolyglutamate synthase:folylpoly-gamma-glutamate synthetase:fpgs (gtcfc:9.6) (ec:6.3.2.17) (keggfc:9.7) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) folC folC Bacillus subtilis 1423 -11528971 72229 folc (ec:6.3.2.17) (de:synthetase) (fpgs)) (db:swissprot) FOLC_BACSU Q05865 BACILLUS SUBTILIS 1423 -11528971 7000685314 folc folyl-polyglutamate synthetase folc (db:pir2.dat) B40646 B40646 Bacillus subtilis 1423 -11528971 7500881705 folc folyl-polyglutamate synthetase (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis valyl trna synthetase (vals) gene, 3' end cds;folyl-polyglutamate synthetase (folc) gene, complete cds; comcgene, 5' end cds.) (le:231) (re:1523) (di:direct) BACFOLC L04520 g142936 Bacillus subtilis 1423 -11528971 215629 folc folyl-polyglutamate synthetase (fn:folate biosynthesis) (db:genpept-bct1) (ec:6.3.2.17) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:69443) (re:70735) (di:complement) BSUB0015 Z99118 g2635273 Bacillus subtilis 1423 -11528971 170004 folc folyl-polyglutamate synthetase folc (db:pir) B40646 B40646 Bacillus subtilis 1423 -11528971 5000688528 (de:(folc) (pn:folylpolyglutamate synthase:fpgs:folylpolyglutamate synthase :folylpoly-gamma-glutamate synthetase:fpgs) (gtcfc:9.06) (ec:6.3.2.17) (folc_bacsu) (keggfc:9.7) (bsorffc:3.4.1) (db:gtc-bacillus subtilis)) folC folC Bacillus subtilis 1423 10014780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741661	1002	23158	192	63

Description

6500725114 pab:pabb para-aminobenzoate synthase:subunit a:para-aminobenzoate synthase component i:adc synthase (gtcfc:9.6) (ec:4.1.3.-) (keggfc:14.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) pabB pabB Bacillus subtilis 1423 -11528972 88415 pabb:pab (ec:4.1.3.-) (de:para-aminobenzoate synthase component i, (adc synthase)) (db:swissprot) PABB_BACSU P28820 BACILLUS SUBTILIS 1423 -11528972 7000686074 pabb para-aminobenzoate synthase:chain a pabb:p-aminobenzoate synthase component i (cl:anthranilate synthase component i) (ec:4.1.3.-) (db:pir2.dat) A37854 A37854 Bacillus subtilis 1423 -11528972 7500887589 pab subunit a of para-aminobenzoate (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:146463) (re:147875) (di:direct) BAC180K D26185 g467463 Bacillus subtilis 1423 -11528972 215063 (sr:b.subtilis (strain vb157) vegetative cell dna, clones pjs(1,2)) (db:genpept-bct1) (de:b.subtilis folic acid biosynthetic operon encodingpara-aminobenzoic acid synthase, component i (pab), glutamineamidotransferase (trpg), pot. p-aminobenzoate synth... BACRFOLA M34053 g143407 Bacillus subtilis 1423 -11528972 216578 pabb para-aminobenzoate synthase subunit a (fn:folate biosynthesis) (db:genpept-bct1) (ec:4.1.3.-) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: pab) (le:82861) (re:84273) (di:direct) BSUB0001 Z99104 g2632341 Bacillus subtilis 1423 -11528972 170410 pabb para-aminobenzoate synthase:chain a pabb:p-aminobenzoate synthase component i (ec:4.1.3.-) (db:pir) A37854 A37854 Bacillus subtilis 1423 -11528972 5000688448 (de:(pabb) (pn:para-aminobenzoate synthase component i:adc synthase:para-aminobenzoate synthase component i :adc synthase) (gn:pab) (gtcfc:5.15:9.12) (ec:4.1.3.-) (pabb_bacsu) (keggfc:1.8:5.9:5.15:9.13) (bsorffc:3.4.1) (db:gtc-b) pabB pabB Bacillus subtilis 1423 10030544

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741674	1003	23159	702	233

Description

6500725115 aminodeoxychorismate lyase:4-amino-4-deoxychorismate lyase:adc lyase (gtcfc:9.6) (ec:4.-.-.-) (keggfc:14.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) pabC pabC Bacillus subtilis 1423 -11528973 88421 pabc (ec:4.-.-.-) (de:4-amino-4-deoxychorismate lyase, (adc lyase)) (db:swissprot) PABC_BACSU P28821 BACILLUS SUBTILIS 1423 -11528973 7000686075 pabc aminodeoxychorismate lyase pabc (db:pir2.dat) C37854 C37854 Bacillus subtilis 1423 -11528973 7500887590 pabc enzyme required for para-aminobenzoate (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:148473) (re:149354) (di:direct) BAC180K D26185 g467465 Bacillus subtilis 1423 -11528973 215065 (sr:b.subtilis (strain vb157) vegetative cell dna, clones pjs(1,2)) (db:genpept-bct1) (de:b.subtilis folic acid biosynthetic operon encodingpara-aminobenzoic acid synthase, component i (pab), glutamineamidotransferase (trpg), pot. p-aminobenzoate synth... BACRFOLA M34053 g143409 Bacillus subtilis 1423 -11528973 216580 pabc aminodeoxychorismate lyase (fn:folate biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:84871) (re:85752) (di:direct) BSUB0001 Z99104 g2632343 Bacillus subtilis 1423 -11528973 170412 pabc aminodeoxychorismate lyase pabc (db:pir) C37854 C37854 Bacillus subtilis 1423 -11528973 5000688542 (de:(pabc) (pn:4-amino-4-deoxychorismate lyase:adc lyase:4-amino-4-deoxychorismate lyase :adc lyase) (gtcfc:9.06) (ec:4.-.-.-) (pabc_bacsu) (keggfc:11.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis)) pabC pabC Bacillus subtilis 1423 10030550

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741678	1004	23160	489	162

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741689	1005	23161	714	237

Description

5000689511 yace:fola dihydroneopterin aldolase:hypothetical 13.5 kd protein in sul-folk intergenic region (gtcfc:9.6) (keggfc:14.2) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) folA folA Bacillus subtilis 1423 -11528974 109593 folb:fola (ec:4.1.2.25) (de:dihydroneopterin aldolase, (dhna)) (db:swissprot) FOLB_BACSU P28823 BACILLUS SUBTILIS 1423 -11528974 7000687151 fola:folb dihydroneopterin aldolase:fola:folate biosynthesis protein 1 sul 3 region (cl:dihydroneopterin aldolase fola:dihydroneopterin aldolase homology) (ec:4.1.2.25) (db:pir2.dat) E37854 E37854 Bacillus subtilis 1423 -11528974 7500881697 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:150186) (re:150548) (di:direct) BAC180K D26185 g467467 Bacillus subtilis 1423 -11528974 215067 (sr:b.subtilis (strain vb157) vegetative cell dna, clones pjs(1,2)) (db:genpept-bct1) (de:b.subtilis folic acid biosynthetic operon encodingpara-aminobenzoic acid synthase, component i (pab), glutamineamidotransferase (trpg), pot. p-aminobenzoate synth... BACRFOLA M34053 g143411 Bacillus subtilis 1423 -11528974 216582 fola dihydroneopterin aldolase (fn:folate biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yace) (le:86584) (re:86946) (di:direct) BSUB0001 Z99104 g2632345 Bacillus subtilis 1423 -11528974 170003 fola dihydroneopterin aldolase fola:folate biosynthesis protein 1 sul 3 region (db:pir) E37854 E37854 Bacillus subtilis 1423 -11528974 6500725116 yace dihydroneopterin aldolase:hypothetical 13.5 kd protein in sul-folk intergenic region (gtcfc:9.6) (keggfc:14.2) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) folA folA Bacillus subtilis 1423 -11528974

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741693	1006	23162	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741771	1007	23163	243	80

Description

6500725117 transcriptional regulator and biotin acetyl-coa-carboxylase synthetase:bira bifunctional protein:biotin operon repressor:biotin--(gtcfc:9.6:10.2) (ec:6.3.4.15) (keggfc:14.1) (bsorffc:3.4.1:6.1.3) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-transcription--mrna synthesis and modi... birA birA Bacillus subtilis 1423 -11528975 61751 bira (ec:6.3.4.15) (de:coa-carboxylase) synthetase), (biotin--protein ligase)) (db:swissprot) BIRA_BACSU P42975 BACILLUS SUBTILIS 1423 -11528975 7000684712 bira transcription repressor of biotin operon bira (cl:bacillus subtilis transcription repressor of biotin operon bira) (db:pir2.dat) A69595 A69595 Bacillus subtilis 1423 -11528975 217161 bira biotin acetyl-coa-carboxylase ligase) (fn:bifunctional biotin operon repressor) (db:genpept-bct1) (ec:6.3.4.15) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth g... BACYPIA L47709 g1146239 Bacillus subtilis 1423 -11528975 7500877839 bira transcriptional regulator and biotin (fn:negative regulation of the biotin operon) (db:genpept-bct1) (ec:6.3.4.15) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:158620) (re:159597) (di:complement) BSUB0012 Z99115 g2634662 Bacillus subtilis 1423 -11528975 5000688880 (de:(bira) (pn:biotin--:bira bifunctional protein:biotin operon repressor:biotin-) (gtcfc:12.13) (ec:6.3.4.15) (bira_bacsu) (keggfc:11.1) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) birA birA Bacillus subtilis 1423 10004459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741772	1008	23164	486	161

Description

6500725118 yqia:fold methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase (gtcfc:9.6:10.7) (keggfc:14.1) (bsorffc:3.4.1:4.3.3) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of macromolecules-protein translation and modification) folD folD Bacillus subtilis 1423 -11528976 72237 fold (ec:1.5.1.5:3.5.4.9) (de:methenyltetrahydrofolate cyclohydrolase,) (db:swissprot) FOLD_BACSU P54382 BACILLUS SUBTILIS 1423 -11528976 7000685316 fold methylenetetrahydrofolate dehydrogenase nadp+:methenyltetrahydrofolate cyclohydrolase (cl:methylenetetrahydrofolate dehydrogenase (nad+):methylenetetrahydrofolate dehydrogenase (nad+) homology) (ec:1.5.1.5:3.5.4.9) (db:pir2.dat) E69626 E69626 Bacillus subtilis 1423 -11528976 216160 yqia (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:190351) (re:191202) (di:direct) BACJH642 D84432 g1303916 Bacillus subtilis 1423 -11528976 7500881709 fold methenyltetrahydrofolate cyclohydrolase (fn:purines and amino acids biosynthesis) (db:genpept-bct1) (ec:1.5.1.5:3.5.4.9) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqia;) (le:132419) (re:133270) (di:complement) BSUB0013 Z99116 g2634865 Bacillus subtilis 1423 -11528976 5000688535 (de:(fold) (pn:methylenetetrahydrofolate dehydrogenase) (gtcfc:9.06) (ec:1.5.1.5) (fold_bacsu) (keggfc:1.9:9.8) (db:gtc-bacillus subtilis)) folD folD Bacillus subtilis 1423 10014788

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741797	1009	23165	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741799	1010	23166	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741807	1011	23167	282	93

Description

6500725119 biotin:bioi:biosynthesis cytochrome p450-like enzyme (gtcfc:9.6) (ec:1.14.-.-) (keggfc:14.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) bioI bioI Bacillus subtilis 1423 -11528977 61744 bioi (ec:1.14.-.-) (de:biotin biosynthesis; cytochrome p450-like enzyme,) (db:swissprot) BIOI_BACSU P53554 BACILLUS SUBTILIS 1423 -11528977 7000684711 bioi cytochrome p450-like enzyme bioi (cl:cytochrome p450) (db:pir2.dat) G69594 G69594 Bacillus subtilis 1423 -11528977 220066 bioi cytochrome p450 enzyme (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:88703) (re:89890) (di:direct) AF008220 AF008220 g2293188 Bacillus subtilis 1423 -11528977 4000706928 bioi cytochrome p450-like enzyme (fn:pimelic acid synthesis) (db:genpept-bct1) (de:bacillus subtilis biotin biosynthetic operon genes, complete andpartial cds.) (le:7164) (re:8351) (di:direct) BSU51868 U51868 g1277030 Bacillus subtilis 1423 -11528977 7500877838 bioi cytochrome p450-like enzyme (fn:biotin biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:90537) (re:91724) (di:complement) BSUB0016 Z99119 g2635503 Bacillus subtilis 1423 -11528977 5000689432 (de:(bioi) (pn:cytochrome p450-like enzyme) (gn:biotin biosynthesis) (gtcfc:13.07) (ec:1.14.-.-) (bioi_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) bioI bioI Bacillus subtilis 1423 10004452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741808	1012	23168	234	77

Description

6500725120 biotin synthetase (gtcfc:9.6) (ec:2.8.1.-) (keggfc:14.1) (bsorffc:3.4.1) (db:gtc-bacillus subtilis) (gtcfc:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) bioB bioB Bacillus subtilis 1423 -11528978 61717 biob (ec:2.8.1.6) (de:biotin synthase, (biotin synthetase)) (db:swissprot) BIOB_BACSU P53557 BACILLUS SUBTILIS 1423 -11528978 7000684707 biob biotin synthetase biob (cl:biotin synthetase) (db:pir2.dat) D69594 D69594 Bacillus subtilis 1423 -11528978 220065 biob biotin synthase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:87627) (re:88634) (di:direct) AF008220 AF008220 g2293187 Bacillus subtilis 1423 -11528978 4000706925 biob biotin synthase (fn:biotin pathway) (db:genpept-bct1) (de:bacillus subtilis biotin biosynthetic operon genes, complete andpartial cds.) (le:6088) (re:7095) (di:direct) BSU51868 U51868 g1277029 Bacillus subtilis 1423 -11528978 7500877807 biob biotin synthetase (fn:biotin biosynthesis) (db:genpept-bct1) (ec:2.8.1.-) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:91793) (re:92800) (di:complement) BSUB0016 Z99119 g2635504 Bacillus subtilis 1423 -11528978

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741816	1013	23169	855	285

Description

GTC ORF with score 278 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, essa i contig fragment no.6.) (nt:similarity to isp4 protein - fission yeast) (le:12085:12896:13233) (re:12810:13151:13802) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741818	1014	23170	477	159

Description

5000688661 hypothetical protein:recf protein (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) recF recF Bacillus subtilis 1423 -11528979 93796 recf (de:recf protein) (db:swissprot) RECF_BACSU P05651 BACILLUS SUBTILIS 1423 -11528979 131410 recf dna repair and genetic recombination protein recf (cl:recf protein) (db:pir1.dat) (mp:0 min) D22930 D22930 Bacillus subtilis 1423 -11528979 214994 recf recombination protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:67039) (re:68151) (di:direct) BAC180K D26185 g467394 Bacillus subtilis 1423 -11528979 7500889569 recf (fn:dna repair and genetic recombination) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:3437) (re:4549) (di:direct) BSUB0001 Z99104 g2632271 Bacillus subtilis 1423 -11528979 6500725121 hypothetical protein:recf protein (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) recF recF Bacillus subtilis 1423 -11528979

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741895	1015	23171	573	191

Description

5000688663 recm:recd:recr hypothetical protein:recombination protein recr (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) recR recR Bacillus subtilis 1423 -11528980 304136 recr:recm:recd (de:recombination protein recr) (db:swissprot) RECR_BACSU P24277 BACILLUS SUBTILIS 1423 -11528980 7000686291 recr dna repair and genetic recombination recr:recm protein (cl:recr protein) (db:pir2.dat) B69691 B69691 Bacillus subtilis 1423 -11528980 7500889589 recr recombination protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:92467) (re:93063) (di:direct) BAC180K D26185 g467411 Bacillus subtilis 1423 -11528980 219569 recr (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (le:2314) (re:2910) (di:direct) BSRECM X17014 g453239 Bacillus subtilis 1423 -11528980 7502851563 recr (fn:dna repair and genetic recombination) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: recm) (le:28865) (re:29461) (di:direct) BSUB0001 Z99104 g2632288 Bacillus subtilis 1423 -11528980 7502851564 recr (db:genpept) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (le:2314) (re:2910) (di:direct) BSRECM X17014 g453239 Bacillus subtilis 1423 -11528980 93829 recr:recm:recd (de:recombination protein recr) (db:swissprot) RECR_BACSU P24277 BACILLUS SUBTILIS 1423 -11528980 206272 recr dna repair and genetic recombination recr (db:pir) B69691 B69691 Bacillus subtilis 1423 -11528980 215011 recr (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (le:2314) (re:2910) (di:direct) BSRECM X17014 g453239 Bacillus subtilis 1423 -11528980 6500725122 recm:recd hypothetical protein:recombination protein recr (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) recR recR Bacillus subtilis 1423 -11528980

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741903	1016	23172	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741905	1017	23173	405	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741908	1018	23174	807	269

Description

5000688658 transcription-repair coupling factor:trcf (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) mfd mfd Bacillus subtilis 1423 -11528981 83619 mfd (de:transcription-repair coupling factor (trcf)) (db:swissprot) MFD_BACSU P37474 BACILLUS SUBTILIS 1423 -11528981 7000685837 mfd transcription-repair coupling factor mfd (cl:transcription-repair coupling protein:dead/h box helicase homology) (db:pir2.dat) S66085 S66085 Bacillus subtilis 1423 -11528981 7500885575 mfd transcription-repair coupling factor (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:124030) (re:127563) (di:direct) BAC180K D26185 g467444 Bacillus subtilis 1423 -11528981 215044 mfd transcription-repair coupling factor (fn:probably involved in homologous dna) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:60428) (re:63961) (di:direct) BSUB0001 Z99104 g2632322 Bacillus subtilis 1423 -11528981 206293 mfd transcription-repair coupling factor mfd (cl:transcription-repair coupling protein:dead/h box helicase homology) (db:pir) S66085 S66085 Bacillus subtilis 1423 -11528981 6500725123 transcription-repair coupling factor:trcf (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) mfd mfd Bacillus subtilis 1423 -11528981

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741909	1019	23175	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741917	1020	23176	570	189

Description

6500725124 dna-3-methyladenine glycosylase:dna-3-methyladenine glycosidase:3-methyladenine-dna glycosylase (gtcfc:10.10) (ec:3.2.2.21) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) alkA alkA Bacillus subtilis 1423 -11528982 57520 alka (ec:3.2.2.21) (de:glycosylase)) (db:swissprot) 3MGA_BACSU P37878 BACILLUS SUBTILIS 1423 -11528982 7000684465 alka dna-3-methyladenine glycosylase alka (db:pir2.dat) E69584 E69584 Bacillus subtilis 1423 -11528982 215146 alka 3-methyladenine dna glycosylase (sr:bacillus subtilis (strain:168t) cell_line:bacillus subtilis 168) (db:genpept-bct1) (de:bacillus subtilis alka gene for 3-methyladenine dna glycosylase,complete cds.) (le:304) (re:1215) (di:direct) BACALKA D14465 g436209 Bacillus subtilis 1423 -11528982 6000684459 alka dna-3-methyladenine glycosylase (fn:adaptative response to dna alkylation) (db:genpept-bct1) (ec:3.2.2.21) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:202533) (re:203444) (di:complement) BSUB0001 Z99104 g2632447 Bacillus subtilis 1423 -11528982 7500876105 alka dna-3-methyladenine glycosylase (fn:adaptative response to dna alkylation) (db:genpept-bct1) (ec:3.2.2.21) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:7883) (re:8794) (di:complement) BSUB0002 Z99105 g2632465 Bacillus subtilis 1423 -11528982 7500876106 alka 3-methyladenine dna glycosylase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:5516) (re:6427) (di:complement) AB006424 AB006424 g3599598 Bacillus subtilis 1423 -11528982 5000688655 (de:(alka) (pn:dna-3-methyladenine glycosidase:dna-3-methyladenine glycosidase :3-methyladenine-dna glycosylase) (gtcfc:10.10) (ec:3.2.2.21) (3mga_bacsu) (keggfc:11.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis)) alkA alkA Bacillus subtilis 1423 10000303

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741918	1021	23177	927	309

Description

5000688651 methylphosphotriester-dna alkyltransferase and transcriptional regulator:arac/xyls family:methylphosphotriester-dna alkyltransferase (gtcfc:10.10:10.2) (keggfc:14.2) (bsorffc:4.1.2:6.1.3) (db:gtc-bacillus subtilis) adaA adaA Bacillus subtilis 1423 -11528983 7500876555 adaa (de:methylphosphotriester-dna alkyltransferase) (db:swissprot) ADAA_BACSU P19219 BACILLUS SUBTILIS 1423 -11528983 123283 adaa methylphosphotriester-dna alkyltransferase:adaab operon transcription activator adaa (cl:methylphosphotriester-dna methyltransferase:methylphosphotriester-dna methyltransferase homology) (ec:2.1.1.-) (db:pir1.dat) XUBSMM S11483 Bacillus subtilis 1423 -11528983 6000684477 (db:genpept-bct1) (de:b.subtilis ada operon adaa and adab genes encodingmethylphosphotriester- dna methyltransferase and methylguanine-dnamethyltransferase.) (nt:adaa) (le:227) (re:862) (di:direct) BSADAAB X53399 g39787 Bacillus subtilis 1423 -11528983 218990 adaa methylphosphotriester-dna alkyltransferase and (fn:adaptative response to dna alkylation; positive) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:203715) (re:204350) (di:direct) BSUB0001 Z99104 g2632448 Bacillus subtilis 1423 -11528983 7500876556 adaa methylphosphotriester-dna alkyltransferase and (fn:adaptative response to dna alkylation; positive) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:9065) (re:9700) (di:direct) BSUB0002 Z99105 g2632466 Bacillus subtilis 1423 -11528983 6500725125 adaa methylphosphotriester-dna alkyltransferase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:6698) (re:7333) (di:direct) AB006424 AB006424 g3599599 Bacillus subtilis 1423 -11528983 7502851565 (db:genpept) (de:b.subtilis ada operon adaa and adab genes encodingmethylphosphotriester-dna methyltransferase and methylguanine-dnamethyltransferase.) (nt:adaa) (le:227) (re:862) (di:direct) BSADAAB X53399 g39787 Bacillus subtilis 1423 -11528983 58590 adaa (de:methylphosphotriester-dna alkyltransferase) (db:swissprot) ADAA_BACSU P19219 BACILLUS SUBTILIS 1423 -11528983 7000684520 adaa methylphosphotriester-dna alkyltransferase:adaab operon transcriptional activator adaa (cl:methylphosphotriester-dna methyltransferase:methylphosphotriester-dna methyltransferase homology) (ec:2.1.1.-) (db:pir) XUBSMM F69582 Bacillus subtilis 1423 -11528983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741926	1022	23178	210	69

Description

6500725126 o6-methylguanine-dna methyltransferase:methylated-dna--protein-cysteine methyltransferase:o-6-methylguanine-dna alkyltransferase (gtcfc:10.10) (ec:2.1.1.63) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) adaB adaB Bacillus subtilis 1423 -11528984 7500876557 adab (ec:2.1.1.63) (de:methylguanine-dna alkyltransferase)) (db:swissprot) ADAB_BACSU P19220 BACILLUS SUBTILIS 1423 -11528984 123277 adab methylated-dna--protein-cysteine s-methyltransferase:adab:o 6 -alkylguanine-dna alkyltransferase:o 6 -methylguanine-dna alkyltransferase:o-methylguanine-dna methyltransferase (cl:methylated-dna--protein-cysteine s-methyltransferase:methylated-dna--protein-cysteine s-methyltransferase homology) (ec:2.1.1.63) (db:pir1.dat) XUBSMB S11564 Bacillus subtilis 1423 -11528984 5000688652 (db:genpept-bct1) (de:b.subtilis ada operon adaa and adab genes encodingmethylphosphotriester- dna methyltransferase and methylguanine-dnamethyltransferase.) (nt:adab) (le:849) (re:1388) (di:direct) BSADAAB X53399 g39788 Bacillus subtilis 1423 -11528984 218991 adab o6-methylguanine-dna methyltransferase (fn:adaptative response to dna alkylation) (db:genpept-bct1) (ec:2.1.1.63) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:204337) (re:204876) (di:direct) BSUB0001 Z99104 g2632449 Bacillus subtilis 1423 -11528984 6000684479 adab o6-methylguanine-dna methyltransferase (fn:adaptative response to dna alkylation) (db:genpept-bct1) (ec:2.1.1.63) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:9687) (re:10226) (di:direct) BSUB0002 Z99105 g2632467 Bacillus subtilis 1423 -11528984 7500876558 adab o-6-methylguanine-dna alkyltransferase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:7320) (re:7859) (di:direct) AB006424 AB006424 g3599600 Bacillus subtilis 1423 -11528984 7502851566 (db:genpept) (de:b.subtilis ada operon adaa and adab genes encodingmethylphosphotriester-dna methyltransferase and methylguanine-dnamethyltransferase.) (nt:adab) (le:849) (re:1388) (di:direct) BSADAAB X53399 g39788 Bacillus subtilis 1423 -11528984 58592 adab (ec:2.1.1.63) (de:methylguanine-dna alkyltransferase)) (db:swissprot) ADAB_BACSU P19220 BACILLUS SUBTILIS 1423 -11528984 7000684521 adab methylated-dna--protein-cysteine s-methyltransferase:adab:o 6 -alkylguanine-dna alkyltransferase:o 6 -methylguanine-dna alkyltransferase:o-methylguanine-dna methyltransferase (cl:methylated-dna--protein-cysteine s-methyltransferase:methylated-dna--protein-cysteine s-methyltransferase homology) (ec:2.1.1.63) (db:pir) XUBSMB G69582 Bacillus subtilis 1423 -11528984

Jc542 U.S. PTO 09/417507 10/14/99

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741927	1023	23179	315	104

Description

6500725127 mutator protein (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) mutT mutT Bacillus subtilis 1423 -11528985 7000694271 mutt mutator protein mutt (cl:mutt domain homology) (db:pir2.dat) D69663 D69663 Bacillus subtilis 1423 -11528985 302688 mutt (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, contains mutt motif, similar) (le:21373) (re:21822) (di:direct) AB001488 AB001488 g1881243 Bacillus subtilis 1423 -11528985 7500964988 mutt mutator protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:85117) (re:85566) (di:direct) BSUB0003 Z99106 g2632733 Bacillus subtilis 1423 -11528985

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501741942	1024	23180	435	145

Description

5000688654 atp-dependent deoxyribonuclease:subunit b:atp-dependent nuclease subunit b (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) addB addB Bacillus subtilis 1423 -11528986 58613 addb (de:atp-dependent nuclease subunit b) (db:swissprot) ADDB_BACSU P23477 BACILLUS SUBTILIS 1423 -11528986 7000684524 addb atp-dependent deoxyribonuclease chain b addb:atp-dependent exonuclease synthesis protein addb (db:pir2.dat) A39432 A39432 Bacillus subtilis 1423 -11528986 7500876568 adda atp-dependent nuclease (sr:b.subtilis dna) (db:genpept-bct1) (de:bacillus subtilis atp-dependent nuclease (adda) and (addb), andopen reading frame 3, partial cds.) (le:502) (re:4002) (di:direct) BACADDAA M63489 g142439 Bacillus subtilis 1423 -11528986 215127 addb atp-dependent deoxyribonuclease subunit b (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:136293) (re:139793) (di:direct) BSUB0006 Z99109 g2633398 Bacillus subtilis 1423 -11528986 4000706895 addb atp-dependent nuclease (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; see ref (3); in embl entry m63489 this) (le:18588) (re:22088) (di:direct) BSY14081 Y14081 g2226191 Bacillus subtilis 1423 -11528986 7502851567 addb atp-dependent nuclease (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; see ref (3); in embl entry m63489 this) (le:18588) (re:22088) (di:direct) BSY14081 Y14081 g2226191 Bacillus subtilis 1423 -11528986 169882 addb atp-dependent deoxyribonuclease chain b addb:atp-dependent exonuclease synthesis protein addb (db:pir) A39432 A39432 Bacillus subtilis 1423 -11528986 6500725128 atp-dependent deoxyribonuclease:subunit b:atp-dependent nuclease subunit b (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) addB addB Bacillus subtilis 1423 -11528986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742023	1025	23181	909	302

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742025	1026	23182	297	98

Description

6500725129 rece5:adda atp-dependent deoxyribonuclease:subunit a:atp-dependent nuclease subunit a (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) addA addA Bacillus subtilis 1423 -11528987 58611 adda (de:atp-dependent nuclease subunit a) (db:swissprot) ADDA_BACSU P23478 BACILLUS SUBTILIS 1423 -11528987 7000684523 adda atp-dependent deoxyribonuclease chain a adda:atp-dependent exonuclease synthesis protein adda (db:pir2.dat) B39432 B39432 Bacillus subtilis 1423 -11528987 7500876567 addb atp-dependent nuclease (sr:b.subtilis dna) (db:genpept-bct1) (de:bacillus subtilis atp-dependent nuclease (adda) and (addb), andopen reading frame 3, partial cds.) (le:3988) (re:7687) (di:direct) BACADDAA M63489 g142440 Bacillus subtilis 1423 -11528987 215128 adda atp-dependent deoxyribonuclease subunit a (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: rece5) (le:139780) (re:143478) (di:direct) BSUB0006 Z99109 g2633399 Bacillus subtilis 1423 -11528987 4000706894 adda atp-dependent nuclease (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:see ref (3); in embl entry m63489 this gene is) (le:22075) (re:25773) (di:direct) BSY14081 Y14081 g2226192 Bacillus subtilis 1423 -11528987 5000688653 adda atp-dependent nuclease (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:see ref (3); in embl entry m63489 this gene is) (le:22075) (re:25773) (di:direct) BSY14081 Y14081 g2226192 Bacillus subtilis 1423 -11528987 169881 adda atp-dependent deoxyribonuclease chain a adda:atp-dependent exonuclease synthesis protein adda (db:pir) B39432 B39432 Bacillus subtilis 1423 -11528987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742026	1027	23183	759	252

Description

6500725130 yixa:sbcd exonuclease sbcd homolog (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) sbcD sbcD Bacillus subtilis 1423 -11528988 7000692975 sbcd exonuclease:sbcd:hypothetical protein addb 3 region (cl:bacillus subtilis exonuclease sbcd:phosphoesterase core homology) (ec:3.1.-.-) (db:pir1.dat) C39432 C39432 Bacillus subtilis 1423 -11528988 7500953292 (sr:b.subtilis dna) (db:genpept-bct1) (de:bacillus subtilis atp-dependent nuclease (adda) and (addb), andopen reading frame 3, partial cds.) (nt:orf 3; putative) (le:7759) (re:8520) (di:direct) BACADDAA M63489 g142441 Bacillus subtilis 1423 -11528988 215129 sbcd exonuclease sbcd homolog (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yixa) (le:143550) (re:144311) (di:direct) BSUB0006 Z99109 g2633400 Bacillus subtilis 1423 -11528988 170065 sbcd exonuclease:sbcd:hypothetical protein addb 3 region (cl:bacillus subtilis exonuclease sbcd) (ec:3.1.-.-) (db:pir) C39432 C39432 Bacillus subtilis 1423 -11528988

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742029	1028	23184	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742057	1029	23185	537	179

Description

GTC ORF with score 472 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome i bac f21m11 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:56649:56854:57200) (re:56768:57120:57376) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742144	1030	23186	198	65

Description

6500725131 dat1:dat o6-methylguanine dna alkyltransferase:methylated-dna--protein-cysteine methyltransferase:6-o-methylguanine-dna methyltransferase:o-6-methylguanine-dna-alkyltransferase (gtcfc:10.10) (ec:2.1.1.63) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) dat dat Bacillus subtilis 1423 -11528989 7500880003 dat:dat1 (ec:2.1.1.63) (de:alkyltransferase)) (db:swissprot) DAT1_BACSU P11742 BACILLUS SUBTILIS 1423 -11528989 123278 dat:dat1 methylated-dna--protein-cysteine s-methyltransferase:dat:o 6 -alkylguanine-dna alkyltransferase:o 6 -methylguanine-dna alkyltransferase:o-methylguanine-dna methyltransferase (cl:methylated-dna--protein-cysteine s-methyltransferase:methylated-dna--protein-cysteine s-methyltransferase homology) (ec:2.1.1.63) (db:pir1.dat) XUBSM1 S04877 Bacillus subtilis 1423 -11528989 5000688656 (db:genpept-bct1) (de:bacillus subtilis dat1 gene for o6-methylguanine-dnaalkyltransferase.) (nt:dat1 protein (aa 1-165)) (le:202) (re:699) (di:direct) BSDAT1 X15659 g39876 Bacillus subtilis 1423 -11528989 219123 dat o6-methylguanine dna alkyltransferase (db:genpept-bct1) (ec:2.1.1.63) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:26102) (re:26599) (di:direct) BSUB0008 Z99111 g2633725 Bacillus subtilis 1423 -11528989 67891 dat:dat1 (ec:2.1.1.63) (de:alkyltransferase)) (db:swissprot) DAT1_BACSU P11742 BACILLUS SUBTILIS 1423 -11528989 7000684985 dat:dat1 methylated-dna--protein-cysteine s-methyltransferase:dat:o 6 -alkylguanine-dna alkyltransferase:o 6 -methylguanine-dna alkyltransferase:o-methylguanine-dna methyltransferase (cl:methylated-dna--protein-cysteine s-methyltransferase:methylated-dna--protein-cysteine s-methyltransferase homology) (ec:2.1.1.63) (db:pir) XUBSM1 A60649 Bacillus subtilis 1423 -11528989

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742149	1031	23187	474	157

Description

6500725132 yloj:pria primosomal replication factor y:primosomal protein n (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) priA priA Bacillus subtilis 1423 -11528990 7500888445 pria (de:primosomal protein n' (replication factor y)) (db:swissprot) PRIA_BACSU P94461 BACILLUS SUBTILIS 1423 -11528990 7000694442 pria primosomal replication factor y pria (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) A69682 A69682 Bacillus subtilis 1423 -11528990 7500888447 pria primosomal replication factor y primosomal (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: yloj) (le:45047) (re:47464) (di:direct) BSUB0009 Z99112 g2633943 Bacillus subtilis 1423 -11528990 5500687795 yloj putative pria protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:6819) (re:9236) (di:direct) BSY13937 Y13937 g2337800 Bacillus subtilis 1423 -11528990

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742150	1032	23188	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742151	1033	23189	423	140

Description

6500725133 rece:reca multifunctional sos repair regulator:reca protein (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) recA recA Bacillus subtilis 1423 -11528991 219566 reca:rece (de:reca protein) (db:swissprot) RECA_BACSU P16971 BACILLUS SUBTILIS 1423 -11528991 7000686286 reca reca protein:multifunctional protein involved in homologous recombination a (cl:reca protein) (db:pir1.dat) RQBSEE S10370 Bacillus subtilis 1423 -11528991 5000688660 (db:genpept-bct1) (de:bacillus subtilis rece gene for rece protein.) (nt:rece protein (aa 1-347)) (le:215) (re:1258) (di:direct) BSRECE X52132 g40070 Bacillus subtilis 1423 -11528991 7500889530 reca multifunctional sos repair regulator (fn:involved in homologous recombination and dna) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: rece) (le:165595) (re:166638) (di:direct) BSUB0009 Z99112 g2634066 Bacillus subtilis 1423 -11528991 93727 reca:rece (de:reca protein) (db:swissprot) RECA_BACSU P16971 BACILLUS SUBTILIS 1423 -11528991

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742156	1034	23190	348	115

Description

6500725134 modification methylase bsu (gtcfc:10.10) (ec:2.1.1.73) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) mtbP mtbP Bacillus subtilis 1423 -11528992 84483 mtbp (ec:2.1.1.73) (de:methyltransferase bsu phi3t) (m.phi3ti)) (db:swissprot) MTBP_BACSU P05795 BACILLUS SUBTILIS 1423 -11528992 7502851568 mtbp (ec:2.1.1.73) (de:methyltransferase bsu phi3t) (m.phi3ti)) (db:swissprot) MTBP_BACSU P05795 BACTERIOPHAGE PHI-3T 10736 -11528992 123264 site-specific dna-methyltransferase cytosine-specific::cytosine-specific dna methylase:cytosine-specific dna methyltransferase:dna cytosine-5 -methyltransferase:dna cytosine methylase:cytosine-specific dna methylase:cytosine-specific dna methyltransferase:dna cytosine-5 -methyltransferase:dna cytosine methylase (cl:site-specific methyltransferase (cytosine-specific) ecorii) (ec:2.1.1.73) (db:pir1.dat) CTBPPT A24465 phage phi-3T 10736 -11528992 7000685872 mtbp modification methylase bsu mtbp (cl:site-specific methyltransferase (cytosine-specific) ecorii) (db:pir2.dat) D69661 D69661 Bacillus subtilis 1423 -11528992 327946 mtbp modification methylase bsu (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:170474) (re:171805) (di:complement) BSUB0011 Z99114 g2634418 Bacillus subtilis 1423 -11528992 7000685873 mtbp modification methylase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:113715) (re:115046) (di:direct) AF020713 AF020713 g3025620 Bacteriophage SPBc2 66797 -11528992 7500886016 (sr:bacteriophage phi-3t dna) (db:genpept-phg) (de:bacteriophage phi-3t methyltransferase (mtase) gene, complete cds.) (nt:methyltransferase (ttg start codon)) (le:714) (re:2045) (di:direct) PH3MTASE M13488 g215471 Bacteriophage phi-3T 10736 -11528992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742165	1035	23191	750	250

Description

6500725135 joob:ypob:nth endonuclease iii:probable endonuclease iii:dna-:apurinic or apyrimidinic site lyase (gtcfc:10.10) (ec:4.2.99.18) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) nth nth Bacillus subtilis 1423 -11528993 70151 nth:joob (ec:4.2.99.18) (de:apyrimidinic site) lyase)) (db:swissprot) END3_BACSU P39788 BACILLUS SUBTILIS 1423 -11528993 7000685157 nth:joob endonuclease iii dna repair nth (cl:apurinic/apyrimidinic endonuclease class ii) (db:pir2.dat) I40525 I40525 Bacillus subtilis 1423 -11528993 7500881013 nth endonuclease iii (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:46.2% of identity to the ... BACYPIA L47709 g1146249 Bacillus subtilis 1423 -11528993 217171 joob endonuclease iii (db:genpept-bct1) (de:bacillus subtilis 168 asparaginyl-trna synthetase (asns) andendonuclease iii (joob) genes, partial cds and dnad protein (dnad)and (jooc) genes, complete cds.) (nt:similar to the e. coli nth gene's endonuclease iii:) (le:1046) (re:... BSU11289 U11289 g533099 Bacillus subtilis 1423 -11528993 219792 nth endonuclease iii (fn:dna repair) (db:genpept-bct1) (ec:4.2.99.18) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: joob, ypob) (le:148457) (re:149116) (di:complement) BSUB0012 Z99115 g2634652 Bacillus subtilis 1423 -11528993 169978 nth:joob endonuclease iii dna repair nth (db:pir) I40525 I40525 Bacillus subtilis 1423 -11528993 5000688659 (de:(nth) (pn:probable endonuclease iii:probable endonuclease iii :dna-:apurinic or apyrimidinic site lyase) (gn:joob) (gtcfc:10.10) (ec:4.2.99.18) (end3_bacsu) (keggfc:11.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis)) nth nth Bacillus subtilis 1423 10012729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742166	1036	23192	282	93

Description

5000688662 hypothetical protein:dna repair protein recn:recombination protein n (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) recN recN Bacillus subtilis 1423 -11528994 93815 recn (de:dna repair protein recn (recombination protein n)) (db:swissprot) RECN_BACSU P17894 BACILLUS SUBTILIS 1423 -11528994 7000686289 recn dna repair and genetic recombination protein recn (cl:recn protein) (db:pir2.dat) B35128 B35128 Bacillus subtilis 1423 -11528994 7500889579 recn (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:197319) (re:199049) (di:direct) BACJH642 D84432 g1303923 Bacillus subtilis 1423 -11528994 216167 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis recombination and sporulation protein (recn, spoivb)genes , complete cds, arginine hydroximate resistance (ahrc) gene,3' end.) (nt:recombination protein (ttg start codon)) (le:131) (re:1... BACRECN M30297 g143402 Bacillus subtilis 1423 -11528994 216575 recn (fn:dna repair and genetic recombination) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:124572) (re:126302) (di:complement) BSUB0013 Z99116 g2634858 Bacillus subtilis 1423 -11528994 154671 recn dna repair and genetic recombination protein recn (cl:recn protein) (db:pir) B35128 B35128 Bacillus subtilis 1423 -11528994 6500725136 hypothetical protein:dna repair protein recn:recombination protein n (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) recN recN Bacillus subtilis 1423 -11528994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742193	1037	23193	372	124

Description

6500725137 uvrb:uvrc excinuclease abc:subunit c:excinuclease abc subunit c (gtcfc:10.10) (ec:4.1.99.3) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) uvrC uvrC Bacillus subtilis 1423 -11528995 104047 uvrc (de:excinuclease abc subunit c) (db:swissprot) UVRC_BACSU P14951 BACILLUS SUBTILIS 1423 -11528995 131426 uvrc excinuclease abc:chain c (cl:excinuclease abc chain c) (db:pir1.dat) (mp:70 min) A37192 A37192 Bacillus subtilis 1423 -11528995 215192 uvrb deoxyribodipyrimidine photolyase (sr:bacillus subtilis (strain 168) (tissue library: atcc 6633) dna) (db:genpept-bct1) (ec:4.1.99.3) (de:bacillus subtilis thioredoxin (trx), uvrb and aspartokinase iigenes, complete cds.) (le:461) (re:2257) (di:direct) BACAPKII J03294 g142521 Bacillus subtilis 1423 -11528995 220321 uvrc excinuclease abc subunit c (fn:excision of ultraviolet light-induced) (db:genpept-bct1) (ec:4.1.99.3) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: uvrb) (le:115064) (re:116860) (di:complement) BSUB0015 Z99118 g2635314 Bacillus subtilis 1423 -11528995 304194 uvrc deoxyribodipyrimidine photolyase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to uvrc in escherichia coli; previously) (le:53047) (re:54843) (di:direct) BSZ75208 Z75208 g1770045 Bacillus subtilis 1423 -11528995 5000688667 (de:(uvrc) (pn:excinuclease abc subunit c:excinuclease abc subunit c) (gtcfc:10.10) (ec:) (uvrc_bacsu) (keggfc:11.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis)) uvrC uvrC Bacillus subtilis 1423 10045817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742274	1038	23194	489	162

Description

6500725138 ytae:mutm formamidopyrimidine-dna glycosidase (gtcfc:10.10) (ec:3.2.2.23) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) mutM mutM Bacillus subtilis 1423 -11528996 7000692999 mutm formamidopyrimidine-dna glycosidase mutm (cl:formamidopyrimidine-dna glycosidase) (db:pir2.dat) B69663 B69663 Bacillus subtilis 1423 -11528996 4000714265 mutm formamidopyrimidine-dna glycosidase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:205959) (re:206795) (di:direct) AF008220 AF008220 g2293273 Bacillus subtilis 1423 -11528996 7500954274 mutm formamidopyrimidine-dna glycosidase (db:genpept-bct1) (ec:3.2.2.23) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ytae) (le:176272) (re:177108) (di:complement) BSUB0015 Z99118 g2635373 Bacillus subtilis 1423 -11528996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742283	1039	23195	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742284	1040	23196	471	156

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742304	1041	23197	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742306	1042	23198	546	182

Description

6500725139 excinuclease abc:subunit a (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) uvrA uvrA Bacillus subtilis 1423 -11528997 7500955284 uvra (de:excinuclease abc subunit a) (db:swissprot) UVRA_BACSU O34863 BACILLUS SUBTILIS 1423 -11528997 7000692972 uvra excinuclease abc chain a:excision endonuclease abc::chain a:uvra protein (cl:excinuclease abc chain a:atp-binding cassette homology) (ec:3.1.-.-) (db:pir2.dat) F69729 F69729 Bacillus subtilis 1423 -11528997 5500701749 uvra excinuclease abc subunit a (fn:excision of ultraviolet light-induced) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:12034) (re:14907) (di:complement) BSUB0019 Z99122 g2636042 Bacillus subtilis 1423 -11528997 7502851569 uvra excinuclease abc subunit a (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:15386) (re:18259) (di:direct) AF017113 AF017113 g2618842 Bacillus subtilis 1423 -11528997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742314	1043	23199	816	271

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742328	1044	23200	372	123

Description

6500725140 dina:uvra:uvrb excinuclease abc:subunit b (gtcfc:10.10) (keggfc:14.2) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) uvrB uvrB Bacillus subtilis 1423 -11528998 7500893892 uvrb:dina:uvr (de:excinuclease abc subunit b (dina protein)) (db:swissprot) UVRB_BACSU P37954 BACILLUS SUBTILIS 1423 -11528998 7000692973 uvrb:uvr:dina excinuclease abc chain b:dna repair protein dina:excision endonuclease abc::chain b:hypothetical protein dna damage-inducible a76 promoter 3 region:urvb homolog dina (cl:excinuclease abc chain b:dead/h box helicase homology) (ec:3.1.-.-) (db:pir2.dat) G69729 G69729 Bacillus subtilis 1423 -11528998 7500893894 uvrb excinuclease abc subunit b (fn:excision of ultraviolet light-induced) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: dina, uvra) (le:14915) (re:16900) (di:complement) BSUB0019 Z99122 g2636043 Bacillus subtilis 1423 -11528998 5500701748 uvrb excinuclease abc subunit b (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:13393) (re:15378) (di:direct) AF017113 AF017113 g2618841 Bacillus subtilis 1423 -11528998

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742329	1045	23201	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742338	1046	23202	396	131

Description

6500725141 ipa-57d:ywdg:ung uracil-dna glycosylase (gtcfc:10.10) (ec:3.2.2.-) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) ung ung Bacillus subtilis 1423 -11528999 7500893807 ung:ipa-57d (ec:3.2.2.-) (de:uracil-dna glycosylase, (udg)) (db:swissprot) UNG_BACSU P39615 BACILLUS SUBTILIS 1423 -11528999 7000686890 ung uracil-dna glycosylase:ung (cl:uracil-dna glycosylase) (ec:3.2.2.-) (db:pir2.dat) S39712 S39712 Bacillus subtilis 1423 -11528999 5000688665 ipa-57d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:59206) (re:59883) (di:direct) BSGENR X73124 g580875 Bacillus subtilis 1423 -11528999 219294 ung uracil-dna glycosylase (db:genpept-bct1) (ec:3.2.2.-) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-57d, ywdg) (le:98079) (re:98756) (di:complement) BSUB0020 Z99123 g2636332 Bacillus subtilis 1423 -11528999 103712 ung:ipa-57d (ec:3.2.2.-) (de:uracil-dna glycosylase, (udg)) (db:swissprot) UNG_BACSU P39615 BACILLUS SUBTILIS 1423 -11528999 140266 ung uracil-dna glycosylase:ung (cl:uracil-dna glycosylase) (ec:3.2.2.-) (db:pir) S39712 S39712 Bacillus subtilis 1423 -11528999

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742410	1047	23203	645	214

Description

6500725142 3-exo-deoxyribonuclease:exodeoxyribonuclease (gtcfc:10.10) (ec:3.1.11.2) (keggfc:14.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis) exoA exoA Bacillus subtilis 1423 -11529000 70812 exoa (ec:3.1.11.2) (de:exodeoxyribonuclease,) (db:swissprot) EXOA_BACSU P37454 BACILLUS SUBTILIS 1423 -11529000 7000685208 exoa 3-exo-deoxyribonuclease exoa (cl:dna-(apurinic or apyrimidinic site) lyase) (db:pir2.dat) S66012 S66012 Bacillus subtilis 1423 -11529000 7500881242 exoa 3-exo-deoxyribonuclease (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:45776) (re:46534) (di:complement) BAC180K D26185 g467372 Bacillus subtilis 1423 -11529000 214972 exoa 3-exo-deoxyribonuclease (db:genpept-bct1) (ec:3.1.11.2) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:197708) (re:198466) (di:complement) BSUB0021 Z99124 g2636635 Bacillus subtilis 1423 -11529000 206151 exoa 3-exo-deoxyribonuclease exoa (db:pir) S66012 S66012 Bacillus subtilis 1423 -11529000 5000688657 (de:(exoa) (pn:exodeoxyribonuclease) (gtcfc:10.10) (ec:3.1.11.2) (exoa_bacsu) (keggfc:11.1) (bsorffc:4.1.2) (db:gtc-bacillus subtilis)) exoA exoA Bacillus subtilis 1423 10013387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742412	1048	23204	435	144

Description

6500725143 nova:gyrb dna gyrase:subunit b:dna gyrase subunit b (gtcfc:10.10) (ec:5.99.1.3) (keggfc:14.1) (bsorffc:6.1.4) (db:gtc-bacillus subtilis) gyrB gyrB Bacillus subtilis 1423 -11529001 214996 gyrb:nova (ec:5.99.1.3) (de:dna gyrase subunit b,) (db:swissprot) GYRB_BACSU P05652 BACILLUS SUBTILIS 1423 -11529001 7000685495 gyrb dna topoisomerase atp-hydrolyzing:chain b gyrb:dna gyrase chain b (cl:dna topoisomerase (atp-hydrolyzing) chain b) (ec:5.99.1.3) (db:pir2.dat) (mp:0) E22930 E22930 Bacillus subtilis 1423 -11529001 7500882881 gyrb b subunit of dna gyrase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:68468) (re:70384) (di:direct) BAC180K D26185 g467396 Bacillus subtilis 1423 -11529001 5000688669 (db:genpept-bct1) (de:bacillus subtilis oric region.) (nt:orf 638 (aa 1-638)) (le:5642) (re:7558) (di:direct) BSORIC X02369 g40018 Bacillus subtilis 1423 -11529001 219455 gyrb dna gyrase subunit b (fn:initation of replication cycle and dna) (db:genpept-bct1) (ec:5.99.1.3) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: nova) (le:4866) (re:6782) (di:direct) BSUB0001 Z99104 g2632273 Bacillus subtilis 1423 -11529001 75215 gyrb:nova (ec:5.99.1.3) (de:dna gyrase subunit b,) (db:swissprot) GYRB_BACSU P05652 BACILLUS SUBTILIS 1423 -11529001 142210 gyrb dna topoisomerase atp-hydrolyzing:chain b gyrb:dna gyrase chain b (cl:dna topoisomerase (atp-hydrolyzing) chain b) (ec:5.99.1.3) (db:pir) (mp:0) E22930 E22930 Bacillus subtilis 1423 -11529001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742423	1049	23205	684	227

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742424	1050	23206	654	217

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742437	1051	23207	576	192

Description

5000688668 nala:cafb:gyra dna gyrase:subunit a:dna gyrase subunit a (gtcfc:10.10) (ec:5.99.1.3) (keggfc:14.1) (bsorffc:6.1.4) (db:gtc-bacillus subtilis) gyrA gyrA Bacillus subtilis 1423 -11529002 214997 gyra:nala:cafb (ec:5.99.1.3) (de:dna gyrase subunit a,) (db:swissprot) GYRA_BACSU P05653 BACILLUS SUBTILIS 1423 -11529002 7000685493 gyra dna topoisomerase atp-hydrolyzing:chain a gyra:dna gyrase chain a (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (ec:5.99.1.3) (db:pir2.dat) (mp:0) F22930 F22930 Bacillus subtilis 1423 -11529002 7500882872 gyra a subunit of dna gyrase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:70595) (re:73060) (di:direct) BAC180K D26185 g467397 Bacillus subtilis 1423 -11529002 219456 (db:genpept-bct1) (de:bacillus subtilis oric region.) (nt:orf 821 (aa 1-821)) (le:7769) (re:10234) (di:direct) BSORIC X02369 g40019 Bacillus subtilis 1423 -11529002 6500725144 gyra dna gyrase subunit a (fn:initation of replication cycle and dna) (db:genpept-bct1) (ec:5.99.1.3) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: nala) (le:6993) (re:9458) (di:direct) BSUB0001 Z99104 g2632274 Bacillus subtilis 1423 -11529002 75191 gyra:nala:cafb (ec:5.99.1.3) (de:dna gyrase subunit a,) (db:swissprot) GYRA_BACSU P05653 BACILLUS SUBTILIS 1423 -11529002 142231 gyra dna topoisomerase atp-hydrolyzing:chain a gyra:dna gyrase chain a (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (ec:5.99.1.3) (db:pir) (mp:0) F22930 F22930 Bacillus subtilis 1423 -11529002

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742441	1052	23208	519	172

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742448	1053	23209	474	157

Description

GTC ORF with score 158 to: (sr:homo sapiens male myeloblast cell-line kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0079 gene, complete cds.) (nt:the ha3543 gene product is related to s.cerevisiae) (le:115) (re:3492) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742456	1054	23210	285	95

Description

6500725145 topi:topa dna topoisomerase i:omega-protein:relaxing enzyme:untwisting enzyme:swivelase (gtcfc:10.10) (ec:5.99.1.2) (keggfc:14.1) (bsorffc:6.1.4) (db:gtc-bacillus subtilis) topA topA Bacillus subtilis 1423 -11529003 101781 topa:topi (ec:5.99.1.2) (de:(untwisting enzyme) (swivelase)) (db:swissprot) TOP1_BACSU P39814 BACILLUS SUBTILIS 1423 -11529003 7000686809 topa dna topoisomerase i topa (cl:dna topoisomerase i) (db:pir2.dat) G69724 G69724 Bacillus subtilis 1423 -11529003 216816 dna topoisomerase i (fn:dna unwinding protein: removes negative) (sr:bacillus subtilis (strain 8g5) dna) (db:genpept-bct1) (de:bacillus subtilis (smf) gene, 3' end, dna topisomase gene, completecds, (gid) gene, 5' end.) (le:673) (re:2748) (di:direct) BACSMF L27797 g520753 Bacillus subtilis 1423 -11529003 5500684752 topa dna topoisomerase i (fn:dna unwinding protein removing negative) (db:genpept-bct1) (ec:5.99.1.2) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: topi) (le:84640) (re:86715) (di:direct) BSUB0009 Z99112 g2633984 Bacillus subtilis 1423 -11529003 7500893256 topa dna topoisomerase i (db:genpept-bct1) (de:bacillus subtilis ylqg to codv gene region.) (le:3808) (re:5883) (di:direct) BSYLQGCOD AJ000975 g2462970 Bacillus subtilis 1423 -11529003 5000688672 (de:(topa) (pn:dna topoisomerase i:dna topoisomerase i :omega-protein:relaxing enzyme:untwisting enzyme:swivelase) (gn:topi) (gtcfc:10.10) (ec:5.99.1.2) (topl_bacsu) (keggfc:11.1) (bsorffc:6.1.4) (db:gtc-bacillus subtilis)) topA topA Bacillus subtilis 1423 10043610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742462	1055	23211	834	278

Description

6500725146 dbpa:hbsu:hbs non-specific dna-binding protein hbsu:dna-binding protein ii:hb:hu (gtcfc:10.10) (keggfc:14.2) (bsorffc:6.1.4) (db:gtc-bacillus subtilis) hbs hbs Bacillus subtilis 1423 -11529004 219351 hbs:hbsu:dbpa (de:dna-binding protein ii (hb) (hu)) (db:swissprot) DBH_BACSU P08821 BACILLUS SUBTILIS 1423 -11529004 7502851570 hbs:hbsu:dbpa (de:dna-binding protein ii (hb) (hu)) (db:swissprot) DBH_BACSU P08821 BACILLUS GLOBIGII 1423 -11529004 148272 hbs:hup:dbpa non-specific dna-binding protein hu:hpb9 protein (cl:bacterial dna-binding protein) (db:pir2.dat) JC1208 JC1208 Bacillus subtilis 1423 -11529004 7000684986 hup dna-binding protein hu:dna-binding protein hb (cl:bacterial dna-binding protein) (db:pir2.dat) JC1209 JC1209 Bacillus sp. 1409 -11529004 7500880020 hubgl hubgl (sr:bacillus globigii dna) (db:genpept-bct1) (de:b.globigii hubgl gene, 5' end.) (le:1) (re:276) (di:direct) BACHUB4 M73503 g143071 Bacillus subtilis 1423 -11529004 215856 hubsub hubsub (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis hubsub gene, 5' end.) (le:1) (re:276) (di:direct) BACHUB5 M73504 g143073 Bacillus subtilis 1423 -11529004 215857 (db:genpept-bct1) (de:bacillus subtilis hbsu gene for hbsu histone-like dna-bindingprotein.) (nt:hbsu (aa 1-92)) (le:111) (re:389) (di:direct) BSHBSU X52418 g39936 Bacillus subtilis 1423 -11529004 5000688670 hbsu (db:genpept-bct1) (de:b.subtilis synthetic gene for histone-like hbsu protein.) (le:4) (re:282) (di:direct) BSHBSUHOM X66448 g39938 Bacillus subtilis 1423 -11529004 219352 hbs non-specific dna-binding protein hbsu (fn:involved in dna repair and homologous) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: dbpa) (le:189240) (re:189518) (di:complement) BSUB0012 Z99115 g2634697 Bacillus subtilis 1423 -11529004 67925 hbs:hbsu:dbpa (de:dna-binding protein ii (hb) (hu)) (db:swissprot) DBH_BACSU P08821 BACILLUS SUBTILIS 1423 -11529004 7502851571 hbs:hbsu:dbpa (de:dna-binding protein ii (hb) (hu)) (db:swissprot) DBH_BACSU P08821 BACILLUS GLOBIGII 1423 -11529004 148280 hup dna-binding protein hu:dna-binding protein hb (cl:bacterial dna-binding protein) (db:pir) JC1209 JC1209 Bacillus sp. 1409 -11529004

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742464	1056	23212	834	278

Description

5000688671 single-strand dna-binding protein:single-strand binding protein:ssb:helix-destabilizing protein (gtcfc:10.10) (keggfc:14.2) (bsorffc:6.1.4) (db:gtc-bacillus subtilis) ssb ssb Bacillus subtilis 1423 -11529005 99525 ssb (de:single-strand binding protein (ssb) (helix-destabilizing protein)) (db:swissprot) SSB_BACSU P37455 BACILLUS SUBTILIS 1423 -11529005 7000686682 ssb single strand dna binding protein ssb (cl:single-stranded dna-binding protein:single-stranded dna-binding protein homology) (db:pir2.dat) S66014 S66014 Bacillus subtilis 1423 -11529005 7500892118 ssb single strand dna binding protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:46882) (re:47400) (di:complement) BAC180K D26185 g467374 Bacillus subtilis 1423 -11529005 214974 ssb single-strand dna-binding protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:198814) (re:199332) (di:complement) BSUB0021 Z99124 g2636637 Bacillus subtilis 1423 -11529005 206282 ssb single strand dna binding protein ssb (cl:single-stranded dna-binding protein homology) (db:pir) S66014 S66014 Bacillus subtilis 1423 -11529005 6500725147 single-strand dna-binding protein:single-strand binding protein:ssb:helix-destabilizing protein (gtcfc:10.10) (keggfc:14.2) (bsorffc:6.1.4) (db:gtc-bacillus subtilis) ssb ssb Bacillus subtilis 1423 -11529005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742465	1057	23213	549	182

Description

6500725148 comi:nuca nuclease (gtcfc:10.1) (keggfc:14.2) (bsorffc:2.3.2) (db:gtc-bacillus subtilis) nucA nucA Bacillus subtilis 1423 -11529006 217140 comi dna entry nuclease (sr:bacillus subtilis (strain:168trpc2) dna, clone_lib:lambda dashi) (db:genpept-bct1) (de:bacillus subtilis dna around 28 degrees region of chromosomecontaining ycka-h genes.) (le:4999) (re:5310) (di:complement) BACYCK D30762 g710634 Bacillus subtilis 1423 -11529006 222609 nuca nuclease (fn:competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: comi) (le:177075) (re:177386) (di:complement) BSUB0002 Z99105 g2632629 Bacillus subtilis 1423 -11529006 7500964928 comi dna-entry nuclease (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:51379) (re:51690) (di:complement) D50453 D50453 g1805415 Bacillus subtilis 1423 -11529006 7000694201 nuca membrane-associated nuclease nuca (db:pir) G69667 G69667 Bacillus subtilis 1423 -11529006

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742471	1058	23214	873	291

Description

GTC ORF with score 143 to: (fn:binds histones) (sr:homo sapiens (library: clontech) male 50 year old adult testis cdn) (db:genpept-pri1) (de:homo sapiens histone-binding protein mrna, complete cds.) (nt:putative histone binding domain i: aa 115-126;) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742548	1059	23215	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742553	1060	23216	843	280

Description

6500725149 nuclease:sporulation-specific extracellular nuclease precursor (gtcfc:10.1) (ec:3.-.-.-) (keggfc:14.1) (bsorffc:2.3.2) (db:gtc-bacillus subtilis) nucB nucB Bacillus subtilis 1423 -11529007 87045 nucb (ec:3.-.-.-) (de:sporulation-specific extracellular nuclease precursor,) (db:swissprot) NUCB_BACSU P42983 BACILLUS SUBTILIS 1423 -11529007 7000685999 nucb sporulation-specific extracellular nuclease nucb precursor:deoxyribonuclease nucb precursor:sporulation-specific (db:pir2.dat) S61273 S61273 Bacillus subtilis 1423 -11529007 7500886931 nucb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:66814) (re:67224) (di:direct) BACJH642 D84432 g1303781 Bacillus subtilis 1423 -11529007 216025 nucb nuclease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:52206) (re:52616) (di:complement) BSUB0014 Z99117 g2635020 Bacillus subtilis 1423 -11529007 258869 nucb deoxyribonuclease (db:genpept-bct1) (de:nucb=competence-specific membrane-associated gene (bacillussubtilis, genomic, 780 nt).) (nt:this sequence comes from fig. 2; dnase) (le:222) (re:632) (di:direct) S78249 S78249 g998941 Bacillus subtilis 1423 -11529007 169958 nucb sporulation-specific extracellular nuclease nucb precursor:deoxyribonuclease nucb precursor:sporulation-specific (db:pir) S61273 S61273 Bacillus subtilis 1423 -11529007

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742562	1061	23217	792	263

Description

6500725150 extracellular metalloprotease:extracellular metalloprotease precursor (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) mpr mpr Bacillus subtilis 1423 -11529008 84187 mpr (ec:3.4.21.-) (de:extracellular metalloprotease precursor,) (db:swissprot) MPR_BACSU P39790 BACILLUS SUBTILIS 1423 -11529008 7000685866 mpr metalloproteinase:mpr precursor:extracellular (ec:3.4.-.-) (db:pir2.dat) A35122 A35122 Bacillus subtilis 1423 -11529008 7500885848 mpr metalloprotease (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis extracellular metalloprotease (mpr) gene,complete cds.) (nt:this is the extracellular metalloprotease) (le:27) (re:968) (di:direct) BACMPR L10505 g143210 Bacillus subtilis 1423 -11529008 216355 mpr extracellular metalloprotease (db:genpept-bct1) (ec:3.4.21.-) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:50529) (re:51470) (di:direct) BSUB0002 Z99105 g2632510 Bacillus subtilis 1423 -11529008 7500885849 mpr extracellular metalloprotease precursor (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:48180) (re:49121) (di:direct) AB006424 AB006424 g3599646 Bacillus subtilis 1423 -11529008 170346 mpr metalloproteinase:mpr precursor:extracellular (ec:3.4.-.-) (db:pir) A35122 A35122 Bacillus subtilis 1423 -11529008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742567	1062	23218	258	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742591	1063	23219	534	178

Description

5000688678 pyrrolidone-carboxylate peptidase:5-oxoprolyl-peptidase:pyroglutamyl-peptidase i (gtcfc:10.11) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) pcp pcp Bacillus subtilis 1423 -11529009 88833 pcp (ec:3.4.19.3) (de:peptidase) (pyroglutamyl-peptidase i)) (db:swissprot) PCP_BACSU P28618 BACILLUS SUBTILIS 1423 -11529009 7000686103 pcp:pep pyroglutamyl-peptidase i:pcp:5-oxoprolyl-peptidase:pyrrolidone-carboxylate peptidase pcp (ec:3.4.19.3) (db:pir2.dat) S23432 S23432 Bacillus subtilis 1423 -11529009 7500887737 pcp pyrrolidone carboxy-peptidase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:19866) (re:20513) (di:complement) BACYCB20 D30808 g710015 Bacillus subtilis 1423 -11529009 325837 pcp l-pyroglutamyl peptide hydrolase (db:genpept-bct1) (ec:3.4.11.8) (de:b.subtilis pcp gene for pyrrolidone carboxyl peptidase.) (nt:transferred entry: 3.4.19.3) (le:520) (re:1167) (di:direct) BSPCPG X66034 g40037 Bacillus subtilis 1423 -11529009 219513 pcp pyrrolidone-carboxylate peptidase (db:genpept-bct1) (ec:3.4.11.8) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:91677) (re:92324) (di:complement) BSUB0002 Z99105 g2632551 Bacillus subtilis 1423 -11529009 7502851572 pcp (db:genpept-pat) (de:b.subtilis pcp gene.) (le:1) (re:645) (di:direct) A25847 A25847 g1247681 Bacillus subtilis 1423 -11529009 170472 pcp:pep pyroglutamyl-peptidase i:pcp:5-oxoprolyl-peptidase:pyrrolidone-carboxylate peptidase pcp (ec:3.4.19.3) (db:pir) S23432 S23432 Bacillus subtilis 1423 -11529009 217133 pcp l-pyroglutamyl peptide hydrolase (db:genpept-bct1) (ec:3.4.11.8) (de:b.subtilis pcp gene for pyrrolidone carboxyl peptidase.) (nt:transferred entry: 3.4.19.3) (le:520) (re:1167) (di:direct) BSPCPG X66034 g40037 Bacillus subtilis 1423 -11529009 6500725151 pyrrolidone-carboxylate peptidase:5-oxoprolyl-peptidase:pyroglutamyl-peptidase i (gtcfc:10.11) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) pcp pcp Bacillus subtilis 1423 -11529009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742706	1064	23220	591	196

Description

6500725152 amidohydrolase (gtcfc:10.11) (ec:3.5.1.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) amhX amhX Bacillus subtilis 1423 -11529010 7500876793 amhx (ec:3.5.1.-) (de:amidohydrolase amhx, (aminoacylase)) (db:swissprot) AMHX_BACSU P54983 BACILLUS SUBTILIS 1423 -11529010 7000692184 amhx amidohydrolase amhx (db:pir2.dat) B69585 B69585 Bacillus subtilis 1423 -11529010 7500876795 amhx amidohydrolase (db:genpept-bct1) (ec:3.5.1.-) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:128923) (re:130092) (di:complement) BSUB0002 Z99105 g2632587 Bacillus subtilis 1423 -11529010 222567 amhx amidohydrolase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:3226) (re:4395) (di:complement) D50453 D50453 g1805373 Bacillus subtilis 1423 -11529010

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742709	1065	23221	231	77

Description

5000689562 ycxt:rsbt switch protein/serine kinase:phosphorylation of rsbs:hypothetical 14.3 kd protein in rsbu 5region:orft (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) rsbT rsbT Bacillus subtilis 1423 -11529011 111056 rsbt (de:anti-sigma b factor rsbt) (db:swissprot) RSBT_BACSU P42411 BACILLUS SUBTILIS 1423 -11529011 7000687506 rsbt positive regulator of sigma-b activity switch protein/serine rsbt (db:pir2.dat) G69701 G69701 Bacillus subtilis 1423 -11529011 216652 orft sigma-b regulator (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:53669) (re:54070) (di:direct) AB001488 AB001488 g1881279 Bacillus subtilis 1423 -11529011 302724 (sr:bacillus subtilis (strain 168 marburg) dna) (db:genpept-bct1) (de:bacillus subtilis (clones paw10, paw50) regulator (rsbu) gene,complete cds, positive regulator (rsbv), 5' end.) (nt:orft; putative) (le:1556) (re:1957) (di:direct) BACRSBU L35574 g642842 Bacillus subtilis 1423 -11529011 7500891134 rsbt switch protein/serine kinase phosphorylation of (fn:positive regulation of sigma-b activity) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ycxt) (le:117413) (re:117814) (di:direct) BSUB0003 Z99106 g2632769 Bacillus subtilis 1423 -11529011 6500725153 ycxt switch protein/serine kinase:phosphorylation of rsbs:hypothetical 14.3 kd protein in rsbu 5region:orft (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) rsbT rsbT Bacillus subtilis 1423 -11529011

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742724	1066	23222	441	146

Description

5000689469 serine protein kinase:prka protein (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) prkA prkA Bacillus subtilis 1423 -11529012 219551 prka (de:prka protein) (db:swissprot) PRKA_BACSU P39134 BACILLUS SUBTILIS 1423 -11529012 123603 prka protein kinase:a:prka protein:serine protein kinase prka:serine/threonine protein kinase a (cl:bacillus protein kinase a) (ec:2.7.1.37) (db:pir1.dat) (mp:169 degrees) JC4602 JC4602 Bacillus subtilis 1423 -11529012 7500888494 prka (db:genpept-bct1) (de:b.subtilis (168) prka gene.) (nt:orf 3) (le:1500) (re:3395) (di:direct) BSPRKA X79388 g494961 Bacillus subtilis 1423 -11529012 6500725154 prka serine protein kinase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:169845) (re:171740) (di:direct) BSUB0005 Z99108 g2633220 Bacillus subtilis 1423 -11529012 91083 prka (de:prka protein) (db:swissprot) PRKA_BACSU P39134 BACILLUS SUBTILIS 1423 -11529012

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742745	1067	23223	519	172

Description

6500725155 spre:apr:apra:apre serine alkaline protease:subtilisin e:subtilisin e precursor (gtcfc:10.11) (ec:3.4.21.62) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) aprE aprE Bacillus subtilis 1423 -11529013 4000714646 apre serine alkaline protease subtilisin e (db:genpept-bct1) (ec:3.4.21.62) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: spre) (le:104395) (re:105540) (di:complement) BSUB0006 Z99109 g2633366 Bacillus subtilis 1423 -11529013 7500954285 apre subtilisin e precursor (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p04189; subt_bacsu) (le:24254) (re:25399) (di:complement) BSY14083 Y14083 g2226248 Bacillus subtilis 1423 -11529013 7000694638 apre subtilisin e:extracellular alkaline serine proteinase apre (cl:subtilisin:subtilisin homology) (db:pir) H69586 H69586 Bacillus subtilis 1423 -11529013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742754	1068	23224	486	161

Description

6500725156 extracellular neutral protease b:neutral protease b precursor (gtcfc:10.11) (ec:3.4.24.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) nprB nprB Bacillus subtilis 1423 -11529014 86400 nprb (ec:3.4.24.-) (de:neutral protease b precursor,) (db:swissprot) NPRB_BACSU P39899 BACILLUS SUBTILIS 1423 -11529014 7000685981 nprb microbial metalloproteinase:nprb precursor:extracellular:extracellular neutral proteinase b nprb (ec:3.4.24.-) (db:pir2.dat) A41042 A41042 Bacillus subtilis 1423 -11529014 7500886560 nprb neutral protease b (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:b.subtillis neutral protease b (nprb) gene, complete cds.) (nt:preproprotease; putative) (le:301) (re:1917) (di:direct) BACNPRB M62845 g143256 Bacillus subtilis 1423 -11529014 216399 nprb (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:39) (re:1655) (di:direct) BS168NPRB Z79580 g1620922 Bacillus subtilis 1423 -11529014 218944 nprb extracellular neutral protease b (db:genpept-bct1) (ec:3.4.24.-) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:186010) (re:187626) (di:direct) BSUB0006 Z99109 g2633446 Bacillus subtilis 1423 -11529014 3500684466 nprb (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (le:43236) (re:44852) (di:direct) BSY09476 Y09476 g2145411 Bacillus subtilis 1423 -11529014 170350 nprb microbial metalloproteinase:nprb precursor:extracellular:extracellular neutral proteinase b nprb (ec:3.4.24.-) (db:pir) A41042 A41042 Bacillus subtilis 1423 -11529014 304064 nprb (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (le:43236) (re:44852) (di:direct) BSY09476 Y09476 g2145411 Bacillus subtilis 1423 -11529014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742849	1069	23225	711	236

Description

5000688675 intracellular proteinase inhibitor bsupi:intracellular proteinase inhibitor:bsupi (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) ipi ipi Bacillus subtilis 1423 -11529015 79798 ipi (de:intracellular proteinase inhibitor (bsupi)) (db:swissprot) IPI_BACSU P39804 BACILLUS SUBTILIS 1423 -11529015 7000685643 ipi major intracellular proteinase inhibitor isp-1 ipi (db:pir2.dat) C49921 C49921 Bacillus subtilis 1423 -11529015 7500884220 ipi bsupi (fn:intracellular proteinase inhibitor) (sr:bacillus subtilis (strain db104) dna, clone ppi-operon) (db:genpept-bct1) (de:b.subtilis ipi gene for intracellular proteinase inhibitor bsupi,complete cds.) (le:1206) (re:1565) (di:direct) BACIPI D16311 g451203 Bacillus subtilis 1423 -11529015 215927 bsupi (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:3648) (re:4007) (di:direct) BS168NPRB Z79580 g1620925 Bacillus subtilis 1423 -11529015 218947 ipi intracellular proteinase inhibitor bsupi (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:189619) (re:189978) (di:direct) BSUB0006 Z99109 g2633449 Bacillus subtilis 1423 -11529015 3500684465 ipi (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:protease) (le:46845) (re:47204) (di:direct) BSY09476 Y09476 g2145414 Bacillus subtilis 1423 -11529015 170330 ipi major intracellular proteinase inhibitor isp-1 ipi (db:pir) C49921 C49921 Bacillus subtilis 1423 -11529015 304067 ipi (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:protease) (le:46845) (re:47204) (di:direct) BSY09476 Y09476 g2145414 Bacillus subtilis 1423 -11529015 6500725157 intracellular proteinase inhibitor bsupi:intracellular proteinase inhibitor:bsupi (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) ipi ipi Bacillus subtilis 1423 -11529015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742882	1070	23226	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742886	1071	23227	840	280

Description

6500725158 ykda:htra serine protease do:heat-shock protein (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) htrA htrA Bacillus subtilis 1423 -11529016 7000694580 htra serine proteinase do:heat-shock protein htra (cl:proteinase hhob) (db:pir2.dat) A69643 A69643 Bacillus subtilis 1423 -11529016 6000689734 ykda ykda (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:putative serine protease, heat-shock inducible;) (le:10063) (re:11412) (di:complement) BSAJ2571 AJ002571 g2632011 Bacillus subtilis 1423 -11529016 7500965179 htra serine protease do heat-shock protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykda) (le:163012) (re:164361) (di:complement) BSUB0007 Z99110 g2633644 Bacillus subtilis 1423 -11529016

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742896	1072	23228	489	163

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742897	1073	23229	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742978	1074	23230	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742984	1075	23231	678	225

Description

GTC ORF with score 885 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c1a4 left hand region 1-26184 bporiginates from chimeric cosmid.) (nt:spbc1a4.08c, len:528aa, similarity: to m. musculus,) (le:18643:20201:20313) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742992	1076	23232	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742995	1077	23233	738	246

Description

GTC ORF with score 251 to: (sr:autographa californica nucleopolyhedrovirus (strain mutant fp-d) (db:genpept-vrl) (de:autographa californica nuclear polyhedrosis virus (acmnpv) mutantfp-d with incorporated trichoplusia ni retrotransposon ted (tn368)and ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501742999	1078	23234	624	208

Description

6500725159 intracellular serine protease:major intracellular serine protease:isp-1 (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) ispA ispA Bacillus subtilis 1423 -11529017 7500884291 ispa (ec:3.4.21.-) (de:major intracellular serine protease, (isp-1)) (db:swissprot) ISP1_BACSU P11018 BACILLUS SUBTILIS 1423 -11529017 6000689776 ispa intracellular serine protease (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:38149) (re:39108) (di:complement) BSAJ2571 AJ002571 g2632039 Bacillus subtilis 1423 -11529017 7500884294 ispa intracellular serine protease (db:genpept-bct1) (ec:3.4.21.-) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:191098) (re:192057) (di:complement) BSUB0007 Z99110 g2633673 Bacillus subtilis 1423 -11529017 7000694183 ispa major intracellular serine proteinase ispa (cl:bacillus intracellular serine protein:subtilisin homology) (db:pir) F69646 F69646 Bacillus subtilis 1423 -11529017

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743007	1079	23235	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743008	1080	23236	408	135

Description

GTC ORF with score 153 to: (sr:deinococcus radiodurans (strain:kr1) dna, clone:pkdl133, pkdl24) (db:genpept-bct1) (ec:1.1.1.27) (de:deinococcus radiodurans gene for l-lactate dehydrogenase, completecds.) (le:143) (re:1057) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743012	1081	23237	639	212

Description

6500725160 ykvh:clpe atp-dependent clp protease-like (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpE clpE Bacillus subtilis 1423 -11529018 7000692247 clpe atp-dependent clp proteinase-like protein clpe (db:pir2.dat) A69601 A69601 Bacillus subtilis 1423 -11529018 7500963439 clpe atp-dependent clp protease-like (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ykvh) (le:40304) (re:42403) (di:complement) BSUB0008 Z99111 g2633741 Bacillus subtilis 1423 -11529018

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743125	1082	23238	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743131	1083	23239	333	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743133	1084	23240	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743136	1085	23241	450	150

Description

6500725161 extracellular neutral metalloprotease:bacillolysin precursor:neutral protease:mcp 76 (gtcfc:10.11) (ec:3.4.24.28) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) nprE nprE Bacillus subtilis 1423 -11529019 86406 npre (ec:3.4.24.28) (de:bacillolysin precursor, (neutral protease) (mcp 76)) (db:swissprot) NPRE_BACSU P06142 BACILLUS SUBTILIS 1423 -11529019 7502851573 npre (ec:3.4.24.28) (de:bacillolysin precursor, (neutral protease) (mcp 76)) (db:swissprot) NPRE_BACSU P06142 BACILLUS SUBTILIS VARAMYLOSACCHARITICUS 99999 -11529019 7502851574 npre (ec:3.4.24.28) (de:bacillolysin precursor, (neutral protease) (mcp 76)) (db:swissprot) NPRE_BACSU P06142 BACILLUS MESENTERICUS 1408 -11529019 7000685982 npre bacillolysin:precursor:extracellular neutral metalloproteinase npre (cl:thermolysin) (ec:3.4.24.28) (db:pir2.dat) JQ2129 JQ2129 Bacillus subtilis 1423 -11529019 7500886562 prepro neutral protease (sr:bacillus subtilis (strain k02, sub_species amylosacchariticus) (db:genpept-bct1) (de:bacillus subtilis gene for neutral protease(monomer), complete cds.) (nt:the possible initiation codon is gtg.) (le:282) (re:1847) (di:direct) BACNP D10773 g912441 Bacillus subtilis 1423 -11529019 219923 npre neutral protease (db:genpept-bct1) (de:bacillus subtilis neutral protease (npre) gene, complete cds.) (le:160) (re:1725) (di:direct) BSU30932 U30932 g1098625 Bacillus subtilis 1423 -11529019 216391 npre extracellular neutral metalloprotease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:144651) (re:146216) (di:complement) BSUB0008 Z99111 g2633841 Bacillus subtilis 1423 -11529019 86407 npre (ec:3.4.24.28) (de:bacillolysin precursor, (neutral protease) (mcp 76)) (db:swissprot) NPRE_BACSU P25268 BACILLUS SUBTILIS 1423 -11529019 7502851575 npre (ec:3.4.24.28) (de:bacillolysin precursor, (neutral protease) (mcp 76)) (db:swissprot) NPRE_BACSU P25268 BACILLUS SUBTILIS VARAMYLOSACCHARITICUS 99999 -11529019 7502851576 npre (ec:3.4.24.28) (de:bacillolysin precursor, (neutral protease) (mcp 76)) (db:swissprot) NPRE_BACSU P25268 BACILLUS MESENTERICUS 1408 -11529019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743152	1086	23242	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743154	1087	23243	411	136

Description

6500725162 bpf:bpr bacillopeptidase f:bacillopeptidase f precursor:esterase:rp-i protease (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) bpr bpr Bacillus subtilis 1423 -11529020 99772 bpr:bpf (ec:3.4.21.-) (de:bacillopeptidase f precursor, (esterase) (rp-i protease)) (db:swissprot) SUBF_BACSU P16397 BACILLUS SUBTILIS 1423 -11529020 7000686695 bpr:ai:7000686695 bacillopeptidase f:precursor bpr (cl:subtilisin homology) (ec:3.4.21.-) (db:pir2.dat) (mp:135 (degrees)) A36734 A36734 Bacillus subtilis 1423 -11529020 7500892217 bacillopeptidase f (sr:b.subtilis (168, strain gp216) dna, clone pcr83) (db:genpept-bct1) (de:b.subtilis bacillopeptidase f (bpr) gene, complete cds.) (nt:bacillopeptidase f precursor) (le:200) (re:4501) (di:direct) BACPEPFA M29035 g143308 Bacillus subtilis 1423 -11529020 216455 bpr bacillopeptidase f (db:genpept-bct1) (ec:3.4.21.-) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: bpf) (le:203888) (re:208189) (di:direct) BSUB0008 Z99111 g2633901 Bacillus subtilis 1423 -11529020 6000685234 bpr bacillopeptidase f (db:genpept-bct1) (ec:3.4.21.-) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: bpf) (le:258) (re:4559) (di:direct) BSUB0009 Z99112 g2633903 Bacillus subtilis 1423 -11529020 169884 bbpf bacillopeptidase f:precursor bpr (cl:subtilisin homology) (ec:3.4.21.-) (db:pir) (mp:135 (degrees)) A36734 A36734 Bacillus subtilis 1423 -11529020

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743164	1088	23244	438	145

Description

6500725163 protease:sporulation sigma-e factor processing peptidase:stage ii sporulation protein ga (gtcfc:10.11:12.15) (ec:3.4.23.-) (keggfc:14.1) (bsorffc:4.3.4:6.2.1) (db:gtc-bacillus subtilis) spoIIGA spoIIGA Bacillus subtilis 1423 -11529021 7500891933 spoiiga (ec:3.4.23.-) (de:ii sporulation protein ga)) (db:swissprot) SP2G_BACSU P13801 BACILLUS SUBTILIS 1423 -11529021 170559 spoiiga sporulation protein spoiiga:pro-sigma-e processing proteinase spoiiga (db:pir2.dat) (mp:135 (degrees)) A29812 S08224 Bacillus subtilis 1423 -11529021 5000688967 spoiiga gene product aa 1-309 (db:genpept-bct1) (de:bacillus subtilis sporulation genes spoiiga and spoiigb, partial.) (le:271) (re:1200) (di:direct) BSSPOII X17344 g580933 Bacillus subtilis 1423 -11529021 219643 spoiiga protease (fn:processing of pro-sigma-e (spoiigb) to active) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:4754) (re:5683) (di:direct) BSUB0009 Z99112 g2633904 Bacillus subtilis 1423 -11529021 99128 spoiiga (ec:3.4.23.-) (de:ii sporulation protein ga)) (db:swissprot) SP2G_BACSU P13801 BACILLUS SUBTILIS 1423 -11529021 7000686630 spoiiga sporulation protein spoiiga:pro-sigma-e processing proteinase spoiiga (db:pir) (mp:135 (degrees)) A29812 C69711 Bacillus subtilis 1423 -11529021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743168	1089	23245	447	148

Description

5000689037 hslv:codw:clpq beta-type subunit of the 20s proteasome:heat shock protein hslv precursor (gtcfc:10.11) (ec:3.4.99.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpQ clpQ Bacillus subtilis 1423 -11529022 77896 hslv:clpq:codw (ec:3.4.99.-) (de:heat shock protein hslv precursor,) (db:swissprot) HSLV_BACSU P39070 BACILLUS SUBTILIS 1423 -11529022 7000685565 clpq:codw 20s proteasome beta-type chain clpq:heat shock protein codw (db:pir2.dat) S61494 S61494 Bacillus subtilis 1423 -11529022 7500883570 codw codw (db:genpept-bct1) (de:bacillus subtilis jh642 dipeptide permease operon regulators, codv,codw, codx, and cody genes, complete cds.) (le:1220) (re:1765) (di:direct) BSU13634 U13634 g535349 Bacillus subtilis 1423 -11529022 219816 clpq beta-type subunit of the 20s proteasome (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: hslv, codw) (le:89093) (re:89638) (di:direct) BSUB0009 Z99112 g2633987 Bacillus subtilis 1423 -11529022 206162 clpq:codw 20s proteasome beta-type chain clpq:heat shock protein codw (db:pir) S61494 S61494 Bacillus subtilis 1423 -11529022 6500725164 hslv:codw beta-type subunit of the 20s proteasome:heat shock protein hslv precursor (gtcfc:10.11) (ec:3.4.99.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpQ clpQ Bacillus subtilis 1423 -11529022

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743180	1090	23246	219	72

Description

5000689036 hslu:codx:clpy atp-dependent clp protease-like:heat shock protein hslu (gtcfc:10.11:12.7) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpY clpY Bacillus subtilis 1423 -11529023 77893 hslu:clpy:codx (de:heat shock protein hslu) (db:swissprot) HSLU_BACSU P39778 BACILLUS SUBTILIS 1423 -11529023 7000685564 clpy:codx atp-dependent clp proteinase-like protein clpy:codx protein (cl:heat shock protein hslu:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir2.dat) E69601 E69601 Bacillus subtilis 1423 -11529023 7500883563 codx codx (db:genpept-bct1) (de:bacillus subtilis jh642 dipeptide permease operon regulators, codv,codw, codx, and cody genes, complete cds.) (le:1782) (re:3185) (di:direct) BSU13634 U13634 g535350 Bacillus subtilis 1423 -11529023 219817 clpy atp-dependent clp protease-like (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: hslu, codx) (le:89655) (re:91058) (di:direct) BSUB0009 Z99112 g2633988 Bacillus subtilis 1423 -11529023 1500685277 clpy atp-dependent clp proteinase-like protein clpy (cl:heat shock protein hslu:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir) E69601 E69601 Bacillus subtilis 1423 -11529023 6500725165 hslu:codx atp-dependent clp protease-like:heat shock protein hslu (gtcfc:10.11:12.7) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpY clpY Bacillus subtilis 1423 -11529023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743181	1091	23247	951	316

Description

6500725166 alkaline serine protease (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) aprX aprX Bacillus subtilis 1423 -11529024 7000694112 aprx intracellular alkaline serine proteinase aprx (cl:subtilisin homology) (db:pir2.dat) A69587 A69587 Bacillus subtilis 1423 -11529024 7500964867 aprx alkaline serine protease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:79426) (re:80754) (di:complement) BSUB0010 Z99113 g2634110 Bacillus subtilis 1423 -11529024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743187	1092	23248	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743194	1093	23249	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743322	1094	23250	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743324	1095	23251	765	254

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743338	1096	23252	579	192

Description

6500725167 yzbd:ctpa carboxy-terminal processing protease (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) ctpA ctpA Bacillus subtilis 1423 -11529025 7000692321 ctpa carboxy-terminal processing proteinase ctpa::tail-specific endopeptidase prc (cl:carboxyl-terminal processing proteinase) (ec:3.4.99.-) (db:pir2.dat) B69610 B69610 Bacillus subtilis 1423 -11529025 5500687368 orfrm1 orfrm1 (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:similar to the e. coli prc and carboxyl-terminal) (le:22886) (re:24286) (di:direct) AF006665 AF006665 g2529476 Bacillus subtilis 1423 -11529025 5500687369 ctpa proteinase (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415395 Bacillus subtilis 1423 -11529025 7500963490 ctpa carboxy-terminal processing protease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yzbd) (le:130976) (re:132376) (di:complement) BSUB0011 Z99114 g2634351 Bacillus subtilis 1423 -11529025

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743356	1097	23253	189	62

Description

Hypothetical protein

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501743366	1098	23254	192	63

Description

6500725168 spore protease (gtcfc:10.11:12.15) (ec:3.4.99.-) (keggfc:14.1) (bsorffc:4.3.4:6.2.1) (db:gtc-bacillus subtilis) gpr gpr Bacillus subtilis 1423 -11529026 74391 gpr (ec:3.4.99.-) (de:spore protease,) (db:swissprot) GPR_BACSU P22322 BACILLUS SUBTILIS 1423 -11529026 7000685441 gpr sasp degradation spore proteinase:gpr precursor (ec:3.4.-.-) (db:pir2.dat) B39198 B39198 Bacillus subtilis 1423 -11529026 7500882683 gpr spore protease (fn:initiates degradation of small, acid-soluble) (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis spore protease (gpr) gene, complete cds.) (le:247) (re:1353) (di:direct) BACGPRAA M55263 g143022 Bacillus subtilis 1423 -11529026 215800 gpr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:84003) (re:85109) (di:direct) BACJH642 D84432 g1303801 Bacillus subtilis 1423 -11529026 216045 gpr spore protease (fn:initiates degradation of small, acid-soluble) (db:genpept-bct1) (ec:3.4.99.-) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:34321) (re:35427) (di:complement) BSUB0014 Z99117 g2635000 Bacillus subtilis 1423 -11529026 170026 gpr sasp degradation spore proteinase gpr precursor (db:pir) B39198 B39198 Bacillus subtilis 1423 -11529026 5000688674 (de:(gpr) (pn:spore protease) (gtcfc:10.11) (ec:3.4.99.-) (gpr_bacsu) (keggfc:11.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis)) gpr gpr Bacillus subtilis 1423 10016908

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501743380	1099	23255	1029	342

Description

6500725169 bofb:spoivfb protease:stage iv sporulation protein fb (gtcfc:10.11:12.15) (keggfc:14.2) (bsorffc:4.3.4:6.2.1) (db:gtc-bacillus subtilis) spoIVFB spoIVFB Bacillus subtilis 1423 -11529027 7500891943 spoivfb:bofb (de:stage iv sporulation protein fb) (db:swissprot) SP4G_BACSU P26937 BACILLUS SUBTILIS 1423 -11529027 7000686639 spoivfb sporulation protein spoivfb:pro-sigma-k processing proteinase spoivfb (db:pir2.dat) S18438 S18438 Bacillus subtilis 1423 -11529027 5000688979 spoivfb sporulation protein (db:genpept-bct1) (de:b.subtilis spoivfa, spoivfb, l20, orfx and l24 genes.) (le:946) (re:1812) (di:direct) BSSPOIVFO X59528 g580934 Bacillus subtilis 1423 -11529027 219647 spoivfb protease (fn:processing of pro-sigma-k to active sigma-k) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:60104) (re:60970) (di:complement) BSUB0015 Z99118 g2635262 Bacillus subtilis 1423 -11529027 99144 spoivfb:bofb (de:stage iv sporulation protein fb) (db:swissprot) SP4G_BACSU P26937 BACILLUS SUBTILIS 1423 -11529027 170588 spoivfb sporulation protein spoivfb:pro-sigma-k processing proteinase spoivfb (db:pir) S18438 S18438 Bacillus subtilis 1423 -11529027

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743381	1100	23256	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743387	1101	23257	426	141

Description

5000688677 lon:lona class iii heat-shock atp-dependent lon protease:atp-dependent protease la 1 (gtcfc:10.11) (ec:3.4.21.53) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) lonA lonA Bacillus subtilis 1423 -11529028 7500885095 lona:lon (ec:3.4.21.53) (de:atp-dependent protease la 1,) (db:swissprot) LON1_BACSU P37945 BACILLUS SUBTILIS 1423 -11529028 7000685755 lona endopeptidase la::class iii heat-shock atp-dependent lona proteinase (cl:atp-dependent serine proteinase la) (ec:3.4.21.53) (db:pir2.dat) I40421 I40421 Bacillus subtilis 1423 -11529028 304227 lon protease la (db:genpept-bct1) (de:b.subtilis lon gene for protease la.) (le:348) (re:2672) (di:direct) BSLONLA X76424 g496557 Bacillus subtilis 1423 -11529028 219377 lona class iii heat-shock atp-dependent lon protease (db:genpept-bct1) (ec:3.4.21.53) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: lon) (le:84436) (re:86760) (di:complement) BSUB0015 Z99118 g2635285 Bacillus subtilis 1423 -11529028 6500725170 lona atp-dependent lon protease (db:genpept-bct1) (ec:3.4.21.53) (de:b.subtilis genomic sequence 89009bp.) (nt:atp-dependent protease; endopeptidase; induced by) (le:83147) (re:85471) (di:direct) BSZ75208 Z75208 g1770078 Bacillus subtilis 1423 -11529028 82310 lona:lon (ec:3.4.21.53) (de:atp-dependent protease la 1,) (db:swissprot) LON1_BACSU P37945 BACILLUS SUBTILIS 1423 -11529028 140624 lona endopeptidase la::class iii heat-shock atp-dependent lona proteinase (cl:atp-dependent serine proteinase la) (ec:3.4.21.53) (db:pir) I40421 I40421 Bacillus subtilis 1423 -11529028 220354 lona atp-dependent lon protease (db:genpept-bct1) (ec:3.4.21.53) (de:b.subtilis genomic sequence 89009bp.) (nt:atp-dependent protease; endopeptidase; induced by) (le:83147) (re:85471) (di:direct) BSZ75208 Z75208 g1770078 Bacillus subtilis 1423 -11529028

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743393	1102	23258	798	266

Description

6500725171 ysxf:lon2:lonb lon-like atp-dependent protease:atp-dependent protease la homolog (gtcfc:10.11) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) lonB lonB Bacillus subtilis 1423 -11529029 82312 lonb:lon2 (ec:3.4.21.-) (de:atp-dependent protease la homolog,) (db:swissprot) LON2_BACSU P42425 BACILLUS SUBTILIS 1423 -11529029 7000685756 lonb lon-like atp-dependent proteinase lonb (db:pir2.dat) G69652 G69652 Bacillus subtilis 1423 -11529029 219846 bslon2 lon-like protease (db:genpept-bct1) (de:bacillus subtilis lon-like protease (bslon2) gene, complete cds,and clpx-like protein (bsclpx) gene, partial cds.) (le:725) (re:2383) (di:direct) BSU18229 U18229 g1142617 Bacillus subtilis 1423 -11529029 220353 lonb lon-like atp-dependent protease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ysxf) (le:86941) (re:88599) (di:complement) BSUB0015 Z99118 g2635286 Bacillus subtilis 1423 -11529029 304226 lonb atp-dependent lon protease (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to lona of bacillus subtilis; identified) (le:81308) (re:82966) (di:direct) BSZ75208 Z75208 g1770077 Bacillus subtilis 1423 -11529029 5000689438 (de:(lon2) (pn:atp-dependent protease la homolog) (gn:lonb) (gtcfc:13.07) (ec:3.4.21.-) (lon2_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) lon2 lon2 Bacillus subtilis 1423 10024542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743397	1103	23259	324	107

Description

Hypothetical protein

ORF_Name	NT_ID	AA_ID	NT LENGTH	AA LENGTH
7501743527	1104	23260	474	157

Description

5000689070 atp-dependent clp protease atp-binding subunit:class iii heat-shock protein:atp-dependent clp protease atp-binding subunit clpx (gtcfc:10.11:12.7) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpX clpX Bacillus subtilis 1423 -11529030 64840 clpx (de:atp-dependent clp protease atp-binding subunit clpx) (db:swissprot) CLPX_BACSU P50866 BACILLUS SUBTILIS 1423 -11529030 7000684842 clpx atp-dependent clp proteinase:regulatory chain x:class iii heat-shock protein (ec:3.4.21.-) (db:pir2.dat) D69601 D69601 Bacillus subtilis 1423 -11529030 220351 clpx atp-dependent clp protease atp-binding subunit (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:88751) (re:90013) (di:complement) BSUB0015 Z99118 g2635287 Bacillus subtilis 1423 -11529030 304224 clpx atp dependent clp protease (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to clpx of escherichia coli and other) (le:79894) (re:81156) (di:direct) BSZ75208 Z75208 g1770075 Bacillus subtilis 1423 -11529030 6500725172 atp-dependent clp protease atp-binding subunit:class iii heat-shock protein:atp-dependent clp protease atp-binding subunit clpx (gtcfc:10.11:12.7) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpX clpX Bacillus subtilis 1423 -11529030

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743536	1105	23261	573	190

Description

5000689466 kinase-associated protein b (gtcfc:10.11:12.13) (keggfc:12.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) kapB kapB Bacillus subtilis 1423 -11529031 80391 kapb (de:kinase-associated protein b) (db:swissprot) KAPB_BACSU Q08429 BACILLUS SUBTILIS 1423 -11529031 7000685661 kapb activator of kinb in the initiation of sporulation kapb (db:pir2.dat) S32936 S32936 Bacillus subtilis 1423 -11529031 4000707155 kapb kinase-associated protein b (fn:required for activation of kinase b in the) (db:genpept-bct1) (de:bacillus subtilis putative aminotransferase (patb), atp-dependentprotein kinase b (kinb), kinase-associated protein b (kapb) andkapd (kapd) genes, complete cds.) (nt:second and last ... BSU63302 U63302 g2231220 Bacillus subtilis 1423 -11529031 219969 kapb kinase-associated protein b (fn:required for activation of kinb in the) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:33479) (re:33865) (di:direct) BSUB0017 Z99120 g2635642 Bacillus subtilis 1423 -11529031 1500685303 kapb kinase b-associated protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuga to yugd.) (le:2912) (re:3298) (di:direct) BSZ93933 Z93933 g1934781 Bacillus subtilis 1423 -11529031 170305 kapb activator of kinb in the initiation of sporulation kapb (db:pir) S32936 S32936 Bacillus subtilis 1423 -11529031 6500725173 kinase-associated protein b (gtcfc:10.11:12.13) (keggfc:12.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) kapB kapB Bacillus subtilis 1423 -11529031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743545	1106	23262	207	68

Description

6500725174 yvdn:clpp class iii heat-shock protein:atp-dependent clp protease proteolytic subunit:endopeptidase clp:caseinolytic protease:protease ti (gtcfc:10.11:12.7) (ec:3.4.21.92) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) clpP clpP Bacillus subtilis 1423 -11529032 7500878860 clpp (ec:3.4.21.92) (de:(endopeptidase clp) (caseinolytic protease) (protease ti)) (db:swissprot) CLPP_BACSU P80244 BACILLUS SUBTILIS 1423 -11529032 7000692245 clpp atp-dependent clp proteinase:chain p:stress protein g7 (cl:atp-dependent clp proteinase chain p) (ec:3.4.21.-) (db:pir2.dat) B69601 B69601 Bacillus subtilis 1423 -11529032 7000692246 clpp atp-dependent clp protease proteolytic subunit (db:genpept-bct1) (ec:3.4.21.92) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvdn) (le:145744) (re:146337) (di:direct) BSUB0018 Z99121 g2635967 Bacillus subtilis 1423 -11529032 1500694039 yvdn hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:similar to clpp_ecoli atp-dependent clp protease) (le:35334) (re:35927) (di:complement) BSZ94043 Z94043 g1945673 Bacillus subtilis 1423 -11529032 7500878863 clpp clpp (db:genpept-bct2) (de:bacillus subtilis clp protease proteolytic component (clpp) gene,complete cds.) (nt:proteolytic component of clp protease) (le:140) (re:733) (di:direct) BSU59754 U59754 g2668494 Bacillus subtilis 1423 -11529032

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743550	1107	23263	462	153

Description

6500725175 subtilisin a:subtilosin a (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) sbo sbo Bacillus subtilis 1423 -11529033 7000694639 sbo subtilosin a sbo (db:pir2.dat) A69704 A69704 Bacillus subtilis 1423 -11529033 4000714661 sbo subtilosin a (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:36711) (re:36842) (di:direct) BSUB0020 Z99123 g2636272 Bacillus subtilis 1423 -11529033 7500965227 sbo subtilosin a (db:genpept-bct1) (de:bacillus subtilis ywia, sbo, ywib, args and nark genes.) (le:811) (re:942) (di:complement) BSZ97024 Z97024 g2224754 Bacillus subtilis 1423 -11529033

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743555	1108	23264	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743560	1109	23265	564	188

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743579	1110	23266	858	286

Description

6500725176 ipa-77d:rocb hypothetical protein:rocb protein (gtcfc:10.11) (keggfc:14.2) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) rocB rocB Bacillus subtilis 1423 -11529034 7500890486 rocb:ipa-77d (de:rocb protein) (db:swissprot) ROCB_BACSU P39635 BACILLUS SUBTILIS 1423 -11529034 7000686434 rocb arginine/ornithine utilization protein rocb:protein ipa-77d (db:pir2.dat) S39732 S39732 Bacillus subtilis 1423 -11529034 219314 ipa-77d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:78668) (re:80368) (di:direct) BSGENR X73124 g414001 Bacillus subtilis 1423 -11529034 7502851577 rocb (fn:involved in arginine and ornithine utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-77d) (le:77591) (re:79291) (di:complement) BSUB0020 Z99123 g2636313 Bacillus subtilis 1423 -11529034 95880 rocb:ipa-77d (de:rocb protein) (db:swissprot) ROCB_BACSU P39635 BACILLUS SUBTILIS 1423 -11529034 170155 rocb arginine / ornithine utilization protein rocb (db:pir) S39732 S39732 Bacillus subtilis 1423 -11529034

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743585	1111	23267	375	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743590	1112	23268	234	78

Description

GTC ORF with score 204 to: (sr:mouse embryonal carcinoma stem cell f9 dna, clone lambda-mkr2) (db:genpept-rod) (de:mouse finger protein containing to drosophila 'krueppel'finger-coding gene, clone lambda-mkr2, (partial).) (nt:finger protein (put.); ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743597	1113	23269	798	266

Description

GTC ORF with score 682 to: (fn:controls phosphorus acquisition) (sr:neurospora crassa strain=74-or23-iva) (db:genpept-pln1) (de:neurospora crassa nuc-2 (nuc-2) gene, complete cds.) (nt:contains six ankyrin repeats; similar to the) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743599	1114	23270	600	199

Description

6500725177 ipa-45r:vpr extracellular serine protease:minor extracellular protease vpr precursor (gtcfc:10.11:12.10) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) vpr vpr Bacillus subtilis 1423 -11529035 217046 vpr:ipa-45r (ec:3.4.21.-) (de:minor extracellular protease vpr precursor,) (db:swissprot) SUBV_BACSU P29141 BACILLUS SUBTILIS 1423 -11529035 7000686696 vpr microbial serine proteinase::minor vpr:precursor (cl:microbial serine proteinase v subtilisin homology) (ec:3.4.21.-) (db:pir2.dat) A41341 A41341 Bacillus subtilis 1423 -11529035 7500892220 vpr minor serine extracellular protease (sr:bacillus subtilis (individual_isolate gp264, strain w168) dna) (db:genpept-bct1) (de:b.subtilis minor serine extracellular protease (vpr) gene, completecds.) (le:232) (re:2652) (di:direct) BACVPR M76590 g143820 Bacillus subtilis 1423 -11529035 219282 ipa-45r::vpr (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:47302) (re:49722) (di:complement) BSGENR X73124 g580871 Bacillus subtilis 1423 -11529035 7502851578 vpr extracellular serine protease (db:genpept-bct1) (ec:3.4.21.-) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-45r) (le:108240) (re:110660) (di:direct) BSUB0020 Z99123 g2636344 Bacillus subtilis 1423 -11529035 99787 vpr:ipa-45r (ec:3.4.21.-) (de:minor extracellular protease vpr precursor,) (db:swissprot) SUBV_BACSU P29141 BACILLUS SUBTILIS 1423 -11529035 170351 vpr microbial serine proteinase::minor vpr:precursor (cl:subtilisin homology) (ec:3.4.21.-) (db:pir) A41341 A41341 Bacillus subtilis 1423 -11529035

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743602	1115	23271	549	183

Description

6500725178 ipa-15r:epr extracellular serine protease:minor extracellular protease epr precursor (gtcfc:10.11:12.10) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) epr epr Bacillus subtilis 1423 -11529036 219252 epr:ipa-15r (ec:3.4.21.-) (de:minor extracellular protease epr precursor,) (db:swissprot) SUBE_BACSU P16396 BACILLUS SUBTILIS 1423 -11529036 124854 epr serine proteinase:epr precursor:minor extracellular serine proteinase epr (cl:serine proteinase e subtilisin homology) (ec:3.4.21.-) (db:pir1.dat) SUBSMP S11504 Bacillus subtilis 1423 -11529036 215580 (sr:b.subtilis (strain 168, isolate gp208) dna, clone pnp1) (db:genpept-bct1) (de:b.subtils extracellular protease (epr) gene, complete cds.) (nt:extracellular protease precursor) (le:447) (re:2384) (di:direct) BACEXCP M22407 g142894 Bacillus subtilis 1423 -11529036 219187 (db:genpept-bct1) (de:bacillus subtilis epr gene for a novel serine protease.) (nt:prepropeptide (aa -27 to 618)) (le:461) (re:2398) (di:direct) BSEPR X53307 g39900 Bacillus subtilis 1423 -11529036 7500892216 ipa-15r::epr (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:15759) (re:17696) (di:complement) BSGENR X73124 g413939 Bacillus subtilis 1423 -11529036 7502851579 epr extracellular serine protease (db:genpept-bct1) (ec:3.4.21.-) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-15r) (le:140263) (re:142200) (di:direct) BSUB0020 Z99123 g2636375 Bacillus subtilis 1423 -11529036 99771 epr:ipa-15r (ec:3.4.21.-) (de:minor extracellular protease epr precursor,) (db:swissprot) SUBE_BACSU P16396 BACILLUS SUBTILIS 1423 -11529036

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743615	1116	23272	201	67

Description

6500725179 peptidase t:aminotripeptidase:tripeptidase (gtcfc:10.11) (ec:3.4.11.-) (keggfc:14.1) (bsorffc:4.3.4) (db:gtc-bacillus subtilis) pepT pepT Bacillus subtilis 1423 -11529037 89031 pept (ec:3.4.11.-) (de:peptidase t, (aminotripeptidase) (tripeptidase)) (db:swissprot) PEPT_BACSU P55179 BACILLUS SUBTILIS 1423 -11529037 7000686113 pept aminotripeptidase::peptidase t (ec:3.4.11.-) (db:pir2.dat) H69674 H69674 Bacillus subtilis 1423 -11529037 303675 pept (fn:unknown) (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (le:5267) (re:6499) (di:direct) BSGALE X99339 g1429259 Bacillus subtilis 1423 -11529037 222861 pept peptidase t tripeptidase (db:genpept-bct1) (ec:3.4.11.-) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:195467) (re:196699) (di:direct) BSUB0020 Z99123 g2636427 Bacillus subtilis 1423 -11529037 301528 pept (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:highly homologous to tripeptidases (peptidase t)) (le:27766) (re:28998) (di:complement) D83026 D83026 g1783235 Bacillus subtilis 1423 -11529037 219223 pept (fn:unknown) (db:genpept-bct1) (de:b.subtilis orfs 1,2,3,4, pept and gale genes.) (le:5267) (re:6499) (di:direct) BSGALE X99339 g1429259 Bacillus subtilis 1423 -11529037 5000689439 (de:(pept) (pn:peptidase t:aminotripeptidase:tripeptidase) (gtcfc:13.07) (ec:3.4.11.-) (pept_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) pepT pepT Bacillus subtilis 1423 10031157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743616	1117	23273	657	219

Description

6500725180 cpsx:abrb transcriptional regulator:transcription state regulatory protein abrb (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) abrB abrB Bacillus subtilis 1423 -11529038 215026 abrb:cpsx (de:transcription state regulatory protein abrb) (db:swissprot) ABRB_BACSU P08874 BACILLUS SUBTILIS 1423 -11529038 7000684487 abrb transition state regulatory protein abrb:transcriptional pleiotropic regulator of transition state genes abrb (db:pir2.dat) S03096 S03096 Bacillus subtilis 1423 -11529038 7500876268 abrb transition state regulatory protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:108448) (re:108738) (di:complement) BAC180K D26185 g467426 Bacillus subtilis 1423 -11529038 5000688876 (db:genpept-bct1) (de:b. subtilis abrb gene involved in transcription regulation.) (nt:abrb protein (aa 1 - 96)) (le:183) (re:473) (di:direct) BSABRB X12820 g39785 Bacillus subtilis 1423 -11529038 218989 abrb transcriptional regulator (fn:regulation of transition state genes (negative) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: cpsx) (le:44846) (re:45136) (di:complement) BSUB0001 Z99104 g2632304 Bacillus subtilis 1423 -11529038 57953 abrb:cpsx (de:transcription state regulatory protein abrb) (db:swissprot) ABRB_BACSU P08874 BACILLUS SUBTILIS 1423 -11529038 170482 abrb transition state regulatory protein abrb:transcriptional pleiotropic regulator of transition state genes abrb (db:pir) S03096 S03096 Bacillus subtilis 1423 -11529038

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743690	1118	23274	342	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743691	1119	23275	210	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743695	1120	23276	453	151

Description

6500725181 yabi:purr transcriptional regulator:pur operon repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) purR purR Bacillus subtilis 1423 -11529039 92476 purr (de:pur operon repressor) (db:swissprot) PURR_BACSU P37551 BACILLUS SUBTILIS 1423 -11529039 7000686246 purr transcription repressor of purine operon purr (db:pir2.dat) S66076 S66076 Bacillus subtilis 1423 -11529039 7500889091 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:118041) (re:118898) (di:direct) BAC180K D26185 g467436 Bacillus subtilis 1423 -11529039 215036 purr transcriptional regulator (fn:negative regulation of the purine operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yabi) (le:54439) (re:55296) (di:direct) BSUB0001 Z99104 g2632314 Bacillus subtilis 1423 -11529039 206236 purr purine operon transcriptional repressor purr (db:pir) S66076 S66076 Bacillus subtilis 1423 -11529039 5000688910 (de:(purr) (pn:pur operon repressor:pur operon repressor) (gtcfc:12.13) (ec:) (purr_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) purR purR Bacillus subtilis 1423 10034508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743711	1121	23277	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743715	1122	23278	318	105

Description

6500725182 yabl:spovt transcriptional regulator:stage v sporulation protein t (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) spoVT spoVT Bacillus subtilis 1423 -11529040 99165 spovt (de:stage v sporulation protein t) (db:swissprot) SP5T_BACSU P37554 BACILLUS SUBTILIS 1423 -11529040 7000686652 spovt transcription regulator spovt (db:pir2.dat) F69716 F69716 Bacillus subtilis 1423 -11529040 7500891957 similar to abrb (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:127699) (re:128235) (di:direct) BAC180K D26185 g467445 Bacillus subtilis 1423 -11529040 215045 spovt transcriptional regulator (fn:positive and negative regulation of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yabl) (le:64097) (re:64633) (di:direct) BSUB0001 Z99104 g2632323 Bacillus subtilis 1423 -11529040 206154 spovt transcriptional regulator spovt (db:pir) F69716 F69716 Bacillus subtilis 1423 -11529040 5000689109 (de:(spovt) (pn:stage v sporulation protein t) (gtcfc:13.07) (ec:) (sp5t_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) spoVT spoVT Bacillus subtilis 1423 10041024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743717	1123	23279	990	329

Description

5000689513 yacg:ctsr transcriptional regulator:hypothetical 17.7 kd protein in lyss-mecb intergenic region (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ctsR ctsR Bacillus subtilis 1423 -11529041 109600 ctsr (de:transcriptional regulator ctsr) (db:swissprot) CTSR_BACSU P37568 BACILLUS SUBTILIS 1423 -11529041 7000687155 ctsr transcription repressor of class iii stress genes ctsr (db:pir2.dat) S66112 S66112 Bacillus subtilis 1423 -11529041 7500879552 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:165048) (re:165512) (di:direct) BAC180K D26185 g467471 Bacillus subtilis 1423 -11529041 215071 ctsr transcriptional regulator (fn:negative regulation of class iii stress genes) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yacg) (le:101446) (re:101910) (di:direct) BSUB0001 Z99104 g2632350 Bacillus subtilis 1423 -11529041 206250 ctsr transcriptional repressor of class iii stress genes ctsr (db:pir) S66112 S66112 Bacillus subtilis 1423 -11529041 6500725183 yacg transcriptional regulator:hypothetical 17.7 kd protein in lyss-mecb intergenic region (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ctsR ctsR Bacillus subtilis 1423 -11529041

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743721	1124	23280	288	96

Description

5000688568 transcription antitermination factor:transcription antitermination protein nusg (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) nusG nusG Bacillus subtilis 1423 -11529042 87241 nusg (de:transcription antitermination protein nusg) (db:swissprot) NUSG_BACSU Q06795 BACILLUS SUBTILIS 1423 -11529042 7000686021 nusg transcription antitermination factor nusg (cl:transcription antitermination factor nusg) (db:pir2.dat) S39859 S39859 Bacillus subtilis 1423 -11529042 7500887015 nusg transcription antitermination factor nusg (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis genes for sigma factor h and ribosomal proteins.) (le:953) (re:1486) (di:direct) BACSHRBPNS D13303 g285628 Bacillus subtilis 1423 -11529042 216737 nusg transcription antitermination factor (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:117887) (re:118420) (di:direct) BSUB0001 Z99104 g2632368 Bacillus subtilis 1423 -11529042 154362 nusg transcription antitermination factor nusg (cl:transcription antitermination factor nusg) (db:pir) S39859 S39859 Bacillus subtilis 1423 -11529042 6500725184 transcription antitermination factor:transcription antitermination protein nusg (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) nusG nusG Bacillus subtilis 1423 -11529042

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743734	1125	23281	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743735	1126	23282	366	121

Description

6500725185 lin-2:yccb:lmra transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) lmrA lmrA Bacillus subtilis 1423 -11529043 7000694807 lmra transcription repressor of lincomycin operon lmra (db:pir2.dat) D69652 D69652 Bacillus subtilis 1423 -11529043 5500687008 yccb lmra (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:lmra gene; probable repressor of) (le:3225) (re:3791) (di:complement) AB000617 AB000617 g2415719 Bacillus subtilis 1423 -11529043 7500965364 lmra transcriptional regulator (fn:negative regulation of the lincomycin operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: lin-2, yccb) (le:95036) (re:95602) (di:complement) BSUB0002 Z99105 g2632554 Bacillus subtilis 1423 -11529043

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743846	1127	23283	225	74

Description

6500725186 regulator of the activity of phosphatase rapc and competence and sporulation stimulating factor:csf (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) phrC phrC Bacillus subtilis 1423 -11529044 7000694393 phrc phosphatase rapc regulator / competence and sporulation stimu phrc (cl:phosphatase regulator) (db:pir2.dat) A69677 A69677 Bacillus subtilis 1423 -11529044 222642 phrc regulator of the activity of phosphatase rapc (fn:csf stimulates competence gene expression) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:26793) (re:26915) (di:direct) BSUB0003 Z99106 g2632679 Bacillus subtilis 1423 -11529044 7500955859 hprc phosphatase regulator c (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:109196) (re:109318) (di:direct) D50453 D50453 g1805448 Bacillus subtilis 1423 -11529044

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743851	1128	23284	405	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743856	1129	23285	531	176

Description

6500725187 ydai:lrpc transcriptional regulator:lrp/asnc family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) lrpC lrpC Bacillus subtilis 1423 -11529045 7000694794 lrpc transcription regulator lrpc (db:pir2.dat) F69653 F69653 Bacillus subtilis 1423 -11529045 7500965353 lrpc transcriptional regulator lrp/asnc family (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ydai) (le:72862) (re:73296) (di:direct) BSUB0003 Z99106 g2632725 Bacillus subtilis 1423 -11529045

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743857	1130	23286	288	96

Description

6500725188 ydzc:sacv transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sacV sacV Bacillus subtilis 1423 -11529046 7000694797 sacv transcription regulator of levansucrase gene sacv (db:pir2.dat) D69703 D69703 Bacillus subtilis 1423 -11529046 7500965356 sacv transcriptional regulator (fn:regulation of the levansucrase gene (sacb)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ydzc) (le:128768) (re:128962) (di:direct) BSUB0003 Z99106 g2632783 Bacillus subtilis 1423 -11529046

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743862	1131	23287	627	209

Description

6500725189 yddo:lrpa transcriptional regulator:lrp/asnc family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) lrpA lrpA Bacillus subtilis 1423 -11529047 7000694792 lrpa transcription regulator of glya trans lrpa (db:pir2.dat) D69653 D69653 Bacillus subtilis 1423 -11529047 302759 yddo (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transcriptional regulator, similar to) (le:84737) (re:85147) (di:direct) AB001488 AB001488 g1881314 Bacillus subtilis 1423 -11529047 7500965351 lrpa transcriptional regulator lrp/asnc family (fn:negative regulation of glya transcription and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: yddo) (le:148482) (re:148892) (di:direct) BSUB0003 Z99106 g2632805 Bacillus subtilis 1423 -11529047

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743865	1132	23288	420	139

Description

6500725190 yddp:lrpb transcriptional regulator:lrp/asnc family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) lrpB lrpB Bacillus subtilis 1423 -11529048 7000694793 lrpb transcription regulator of glya trans lrpb (db:pir2.dat) E69653 E69653 Bacillus subtilis 1423 -11529048 302760 yddp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transcriptional regulator, similar to) (le:85270) (re:85719) (di:complement) AB001488 AB001488 g1881315 Bacillus subtilis 1423 -11529048 7500965352 lrpb transcriptional regulator lrp/asnc family (fn:negative regulation of glya transcription and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: yddp) (le:149015) (re:149464) (di:complement) BSUB0003 Z99106 g2632806 Bacillus subtilis 1423 -11529048

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743868	1133	23289	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743872	1134	23290	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743876	1135	23291	717	238

Description

5000688897 transcriptional regulator:transcription activator gutr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) gutR gutR Bacillus subtilis 1423 -11529049 75117 gutr (de:transcription activator gutr) (db:swissprot) GUTR_BACSU P39143 BACILLUS SUBTILIS 1423 -11529049 7000685480 gutr sorbitol dehydrogenase gene transcription activator gutr (db:pir2.dat) I40014 I40014 Bacillus subtilis 1423 -11529049 7500882859 gutr gutr (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:transcription activator gutr) (le:14864) (re:17353) (di:complement) AB007637 AB007637 g2522005 Bacillus subtilis 1423 -11529049 216944 gutr transcription activator (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis transcription activator (gutr) gene, completecds.) (le:342) (re:2831) (di:direct) BACTAA L19113 g437318 Bacillus subtilis 1423 -11529049 5500684555 gutr transcriptional regulator (fn:positive regulation of the sorbitol) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:63792) (re:66281) (di:complement) BSUB0004 Z99107 g2632927 Bacillus subtilis 1423 -11529049 170633 gutr sorbitol dehydrogenase gene transcription activator gutr (db:pir) I40014 I40014 Bacillus subtilis 1423 -11529049 6500725191 transcriptional regulator:transcription activator gutr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) gutR gutR Bacillus subtilis 1423 -11529049

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743879	1136	23292	294	97

Description

6500725192 yfxa:trer transcriptional regulator:gntr family:trehalose operon transcriptional repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) treR treR Bacillus subtilis 1423 -11529050 7500893380 trer (de:trehalose operon transcriptional repressor) (db:swissprot) TRER_BACSU P39796 BACILLUS SUBTILIS 1423 -11529050 7000686826 trer transcription repressor of trehalose operon trer (db:pir2.dat) JC5038 JC5038 Bacillus subtilis 1423 -11529050 5000689110 trer trer (fn:repressor of the trehalose operon) (db:genpept-bct1) (de:b.subtilis trea, trep and trer genes.) (nt:position 3684 corresponds to position 2543 of) (le:3352) (re:4068) (di:direct) BSTREAPR Z54245 g1000453 Bacillus subtilis 1423 -11529050 7500893381 trer transcriptional regulator gntr family (fn:negative regulation of the trehalose operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfxa) (le:50243) (re:50959) (di:direct) BSUB0005 Z99108 g2633106 Bacillus subtilis 1423 -11529050 6000685278 trer (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:16962) (re:17678) (di:complement) D83967 D83967 g2626829 Bacillus subtilis 1423 -11529050 102167 trer (de:trehalose operon transcriptional repressor) (db:swissprot) TRER_BACSU P39796 BACILLUS SUBTILIS 1423 -11529050 1500685596 trer trehalose operon transcriptional repressor trer (db:pir) JC5038 JC5038 Bacillus subtilis 1423 -11529050 219743 trer (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:16962) (re:17678) (di:complement) D83967 D83967 g2626829 Bacillus subtilis 1423 -11529050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743880	1137	23293	588	195

Description

6500725193 yfjg:yzcb:acor transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) acoR acoR Bacillus subtilis 1423 -11529051 7000694703 acor transcription activator of acetoin dehydrogenase operon acor (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) H69581 H69581 Bacillus subtilis 1423 -11529051 7000694704 acor transcriptional regulator (fn:positive regulation of the acetoin) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfjg, yzcb) (le:80444) (re:82261) (di:direct) BSUB0005 Z99108 g2633134 Bacillus subtilis 1423 -11529051 7500965278 yfjg (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:4064) (re:5881) (di:complement) D78509 D78509 g2780391 Bacillus subtilis 1423 -11529051

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743896	1138	23294	546	182

Description

6500725194 transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) senS senS Bacillus subtilis 1423 -11529052 7000694796 sens transcription regulator of extracellular enzyme genes sens (db:pir2.dat) B69705 B69705 Bacillus subtilis 1423 -11529052 7500965355 sens transcriptional regulator (fn:positive regulation of extracellular enzyme) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:155978) (re:156196) (di:direct) BSUB0005 Z99108 g2633204 Bacillus subtilis 1423 -11529052

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743898	1139	23295	672	223

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743905	1140	23296	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501743912	1141	23297	456	151

Description

GTC ORF with score 179 to: (sr:aspergillus fumigatus (library: cbs 144.89) (clone: fp4) myceliu) (db:genpept-pln1) (de:aspergillus fumigatus 88 kda secreted dipetidyl peptidase gene,complete cds.) (nt:putative) (le:326:461:571:860:1922) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744017	1142	23298	588	196

Description

5000688894 transcription antiterminator:glycerol uptake operon antiterminator regulatory protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) glpP glpP Bacillus subtilis 1423 -11529053 74044 glpp (de:glycerol uptake operon antiterminator regulatory protein) (db:swissprot) GLPP_BACSU P30300 BACILLUS SUBTILIS 1423 -11529053 7000685418 glpp glycerol metabolism regulatory protein glpp (db:pir2.dat) (mp:75 (degrees)) B47700 B47700 Bacillus subtilis 1423 -11529053 7500882512 glpp regulatory protein (fn:putative antiterminator) (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis antiterminator regulatory protein (glpp),glycerol uptake facilitator (glpf) genes, complete cds, glycerolkinase (glpk) gene, 5' end.) (le:328) (re:906) (di:... BACGLPPFK M99611 g142996 Bacillus subtilis 1423 -11529053 215686 glpp transcription antiterminator (fn:control of mrna stability of glpd) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:198429) (re:199007) (di:direct) BSUB0005 Z99108 g2633250 Bacillus subtilis 1423 -11529053 4000707102 glpp transcription antiterminator (fn:control of mrna stability of glpd) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:1749) (re:2327) (di:direct) BSUB0006 Z99109 g2633262 Bacillus subtilis 1423 -11529053 6000684763 glpp regulatory protein (fn:putative antiterminator) (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:see embl m99611 and swiss prot p30300.) (le:1397) (re:1975) (di:direct) BSY14079 Y14079 g2226135 Bacillus subtilis 1423 -11529053 170020 glpp glycerol metabolism regulatory protein glpp (db:pir) (mp:75 (degrees)) B47700 B47700 Bacillus subtilis 1423 -11529053 6500725195 transcription antiterminator:glycerol uptake operon antiterminator regulatory protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) glpP glpP Bacillus subtilis 1423 -11529053

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744025	1143	23299	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744031	1144	23300	585	195

Description

5000688885 transcriptional regulator:lysr family:citrate synthase i repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) citR citR Bacillus subtilis 1423 -11529054 64710 citr (de:citrate synthase i repressor) (db:swissprot) CITR_BACSU P39127 BACILLUS SUBTILIS 1423 -11529054 7000684831 citr transcription repressor of citrate synthase i citr (cl:bacillus subtilis transcription repressor of citrate synthase i citr) (db:pir2.dat) I40379 I40379 Bacillus subtilis 1423 -11529054 7500878781 citr citr (fn:repressor of cita) (db:genpept-bct1) (de:bacillus subtilis smy citrate synthase i (cita) and repressor ofcita (citr) genes, complete cds.) (le:96) (re:1022) (di:complement) BSCITRA U05256 g452564 Bacillus subtilis 1423 -11529054 219074 citr transcriptional regulator lysr family (fn:negative regulation of the citrate synthase i) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:20002) (re:20928) (di:complement) BSUB0006 Z99109 g2633278 Bacillus subtilis 1423 -11529054 4000706968 citr (fn:negative regulatory protein for the cita gene) (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:see subtilist bg10853, embl u05256 and swiss prot) (le:6650) (re:7576) (di:complement) BSY14082 Y14082 g2226199 Bacillus subtilis 1423 -11529054 169918 citr citrate synthase i transcriptional repressor citr (db:pir) I40379 I40379 Bacillus subtilis 1423 -11529054 6500725196 transcriptional regulator:lysr family:citrate synthase i repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) citR citR Bacillus subtilis 1423 -11529054

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744033	1145	23301	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744044	1146	23302	411	136

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744052	1147	23303	240	79

Description

5000688898 cata:scoc:hpr transcriptional regulator:protease production regulatory protein hpr (gtcfc:10.2:12.13) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) hpr hpr Bacillus subtilis 1423 -11529055 77572 hpr:cata:scoc (de:protease production regulatory protein hpr) (db:swissprot) HPR_BACSU P11065 BACILLUS SUBTILIS 1423 -11529055 7000685557 hpr sporulation repressor hpr (db:pir2.dat) A32009 A32009 Bacillus subtilis 1423 -11529055 7500883507 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis hpr gene encoding a negative regulatory protein forsporulation and protease production.) (nt:hpr protein) (le:95) (re:706) (di:direct) BACHPR M20237 g143052 Bacillus subtilis 1423 -11529055 215843 hpr transcriptional regulator (fn:negative regulation of sporulation and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: cata, scoc) (le:73081) (re:73692) (di:complement) BSUB0006 Z99109 g2633335 Bacillus subtilis 1423 -11529055 4000707132 hpr regulatory protein (fn:regulator of protease production and) (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:see swiss prot m20237) (le:7221) (re:7832) (di:direct) BSY14077 Y14077 g2226120 Bacillus subtilis 1423 -11529055 170465 hpr sporulation repressor hpr (db:pir) A32009 A32009 Bacillus subtilis 1423 -11529055 6500725197 cata:scoc transcriptional regulator:protease production regulatory protein hpr (gtcfc:10.2:12.13) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) hpr hpr Bacillus subtilis 1423 -11529055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744053	1148	23304	369	122

Description

6500725198 transcriptional regulator:laci family:degradation activator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) degA degA Bacillus subtilis 1423 -11529056 7000694699 dega sporulation-specific degradation regulator protein dega (cl:lac repressor) (db:pir1.dat) A36940 G69613 Bacillus subtilis 1423 -11529056 3000694800 dega transcriptional regulator laci family (fn:stimulates degradation of glutamine) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:163121) (re:164134) (di:direct) BSUB0006 Z99109 g2633419 Bacillus subtilis 1423 -11529056 7500955299 dega (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (le:20347) (re:21360) (di:direct) BSY09476 Y09476 g2145384 Bacillus subtilis 1423 -11529056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744061	1149	23305	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744062	1150	23306	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744063	1151	23307	1080	360

Description

GTC ORF with score 219 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744071	1152	23308	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744078	1153	23309	222	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744084	1154	23310	249	82

Description

5000688921 transcriptional regulator:transcriptional activator tena (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) tenA tenA Bacillus subtilis 1423 -11529057 101000 tena (de:transcriptional activator tena) (db:swissprot) TENA_BACSU P25052 BACILLUS SUBTILIS 1423 -11529057 131462 tena transcription activator of extracellular enzyme genes tena (cl:transcription activator tena) (db:pir1.dat) XMBSTA A39184 Bacillus subtilis 1423 -11529057 216951 tena transcription activator (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis transcription activator (tena and teni) genes,complete cds.) (le:407) (re:1117) (di:direct) BACTENAI M73546 g143729 Bacillus subtilis 1423 -11529057 7500892932 tena transcriptional regulator (fn:positive regulation of extracellular enzyme) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:47530) (re:48240) (di:direct) BSUB0007 Z99110 g2633519 Bacillus subtilis 1423 -11529057 6500725199 transcriptional regulator:transcriptional activator tena (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) tenA tenA Bacillus subtilis 1423 -11529057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744090	1155	23311	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744096	1156	23312	549	183

Description

5000688922 transcriptional regulator:regulatory protein teni (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) tenI tenI Bacillus subtilis 1423 -11529058 101006 teni (de:regulatory protein teni) (db:swissprot) TENI_BACSU P25053 BACILLUS SUBTILIS 1423 -11529058 131464 teni regulatory protein teni:extracellular enzyme genes transcriptional activator teni (cl:regulatory protein teni) (db:pir1.dat) XMBSTI B39184 Bacillus subtilis 1423 -11529058 216952 teni transcription activator (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis transcription activator (tena and teni) genes,complete cds.) (le:1092) (re:1709) (di:direct) BACTENAI M73546 g143730 Bacillus subtilis 1423 -11529058 7500892934 teni transcriptional regulator (fn:positive regulation of extracellular enzyme) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:48215) (re:48832) (di:direct) BSUB0007 Z99110 g2633520 Bacillus subtilis 1423 -11529058 6500725200 transcriptional regulator:regulatory protein teni (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) tenI tenI Bacillus subtilis 1423 -11529058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744189	1157	23313	486	162

Description

GTC ORF with score 169 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1635.) (nt:similar to saccharomyces cerevisiae nam9 protein) (le:59) (re:1042) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744191	1158	23314	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744192	1159	23315	252	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744200	1160	23316	1203	400

Description

5000689464 gsiab:phra inhibitor of the activity of phosphatase rapa:hypothetical 4.8 kd protein in gsiaa 3region (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) phrA phrA Bacillus subtilis 1423 -11529059 219349 phra:gsiab (de:phosphatase rapa inhibitor) (db:swissprot) PHRA_BACSU Q00829 BACILLUS SUBTILIS 1423 -11529059 7000685386 phra phosphatase rapa inhibitor phra:glucose starvation-inducible protein gsiab (db:pir2.dat) H69676 H69676 Bacillus subtilis 1423 -11529059 7500888065 phra pre-inhibitor protein of rapa (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (le:1... AF034138 AF034138 g2645864 Bacillus subtilis 1423 -11529059 6000684785 gsiab (db:genpept-bct1) (de:b.subtilis gsiaa and gsiab genes.) (le:1421) (re:1555) (di:direct) BSGSIAAB X56679 g39932 Bacillus subtilis 1423 -11529059 6500725201 phra inhibitor of the activity of phosphatase rapa (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: gsiab) (le:122074) (re:122208) (di:direct) BSUB0007 Z99110 g2633598 Bacillus subtilis 1423 -11529059 74593 phra:gsiab (de:phosphatase rapa inhibitor) (db:swissprot) PHRA_BACSU Q00829 BACILLUS SUBTILIS 1423 -11529059 170028 phra phosphatase rapa inhibitor phra:glucose starvation-inducible protein gsiab (db:pir) H69676 H69676 Bacillus subtilis 1423 -11529059

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744201	1161	23317	408	135

Description

5000689028 transcriptional regulator:putative pbsx repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) xre xre Bacillus subtilis 1423 -11529060 217062 xre (de:putative pbsx repressor) (db:swissprot) XRE_BACSU P23789 BACILLUS SUBTILIS 1423 -11529060 7000687050 xre transcription repressor of pbsx genes xre:pbsx repressor 2 (cl:probable transcription repressor yowr) (db:pir2.dat) JQ0810 JQ0810 Bacillus subtilis 1423 -11529060 7500894478 (sr:b.subtilis (strain 168, isolate so113) dna) (db:genpept-bct1) (de:b.subtilis pbsx repressor (xre) gene, complete cds.) (nt:pbsx repressor) (le:397) (re:738) (di:direct) BACXREA M36478 g143835 Bacillus subtilis 1423 -11529060 219478 xre (fn:the pbsx repressor; see also m36477 and m36478) (db:genpept-bct1) (de:b.subtilis (so113) genomic dna (5425bp).) (le:463) (re:804) (di:complement) BSGENDNA Z34287 g498812 Bacillus subtilis 1423 -11529060 219230 xre pbsx repressor (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqae of the skin element) (le:460) (re:801) (di:complement) BSPBSXSE Z70177 g1225936 Bacillus subtilis 1423 -11529060 6500725202 xre transcriptional regulator (fn:negative regulation of the defective prophage) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:126409) (re:126750) (di:complement) BSUB0007 Z99110 g2633605 Bacillus subtilis 1423 -11529060 108162 xre (de:putative pbsx repressor) (db:swissprot) XRE_BACSU P23789 BACILLUS SUBTILIS 1423 -11529060 158713 xre repressor protein xre (db:pir) JQ0810 JQ0810 Bacillus subtilis phage PBSX 10667 -11529060 170670 xre transcriptional repressor of pbsx genes xre:pbsx repressor 2 (db:pir) I40038 I40038 Bacillus subtilis 1423 -11529060

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744207	1162	23318	198	65

Description

6500725203 scgr:tnra transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) tnrA tnrA Bacillus subtilis 1423 -11529061 7000694711 tnra:scgr transcription regulator scgr:transcription regulator tnra (cl:transcription repressor glnr) (db:pir2.dat) S70466 S70466 Bacillus subtilis 1423 -11529061 219615 tnra tnra (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:transcriptional regulator) (le:49538) (re:49870) (di:complement) BSAJ2571 AJ002571 g2632050 Bacillus subtilis 1423 -11529061 220095 scgr (db:genpept-bct1) (de:b.subtilis scgr gene.) (le:83) (re:415) (di:direct) BSSCGR X98512 g1405480 Bacillus subtilis 1423 -11529061 6000689799 tnra transcriptional regulator (fn:global nitrogen regulation (positive regulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: scgr) (le:202487) (re:202819) (di:complement) BSUB0007 Z99110 g2633685 Bacillus subtilis 1423 -11529061 6000689801 tnra transcriptional regulator (fn:global nitrogen regulation (positive regulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: scgr) (le:2087) (re:2419) (di:complement) BSUB0008 Z99111 g2633702 Bacillus subtilis 1423 -11529061 7500955788 tnra transcription factor tnra (db:genpept-bct2) (de:bacillus subtilis transcription factor tnra (tnra) gene, completecds.) (le:312) (re:644) (di:direct) BSU55004 U55004 g1518970 Bacillus subtilis 1423 -11529061

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744214	1163	23319	546	181

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744222	1164	23320	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744228	1165	23321	576	191

Description

6500725204 ykwa:glct transcriptional antiterminator:bglg family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) glcT glcT Bacillus subtilis 1423 -11529062 7000694708 glct transcription antiterminator glct (cl:bacillus subtilis transcription antiterminator lict) (db:pir2.dat) D69632 D69632 Bacillus subtilis 1423 -11529062 7500965281 glct transcriptional antiterminator bglg family (fn:essential for the expression of the ptsghi) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ykwa) (le:60768) (re:61625) (di:direct) BSUB0008 Z99111 g2633759 Bacillus subtilis 1423 -11529062

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744234	1166	23322	783	261

Description

5000689574 ykxi:spla transcriptional regulator:hypothetical 9.2 kd protein in ptsi-spl intergenic region (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) splA splA Bacillus subtilis 1423 -11529063 114279 spla (de:transcriptional regulator spla) (db:swissprot) SPLA_BACSU P37955 BACILLUS SUBTILIS 1423 -11529063 7000688113 spla transcription regulator of spore photoproduct lyase operon spla:hypothetical protein 5 of spl (db:pir2.dat) E69709 E69709 Bacillus subtilis 1423 -11529063 7500891978 9000 kda protein (fn:unknown) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis 168 enzyme i of the pep:phototransferase systemgene, 3' end, and spore photoproduct lyase gene, complete cds.) (le:613) (re:852) (di:direct) BACENZYMEI L08809 g289269 Bacillus subtilis 1423 -11529063 215571 spla transcriptional regulator (fn:regulation of the spore photoproduct lyase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ykxi) (le:66070) (re:66309) (di:direct) BSUB0008 Z99111 g2633763 Bacillus subtilis 1423 -11529063 170388 spla transcriptional regulator of the spore photoproduct lyase opero spla (db:pir) E69709 E69709 Bacillus subtilis 1423 -11529063 6500725205 ykxi transcriptional regulator:hypothetical 9.2 kd protein in ptsi-spl intergenic region (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) splA splA Bacillus subtilis 1423 -11529063

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744245	1167	23323	474	158

Description

6500725206 transcriptional regulator:deor family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) fruR fruR Bacillus subtilis 1423 -11529064 7000694805 frur transcription repressor of fructose operon frur (cl:regulatory protein gutr) (db:pir2.dat) B69627 B69627 Bacillus subtilis 1423 -11529064 7500955786 frur frur (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to l. lactis lactose pts system repressor,) (le:12681) (re:13436) (di:direct) AF012285 AF012285 g3282123 Bacillus subtilis 1423 -11529064 7500955785 frur transcriptional regulator deor family (fn:negative regulation of the fructose operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:112193) (re:112948) (di:direct) BSUB0008 Z99111 g2633809 Bacillus subtilis 1423 -11529064

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744322	1168	23324	780	260

Description

6500725207 ylxt:yzaa:abh transcriptional regulator:putative transition state regulator abh (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) abh abh Bacillus subtilis 1423 -11529065 57920 abh (de:putative transition state regulator abh) (db:swissprot) ABH_BACSU P39758 BACILLUS SUBTILIS 1423 -11529065 7000684485 abh transcription regulator of transition state genes abrb-like abh (db:pir2.dat) I39925 I39925 Bacillus subtilis 1423 -11529065 220072 abh putative transition state regulator abh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to orf1 product encoded by genbank) (le:22968) (re:23246) (di:direct) AF012285 AF012285 g3282133 Bacillus subtilis 1423 -11529065 7500876266 orf1 (sr:bacillus subtilis (sub_species:marburg, strain:168) (db:genpept-bct1) (de:bacillus subtilis genes for amps, mrebh, orf1, kinc, orf3, orf4 andorf5.) (le:2509) (re:2787) (di:direct) BACAMOKOOO D37799 g520841 Bacillus subtilis 1423 -11529065 215163 orf1 (sr:bacillus subtilis (sub_species marburg) (sub_strain jh642,strai) (db:genpept-bct1) (de:bacillus subtilis genes for orf1 and kinc.) (le:443) (re:721) (di:direct) BACORFKINC D37798 g520576 Bacillus subtilis 1423 -11529065 216417 abh transcriptional regulator (fn:regulation of transition state genes) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ylxt, yzaa) (le:122480) (re:122758) (di:direct) BSUB0008 Z99111 g2633819 Bacillus subtilis 1423 -11529065 170248 abh transcriptional regulator of transition state genes abrb-like abh (db:pir) I39925 I39925 Bacillus subtilis 1423 -11529065 5000689066 (de:(abh) (pn:putative transition state regulator abh) (gtcfc:13.07) (ec:) (abh_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) abh abh Bacillus subtilis 1423 10000700

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744331	1169	23325	858	286

Description

6500725208 transcriptional attenuator and uracil phosphoribosyltransferase activity:minor:pyrimidine operon regulatory protein pyrr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) pyrR pyrR Bacillus subtilis 1423 -11529066 7500965282 pyrr transcriptional attenuator and uracil (fn:attenuation (antitermination) of the pyrimidine) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:19288) (re:19833) (di:direct) BSUB0009 Z99112 g2633920 Bacillus subtilis 1423 -11529066 7000694710 pyrr transcriptional attenuation of the pyrimidine operon / uracil pyrr (db:pir) A69687 A69687 Bacillus subtilis 1423 -11529066

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744355	1170	23326	396	132

Description

GTC ORF with score 112 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744358	1171	23327	627	209

Description

GTC ORF with score 112 to: (sr:african clawed frog) (db:genpept-vrt) (de:xenopus laevis middle molecular weight neurofilament proteinnf-m(2) mrna, complete cds.) (nt:neuronal intermediate filament protein; duplicated) (le:31) (re:2772) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744459	1172	23328	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744463	1173	23329	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744467	1174	23330	486	161

Description

5000689460 transcriptional regulator:cody protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) codY codY Bacillus subtilis 1423 -11529067 7000684862 cody transcription pleiotropic repressor cody (db:pir2.dat) S61496 S61496 Bacillus subtilis 1423 -11529067 219818 cody cody (db:genpept-bct1) (de:bacillus subtilis jh642 dipeptide permease operon regulators, codv,codw, codx, and cody genes, complete cds.) (le:3225) (re:4004) (di:direct) BSU13634 U13634 g535351 Bacillus subtilis 1423 -11529067 7500965285 cody transcriptional regulator (fn:negative regulation of srfa and comk genes (in) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:91098) (re:91877) (di:direct) BSUB0009 Z99112 g2633989 Bacillus subtilis 1423 -11529067 6500725209 transcriptional regulator:cody protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) codY codY Bacillus subtilis 1423 -11529067 65301 cody_bacsu (de:cody protein.) P39779 P39779 Bacillus subtilis 1423 -11529067

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744471	1175	23331	690	230

Description

6500725210 hypothetical protein:n utilization substance protein a homolog:nusa protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) nusA nusA Bacillus subtilis 1423 -11529068 7500955886 nusa (fn:transcription termination) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:133252) (re:134367) (di:direct) BSUB0009 Z99112 g2634032 Bacillus subtilis 1423 -11529068 7000694698 nusa transcription termination nusa (cl:bacillus transcription termination factor nusa:transcription termination factor nusa homology) (db:pir) B69668 B69668 Bacillus subtilis 1423 -11529068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744490	1176	23332	486	162

Description

6500725211 transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) pksA pksA Bacillus subtilis 1423 -11529069 7000694798 pksa transcription regulator of polyketide synthase operon pksa (db:pir2.dat) G69677 G69677 Bacillus subtilis 1423 -11529069 6000690884 pksa transcriptional regulator (fn:regulation of the polyketide synthase operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:182855) (re:183472) (di:direct) BSUB0009 Z99112 g2634079 Bacillus subtilis 1423 -11529069 7500965357 pksa transcriptional regulator (fn:regulation of the polyketide synthase operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:75) (re:692) (di:direct) BSUB0010 Z99113 g2634091 Bacillus subtilis 1423 -11529069

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744491	1177	23333	234	77

Description

5000688893 transcriptional regulator:regulatory protein glnr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) glnR glnR Bacillus subtilis 1423 -11529070 73996 glnr (de:regulatory protein glnr) (db:swissprot) GLNR_BACSU P37582 BACILLUS SUBTILIS 1423 -11529070 7000685411 glnr transcription repressor of glutamine synthetase glnr (cl:transcription repressor glnr) (db:pir2.dat) JT0393 JT0393 Bacillus subtilis 1423 -11529070 7500882477 unknown protein (sr:bacillus subtilis (sub_strain jh642/168, strain marburg) dna) (db:genpept-bct1) (de:bacillus subtilis glutamine synthetase (glna) gene, complete cds.) (nt:orf1; putative) (le:162) (re:569) (di:direct) BACGLNAZ M22811 g1119204 Bacillus subtilis 1423 -11529070 215675 glnr glnr (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750110 Bacillus subtilis 1423 -11529070 220164 glnr transcriptional regulator (fn:negative regulation of the glutamine synthetase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:96001) (re:96408) (di:direct) BSUB0010 Z99113 g2634129 Bacillus subtilis 1423 -11529070 170485 glnr glutamine synthetase transcriptional repressor glnr (cl:transcriptional repressor glnr) (db:pir) JT0393 JT0393 Bacillus subtilis 1423 -11529070 6500725212 transcriptional regulator:regulatory protein glnr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) glnR glnR Bacillus subtilis 1423 -11529070

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744493	1178	23334	699	232

Description

6500725213 transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) xylR xylR Bacillus subtilis 1423 -11529071 220177 xylr xylose repressor (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750123 Bacillus subtilis 1423 -11529071 7500955302 xylr transcriptional regulator (fn:negative regulation of the xylose operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:108566) (re:109618) (di:complement) BSUB0010 Z99113 g2634143 Bacillus subtilis 1423 -11529071 7000694809 xylr transcriptional repressor of the xylose operon xylr (cl:xylose repressor:glucose kinase homology) (db:pir) E69735 E69735 Bacillus subtilis 1423 -11529071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744495	1179	23335	738	245

Description

6500725214 dinr:lexa transcriptional regulator:sos regulatory protein lexa/ (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) lexA lexA Bacillus subtilis 1423 -11529072 81974 lexa:dinr (de:sos regulatory protein lexa/dinr) (db:swissprot) LEXA_BACSU P31080 BACILLUS SUBTILIS 1423 -11529072 7000685738 lexa:dinr transcription repressor of sos regulon lexa/dinr (cl:lexa protein) (db:pir2.dat) A41315 A41315 Bacillus subtilis 1423 -11529072 7500884970 lexa (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis lexa gene, 3' end.) (le:390) (re:1007) (di:direct) BACLEXA M64684 g289288 Bacillus subtilis 1423 -11529072 216288 lexa transcriptional regulator (fn:negative regulation of the sos regulon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: dinr) (le:135694) (re:136311) (di:complement) BSUB0010 Z99113 g2634169 Bacillus subtilis 1423 -11529072 170549 lexa:dinr sos regulon transcriptional repressor lexa/dinr (db:pir) A41315 A41315 Bacillus subtilis 1423 -11529072 5000688902 (de:(lexa) (pn:sos regulatory protein lexa:sos regulatory protein lexa) (gn:dinr) (gtcfc:12.13) (ec:) (lexa_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) lexA lexA Bacillus subtilis 1423 10024208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744499	1180	23336	264	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744502	1181	23337	618	205

Description

5000688895 transcriptional regulator:lysr family:transcriptional regulatory protein gltc (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) gltC gltC Bacillus subtilis 1423 -11529073 74119 gltc (de:transcriptional regulatory protein gltc) (db:swissprot) GLTC_BACSU P20668 BACILLUS SUBTILIS 1423 -11529073 7000685424 gltc transcription activator of glutamate synthase operon gltc:regulatory protein gltc (cl:probable transcription regulator lsyr) (db:pir2.dat) A69635 A69635 Bacillus subtilis 1423 -11529073 245394 gltc transcriptional regulator lysr family (fn:positive regulation of the glutamate synthase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:232835) (re:233737) (di:direct) BSUB0010 Z99113 g2634229 Bacillus subtilis 1423 -11529073 6000684767 gltc transcriptional regulator lysr family (fn:positive regulation of the glutamate synthase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:13865) (re:14767) (di:direct) BSUB0011 Z99114 g2634240 Bacillus subtilis 1423 -11529073 7500882555 gltc (fn:positive transcriptional regulator) (db:genpept-bct1) (de:bacillus subtilis (gltc) gene, complete cds and glutamate synthase,large subunit (glta) gene, partial cds. gene.) (le:34) (re:936) (di:complement) M28509 M28509 g457514 Bacillus subtilis 1423 -11529073 6500725215 transcriptional regulator:lysr family:transcriptional regulatory protein gltc (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) gltC gltC Bacillus subtilis 1423 -11529073

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744504	1182	23338	369	122

Description

6500725216 prtr:degr hypothetical protein:regulatory protein degr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) degR degR Bacillus subtilis 1423 -11529074 68234 degr:prtr (de:regulatory protein degr) (db:swissprot) DEGR_BACSU P06563 BACILLUS SUBTILIS 1423 -11529074 7502851580 degr:prtr (de:regulatory protein degr) (db:swissprot) DEGR_BACSU P06563 BACILLUS SUBTILIS VARNATTO 99999 -11529074 7000685003 degr degradative enzyme production factor degr (db:pir2.dat) I39957 I39957 Bacillus subtilis 1423 -11529074 7500880150 (sr:b.natto (strain if03936) dna, clone pnc61) (db:genpept-bct1) (de:bacillus natto prtr gene encoding protease, complete cds.) (nt:protease) (le:417) (re:599) (di:direct) BACPRTR M12917 g143355 Bacillus subtilis 1423 -11529074 216518 (sr:b.subtilis (strain i168 (trpc)) dna, clone pprtr1) (db:genpept-bct1) (de:b.subtilis prtr gene encoding protease, complete cds.) (nt:protease) (le:417) (re:599) (di:direct) BACPRTRA M15318 g143357 Bacillus subtilis 1423 -11529074 216519 degr (fn:regulation of degradative enzymes byosynthesis) (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (le:13111) (re:13293) (di:direct) BACYACA L77246 g1256628 Bacillus subtilis 1423 -11529074 217085 degr (fn:activation of degradative enzymes (apre, npre,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: prtr) (le:111859) (re:112041) (di:complement) BSUB0012 Z99115 g2634614 Bacillus subtilis 1423 -11529074 170464 degr degradative enzyme production factor degr (db:pir) I39957 I39957 Bacillus subtilis 1423 -11529074 5000688889 (de:(degr) (pn:regulatory protein degr) (gn:prtr) (gtcfc:12.13) (ec:) (degr_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) degR degR Bacillus subtilis 1423 10010827

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744505	1183	23339	489	162

Description

5000689090 transcriptional regulator:laci family:kdg operon repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) kdgR kdgR Bacillus subtilis 1423 -11529075 80587 kdgr (de:kdg operon repressor) (db:swissprot) KDGR_BACSU P50844 BACILLUS SUBTILIS 1423 -11529075 7000685672 kdgr transcription repressor of pectin utilization operon kdgr (db:pir2.dat) B69648 B69648 Bacillus subtilis 1423 -11529075 216507 kdgr repressor protein (fn:regulation of transcription of kdg operon) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene,... BACPONAYPP L47838 g1146188 Bacillus subtilis 1423 -11529075 7500884552 kdgr transcriptional regulator laci family (fn:negative regulation of the pectin utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:128315) (re:129334) (di:complement) BSUB0012 Z99115 g2634631 Bacillus subtilis 1423 -11529075 6500725217 transcriptional regulator:laci family:kdg operon repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) kdgR kdgR Bacillus subtilis 1423 -11529075

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744507	1184	23340	591	197

Description

5000688904 tryptophan operon rna-binding attenuation protein:transcription attenuation protein mtrb:tryptophan rna-binding attenuator protein:trap (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) mtrB mtrB Bacillus subtilis 1423 -11529076 84589 mtrb (de:attenuator protein) (trap)) (db:swissprot) MTRB_BACSU P19466 BACILLUS SUBTILIS 1423 -11529076 7000685880 mtrb tryptophan biosynthetic enzyme transcription regulatory protein mtrb:trp rna-binding attenuation protein:tryptophan operon rna-binding attenuation protein trap mtrb (db:pir2.dat) B38256 B38256 Bacillus subtilis 1423 -11529076 7500886044 mtrb rna binding regulatory protein (sr:b.subtilis (strain w168) cell line bg2087 dna, clone 7a) (db:genpept-bct1) (de:b.subtilis regulatory protein (mtra and mtrb) genes, complete cds.) (le:990) (re:1217) (di:direct) BACMTRAA M37320 g143234 Bacillus subtilis 1423 -11529076 216369 mtrb mtrb (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:990) (re:1217) (di:direct) BACVARGNS M80245 g143800 Bacillus subtilis 1423 -11529076 217026 mtrb tryptophan operon rna-binding attenuation (fn:regulation of tryptophan biosynthesis (required) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:188231) (re:188458) (di:complement) BSUB0012 Z99115 g2634695 Bacillus subtilis 1423 -11529076 170650 mtrb tryptophan biosynthetic enzyme transcription regulatory protein mtrb:trp rna-binding attenuation protein:tryptophan operon rna-binding attenuation protein trap mtrb (db:pir) B38256 B38256 Bacillus subtilis 1423 -11529076 6500725218 tryptophan operon rna-binding attenuation protein:transcription attenuation protein mtrb:tryptophan rna-binding attenuator protein:trap (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) mtrB mtrB Bacillus subtilis 1423 -11529076

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744509	1185	23341	303	100

Description

5000688879 transcriptional regulator:xre family:ans operon repressor protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ansR ansR Bacillus subtilis 1423 -11529077 59645 ansr (de:ans operon repressor protein) (db:swissprot) ANSR_BACSU Q07683 BACILLUS SUBTILIS 1423 -11529077 7000684583 ansr transcription repressor of ansab operon ansr (db:pir2.dat) B40617 B40617 Bacillus subtilis 1423 -11529077 7500876924 (fn:ans repressor) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis ansr gene, complete cds.) (le:658) (re:1008) (di:complement) BACANSRX L08205 g387575 Bacillus subtilis 1423 -11529077 215188 ansr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:262311) (re:262661) (di:complement) BACJH642 D84432 g1303986 Bacillus subtilis 1423 -11529077 216230 ansr transcriptional regulator xre family (fn:negative regulation of the ansab operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:60958) (re:61308) (di:direct) BSUB0013 Z99116 g2634794 Bacillus subtilis 1423 -11529077 170500 ansr ansab operon transcriptional repressor ansr (db:pir) B40617 B40617 Bacillus subtilis 1423 -11529077 6500725219 transcriptional regulator:xre family:ans operon repressor protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ansR ansR Bacillus subtilis 1423 -11529077

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744510	1186	23342	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744520	1187	23343	243	80

Description

6500725220 transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) bmrR bmrR Bacillus subtilis 1423 -11529078 7500877872 bmrr:bmr1r (de:multidrug-efflux transporter 1 regulator) (db:swissprot) BMRR_BACSU P39075 BACILLUS SUBTILIS 1423 -11529078 7000694705 bmrr transcription activator of bmrur operon bmrr (db:pir2.dat) E69595 E69595 Bacillus subtilis 1423 -11529078 5500703921 bmrr multidrug-efflux transporter regulator (fn:dna-binding protein activating transcription of) (db:genpept-bct1) (de:bacillus subtilis bmru, multidrug efflux transporter (bmr) and itsregulator (bmrr) genes, complete cds, and branched-chain 2-oxo aciddehydrogenase (bfmb) gene, 3' end.) (le:2463... BACBMRURBE L25604 g2558637 Bacillus subtilis 1423 -11529078 7500877875 bmrr transcriptional regulator (fn:positive regulation of the bmrur operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:99870) (re:100709) (di:direct) BSUB0013 Z99116 g2634836 Bacillus subtilis 1423 -11529078

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744521	1188	23344	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744625	1189	23345	480	159

Description

5000688877 transcriptional regulator:arginine hydroximate resistance protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ahrC ahrC Bacillus subtilis 1423 -11529079 58996 ahrc (de:arginine hydroximate resistance protein) (db:swissprot) AHRC_BACSU P17893 BACILLUS SUBTILIS 1423 -11529079 7000684545 ahrc arginine metabolism regulatory protein ahrc (db:pir2.dat) JS0275 JS0275 Bacillus subtilis 1423 -11529079 7500876697 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis ahrc gene, encoding an arginine repressor/activatorprotein.) (nt:ahrc protein) (le:333) (re:782) (di:direct) BACAHRCA M27869 g142450 Bacillus subtilis 1423 -11529079 215136 ahrc (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:196833) (re:197282) (di:direct) BACJH642 D84432 g1303922 Bacillus subtilis 1423 -11529079 216166 ahrc transcriptional regulator (fn:negative regulation of arginine biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:126339) (re:126788) (di:complement) BSUB0013 Z99116 g2634859 Bacillus subtilis 1423 -11529079 169871 ahrc arginine metabolism regulatory protein ahrc (db:pir) JS0275 JS0275 Bacillus subtilis 1423 -11529079 6500725221 transcriptional regulator:arginine hydroximate resistance protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ahrC ahrC Bacillus subtilis 1423 -11529079

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744636	1190	23346	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744637	1191	23347	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744668	1192	23348	1107	369

Description

5000688919 antagonist of sinr:sini protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sinI sinI Bacillus subtilis 1423 -11529080 98530 sini (de:sini protein) (db:swissprot) SINI_BACSU P23308 BACILLUS SUBTILIS 1423 -11529080 7000686602 sini sinr antagonist sini (db:pir2.dat) A25159 A25159 Bacillus subtilis 1423 -11529080 7500891642 sini (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:166986) (re:167159) (di:complement) BACJH642 D84432 g1303887 Bacillus subtilis 1423 -11529080 216131 sini antagonist of sinr (fn:prevents sinr from binding to its target) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:156462) (re:156635) (di:direct) BSUB0013 Z99116 g2634894 Bacillus subtilis 1423 -11529080 170048 sini sinr antagonist sini (db:pir) A25159 A25159 Bacillus subtilis 1423 -11529080 6500725222 antagonist of sinr:sini protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sinI sinI Bacillus subtilis 1423 -11529080

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744681	1193	23349	1122	373

Description

5000688920 sin:flad:sinr transcriptional regulator:sinr protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sinR sinR Bacillus subtilis 1423 -11529081 98532 sinr:sin:flad (de:sinr protein) (db:swissprot) SINR_BACSU P06533 BACILLUS SUBTILIS 1423 -11529081 7000686603 sinr 13k sin operon hypothetical protein sinr:post-exponential-phase transcriptional regulator sinr (db:pir2.dat) B25159 B25159 Bacillus subtilis 1423 -11529081 7500891643 sinr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:166617) (re:166952) (di:complement) BACJH642 D84432 g1303886 Bacillus subtilis 1423 -11529081 216130 (sr:bacillus subtilis (strain is190) dna, clone pis74) (db:genpept-bct1) (de:b.subtilis sin gene causing inhibition of both sporulation andexoprotease production, complete cds.) (nt:sin regulatory protein (ttg start codon)) (le:490) (re:825) (di:direct) BACSIN M14112 g143547 Bacillus subtilis 1423 -11529081 216747 sinr transcriptional regulator (fn:regulation of post-exponential-phase responses) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: sin, flad) (le:156669) (re:157004) (di:direct) BSUB0013 Z99116 g2634895 Bacillus subtilis 1423 -11529081 169829 sinr 13k sin operon hypothetical protein sinr:post-exponential-phase transcriptional regulator sinr (db:pir) B25159 B25159 Bacillus subtilis 1423 -11529081 6500725223 sin:flad transcriptional regulator:sinr protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sinR sinR Bacillus subtilis 1423 -11529081

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744685	1194	23350	543	180

Description

6500725224 yqxe:yqes:hrca transcriptional regulator:heat-inducible transcription repressor hrca (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) hrcA hrcA Bacillus subtilis 1423 -11529082 77603 hrca (de:heat-inducible transcription repressor hrca) (db:swissprot) HRCA_BACSU P25499 BACILLUS SUBTILIS 1423 -11529082 7000685558 hrca transcription repressor of class i heat-shock gene hrca:hypothetical protein 39 (cl:conserved hypothetical protein mg205) (db:pir2.dat) A41874 A41874 Bacillus subtilis 1423 -11529082 7500883512 (sr:bacillus subtilis (strain mb11) dna) (db:genpept-bct1) (de:b.subtilis orf39, grpe, dnak, and dnaj genes, complete cds's.) (nt:orf39) (le:242) (re:1273) (di:direct) BACHSP M84964 g143057 Bacillus subtilis 1423 -11529082 215846 yqes (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:89977) (re:91008) (di:direct) BACJH642 D84432 g1303806 Bacillus subtilis 1423 -11529082 216050 hrca transcriptional regulator (fn:negative regulation of class i heat-shock genes) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqxe, yqes) (le:28422) (re:29453) (di:complement) BSUB0014 Z99117 g2634995 Bacillus subtilis 1423 -11529082 170034 hrca class i heat-shock gene transcriptional repressor hrca:hypothetical protein 39 (db:pir) A41874 A41874 Bacillus subtilis 1423 -11529082 5000689087 (de:(hrca) (pn:heat-inducible transcription repressor hrca) (gtcfc:13.07) (ec:) (hrca_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) hrcA hrcA Bacillus subtilis 1423 10019963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744686	1195	23351	852	283

Description

6500725225 regulator of the activity of phosphatase rape (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) phrE phrE Bacillus subtilis 1423 -11529083 7000694394 phre phosphatase rape regulator phre (db:pir2.dat) B69677 B69677 Bacillus subtilis 1423 -11529083 7500965061 phre regulator of the activity of phosphatase rape (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:60150) (re:60284) (di:direct) BSUB0014 Z99117 g2635029 Bacillus subtilis 1423 -11529083

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744688	1196	23352	1149	382

Description

6500725226 bmr2r:bmtr:bltr transcriptional regulator:multidrug-efflux transporter 2 regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) bltR bltR Bacillus subtilis 1423 -11529084 61857 bltr:bmtr:bmr2r (de:multidrug-efflux transporter 2 regulator) (db:swissprot) BLTR_BACSU P39842 BACILLUS SUBTILIS 1423 -11529084 7000684723 bltr transcription regulator of bltd operon bltr (db:pir2.dat) I39791 I39791 Bacillus subtilis 1423 -11529084 7500877866 bltr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:2757) (re:3578) (di:direct) BACJH642 D84432 g1303700 Bacillus subtilis 1423 -11529084 215287 bltr transcriptional regulator (fn:regulation of the bltd operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: bmr2r, bmtr) (le:115854) (re:116675) (di:complement) BSUB0014 Z99117 g2635103 Bacillus subtilis 1423 -11529084 215944 bltr transcription regulator (fn:transcriptional regulator of blt) (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct2) (de:bacillus subtilis multidrug efflux transporter (blt) gene;transcription regulator (bltr) gene; transacetylase (bltd) gene.) (le:299) (re:1120) (di:compl... BACBLTRD L32599 g483940 Bacillus subtilis 1423 -11529084 170637 bltr bltd operon transcriptional regulator bltr (db:pir) I39791 I39791 Bacillus subtilis 1423 -11529084 5000688881 (de:(bltr) (pn:multidrug-efflux transporter 2 regulator) (gn:bmtr:bmr2r) (gtcfc:12.13) (ec:) (bltr_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) bltR bltR Bacillus subtilis 1423 10004561

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744691	1197	23353	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744693	1198	23354	687	228

Description

6500725227 yrdl:gltr transcriptional regulator:lysr family:transcriptional regulatory protein gltr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) gltR gltR Bacillus subtilis 1423 -11529085 7000694806 gltr transcription repressor of glutamate synthase operon gltr (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) C69635 C69635 Bacillus subtilis 1423 -11529085 1500692684 yrdl lysr family regulatory protein yrdl (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934654 Bacillus subtilis 1423 -11529085 7500965363 gltr transcriptional regulator lysr family (fn:negative regulation of the glutamate synthase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrdl) (le:125656) (re:126546) (di:direct) BSUB0014 Z99117 g2635112 Bacillus subtilis 1423 -11529085

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744835	1199	23355	507	168

Description

6500725228 yrdi:azld hypothetical protein:branched-chain amino acid transport (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) azlD azlD Bacillus subtilis 1423 -11529086 7500877630 azld (de:branched-chain amino acid transport protein azld) (db:swissprot) AZLD_BACSU O07923 BACILLUS SUBTILIS 1423 -11529086 7000692292 azld branched-chain amino acid transport protein azld (cl:branched-chain amino acid transport protein azld) (db:pir2.dat) H69592 H69592 Bacillus subtilis 1423 -11529086 500685416 azld (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (nt:product similar to haemophilus influenzae) (le:4552) (re:4884) (di:direct) BSCYPAZL Y11043 g1926282 Bacillus subtilis 1423 -11529086 7500877632 yrdi hypothetical protein yrdi (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934651 Bacillus subtilis 1423 -11529086 7500877633 azld (fn:branched-chain amino acid transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrdi) (le:128466) (re:128798) (di:complement) BSUB0014 Z99117 g2635115 Bacillus subtilis 1423 -11529086 1500689776 azld (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (nt:product similar to haemophilus influenzae) (le:4552) (re:4884) (di:direct) BSCYPAZL Y11043 g1926282 Bacillus subtilis 1423 -11529086

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744839	1200	23356	519	172

Description

6500725229 yrdh:azlc hypothetical protein:branched-chain amino acid transport (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) azlC azlC Bacillus subtilis 1423 -11529087 7500877626 azlc (de:branched-chain amino acid transport protein azlc) (db:swissprot) AZLC_BACSU O07942 BACILLUS SUBTILIS 1423 -11529087 7000692291 azlc branched-chain amino acid transport azlc (cl:hypothetical protein b2682) (db:pir2.dat) G69592 G69592 Bacillus subtilis 1423 -11529087 500685415 azlc (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (nt:product similar to haemophilus influenzae) (le:3791) (re:4555) (di:direct) BSCYPAZL Y11043 g1926281 Bacillus subtilis 1423 -11529087 7500877628 yrdh hypothetical protein yrdh (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934650 Bacillus subtilis 1423 -11529087 7500877629 azlc (fn:branched-chain amino acid transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrdh) (le:128795) (re:129559) (di:complement) BSUB0014 Z99117 g2635116 Bacillus subtilis 1423 -11529087 1500689775 azlc (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (nt:product similar to haemophilus influenzae) (le:3791) (re:4555) (di:direct) BSCYPAZL Y11043 g1926281 Bacillus subtilis 1423 -11529087

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744847	1201	23357	429	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744853	1202	23358	318	105

Description

6500725230 yrdg:azlb transcriptional regulator:lrp/asnc family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) azlB azlB Bacillus subtilis 1423 -11529088 7500877622 azlb (de:transcriptional regulator azlb) (db:swissprot) AZLB_BACSU O07920 BACILLUS SUBTILIS 1423 -11529088 7000694803 azlb transcription repressor of azlbcd operon azlb (db:pir2.dat) F69592 F69592 Bacillus subtilis 1423 -11529088 500685414 azlb transcriptional regulator (fn:transcriptional regulator of the lrp/asnc) (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (le:3305) (re:3778) (di:direct) BSCYPAZL Y11043 g1926280 Bacillus subtilis 1423 -11529088 7500877624 yrdg regulatory protein yrdg (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934649 Bacillus subtilis 1423 -11529088 7500877625 azlb transcriptional regulator lrp/asnc family (fn:negative regulation of the azlbcd operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrdg) (le:129572) (re:130045) (di:complement) BSUB0014 Z99117 g2635117 Bacillus subtilis 1423 -11529088 1500689774 azlb transcriptional regulator (fn:transcriptional regulator of the lrp/asnc) (db:genpept-bct1) (de:b.subtilis cypa, azlb, azlc and azld genes orf49 and orf91.) (le:3305) (re:3778) (di:direct) BSCYPAZL Y11043 g1926280 Bacillus subtilis 1423 -11529088

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744856	1203	23359	261	86

Description

5000688901 transcriptional regulator:nifa/ntrc family:transcriptional regulatory protein levr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) levR levR Bacillus subtilis 1423 -11529089 81972 levr (de:transcriptional regulatory protein levr) (db:swissprot) LEVR_BACSU P23914 BACILLUS SUBTILIS 1423 -11529089 7000685737 levr transcription activator of levanase operon levr (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) A39160 A39160 Bacillus subtilis 1423 -11529089 7500884968 levr (sr:b.subtilis (168 marburg) dna) (db:genpept-bct1) (de:bacillus subtilis levr gene, complete cds.) (le:49) (re:2865) (di:direct) BACLEVRA M60105 g143150 Bacillus subtilis 1423 -11529089 216287 levr transcriptional regulatory protein (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:2472) (re:5288) (di:direct) BS233DEG X92868 g2108261 Bacillus subtilis 1423 -11529089 1500685317 levr transcriptional regulator nifa/ntrc family (fn:positive regulation of the levanase operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:162843) (re:165659) (di:complement) BSUB0014 Z99117 g2635154 Bacillus subtilis 1423 -11529089 170314 levr levanase operon transcriptional activator levr (cl:rna polymerase sigma factor interaction domain homology) (db:pir) A39160 A39160 Bacillus subtilis 1423 -11529089 6500725231 transcriptional regulator:nifa/ntrc family:transcriptional regulatory protein levr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) levR levR Bacillus subtilis 1423 -11529089

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744861	1204	23360	894	298

Description

6500725232 transcription elongation factor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) greA greA Bacillus subtilis 1423 -11529090 7000694696 grea transcription elongation factor grea (cl:transcription elongation factor greb) (db:pir2.dat) A69637 A69637 Bacillus subtilis 1423 -11529090 7500965275 grea transcription elongation factor (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:191314) (re:191787) (di:complement) BSUB0014 Z99117 g2635178 Bacillus subtilis 1423 -11529090

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744878	1205	23361	651	217

Description

6500725233 ytnk:ribr transcriptional regulator:regulatory protein ribr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ribR ribR Bacillus subtilis 1423 -11529091 5500685834 ribr (de:regulatory protein ribr) (db:swissprot) RIBR_BACSU P94465 BACILLUS SUBTILIS 1423 -11529091 7000686330 ribr transcription regulator of riboflavin biosynthesis genes ribr (db:pir2.dat) G69692 G69692 Bacillus subtilis 1423 -11529091 219612 ribr ribr (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:this protein probably involved in riboflavin) (le:177447) (re:178139) (di:direct) AF008220 AF008220 g2293255 Bacillus subtilis 1423 -11529091 4000714247 ribr regulatory protein (fn:involved in riboflavin biosynthesis) (db:genpept-bct1) (de:b.subtilis sb25 ribr gene.) (le:182) (re:874) (di:direct) BSSB25 Y09721 g1707406 Bacillus subtilis 1423 -11529091 6000686086 ribr transcriptional regulator (fn:regulation of riboflavin biosynthesis genes) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ytnk) (le:204928) (re:205620) (di:complement) BSUB0015 Z99118 g2635395 Bacillus subtilis 1423 -11529091 7500889777 ribr transcriptional regulator (fn:regulation of riboflavin biosynthesis genes) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ytnk) (le:2288) (re:2980) (di:complement) BSUB0016 Z99119 g2635414 Bacillus subtilis 1423 -11529091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744892	1206	23362	630	210

Description

5000688883 grar:alsa:amyr:ccpa transcriptional regulator:lacl family:glucose-resistance amylase regulator:catabolite control protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ccpA ccpA Bacillus subtilis 1423 -11529092 63486 ccpa:grar:amyr:alsa (de:glucose-resistance amylase regulator (catabolite control protein)) (db:swissprot) CCPA_BACSU P25144 BACILLUS SUBTILIS 1423 -11529092 7000684775 ccpa transcription regulator for carbon catabolite control ccpa (cl:lac repressor) (db:pir2.dat) S15318 S15318 Bacillus subtilis 1423 -11529092 7500878373 ccpa laci-family transcription regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:133953) (re:134957) (di:direct) AF008220 AF008220 g2293221 Bacillus subtilis 1423 -11529092 215801 grar glucose-resistance amylase regulator (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis glucose-resistance amylase regulator (grar) gene,complete cds.) (le:330) (re:1334) (di:direct) BACGRAR M85182 g143024 Bacillus subtilis 1423 -11529092 4000706955 ccpa transcriptional regulator lacl family (fn:carbon catabolite control protein involved in) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: grar, alsa) (le:45470) (re:46474) (di:complement) BSUB0016 Z99119 g2635458 Bacillus subtilis 1423 -11529092 169898 ccpa carbon catabolite control transcriptional regulator ccpa (cl:lac repressor) (db:pir) S15318 S15318 Bacillus subtilis 1423 -11529092 6500725234 grar:alsa:amyr transcriptional regulator:lacl family:glucose-resistance amylase regulator:catabolite control protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) ccpA ccpA Bacillus subtilis 1423 -11529092

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744894	1207	23363	426	142

Description

6500725235 transcriptional regulator:laci family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) msmR msmR Bacillus subtilis 1423 -11529093 7000694795 msmr transcription regulator msmr (cl:lac repressor) (db:pir2.dat) A69661 A69661 Bacillus subtilis 1423 -11529093 4000714176 msmr laci-family transcription regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:81300) (re:82334) (di:complement) AF008220 AF008220 g2293309 Bacillus subtilis 1423 -11529093 7500965354 msmr transcriptional regulator laci family (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:98093) (re:99127) (di:direct) BSUB0016 Z99119 g2635510 Bacillus subtilis 1423 -11529093

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744898	1208	23364	942	313

Description

GTC ORF with score 213 to: (sr:yeast (s.cerevisiae; dby939) dna) (db:genpept-pln1) (de:yeast (s.cerevisiae) mod5 gene encoding trna isopentenyltransferase, complete cds.) (nt:trna isopentenyl transferase) (le:274:1213) (re:1209:1560) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744903	1209	23365	219	73

Description

5000688888 sacq:amyb:degq hypothetical protein:degradation enzyme regulation protein degq:sacq regulatory factor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) degQ degQ Bacillus subtilis 1423 -11529094 68233 degq:sacq:amyb (de:degradation enzyme regulation protein degq (sacq regulatory factor)) (db:swissprot) DEGQ_BACSU Q99039 BACILLUS SUBTILIS 1423 -11529094 7000685002 degq degradative enzyme production factor degq (db:pir2.dat) H69613 H69613 Bacillus subtilis 1423 -11529094 216667 (sr:b.subtilis (strain w168) dna, clone pnprs1; and (strain b629) (db:genpept-bct1) (de:b.subtilis sacq gene encoding a regulatory factor affectingproduction or excretion of a number of excreted proteins.) (nt:sacq regulatory factor) (le:471) (re:611) ... BACSACQB M12501 g143496 Bacillus subtilis 1423 -11529094 1500685196 degq (fn:hyperproduction of levansucrase and other) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: sacq) (le:59168) (re:59308) (di:complement) BSUB0017 Z99120 g2635667 Bacillus subtilis 1423 -11529094 7500880148 degq (fn:regulatory factor of degradation enzyme) (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufa to yufe.) (le:2220) (re:2360) (di:direct) BSZ93932 Z93932 g1934769 Bacillus subtilis 1423 -11529094 6500725236 sacq:amyb hypothetical protein:degradation enzyme regulation protein degq:sacq regulatory factor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) degQ degQ Bacillus subtilis 1423 -11529094

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501744909	1210	23366	693	230

Description

6500725237 yume:paib transcriptional regulator:protease synthase and sporulation negative regulatory protein pai 2 (gtcfc:10.2:12.13:12.15) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) paiB paiB Bacillus subtilis 1423 -11529095 7000694800 paib transcription repressor of sporulation and degradative enzymes paib (db:pir2.dat) F69671 F69671 Bacillus subtilis 1423 -11529095 7500965359 paib transcriptional regulator (fn:negative regulation of sporulation and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: yume) (le:106153) (re:106776) (di:complement) BSUB0017 Z99120 g2635711 Bacillus subtilis 1423 -11529095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745015	1211	23367	639	212

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745019	1212	23368	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745029	1213	23369	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745030	1214	23370	414	137

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745031	1215	23371	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745032	1216	23372	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745036	1217	23373	426	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745040	1218	23374	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745041	1219	23375	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745047	1220	23376	519	173

Description

6500725238 transcriptional regulator:protease synthase and sporulation negative regulatory protein pai 1 (gtcfc:10.2:12.13:12.15) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) paiA paiA Bacillus subtilis 1423 -11529096 7500965360 paia transcriptional regulator (fn:negative regulation of sporulation, septation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:106800) (re:107318) (di:complement) BSUB0017 Z99120 g2635712 Bacillus subtilis 1423 -11529096 7000694801 paia transcriptional repressor of sporulation:septation and degrad paia (db:pir) E69671 E69671 Bacillus subtilis 1423 -11529096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745058	1221	23377	750	250

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745175	1222	23378	360	119

Description

6500725239 arac:yvbs:arar transcriptional regulator:laci family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) araR araR Bacillus subtilis 1423 -11529097 7000694802 arar transcription repressor of arabinose operon arar (db:pir2.dat) D69588 D69588 Bacillus subtilis 1423 -11529097 7500965361 arar transcriptional regulator laci family (fn:negative regulation of the l-arabinose) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: arac, yvbs) (le:85117) (re:86271) (di:direct) BSUB0018 Z99121 g2635910 Bacillus subtilis 1423 -11529097

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745181	1223	23379	459	152

Description

6500725240 yvfj:lacr transcriptional regulator:laci family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) lacR lacR Bacillus subtilis 1423 -11529098 7000694804 lacr transcription repressor of beta-galactosidase gene lacr (cl:lac repressor) (db:pir2.dat) C69649 C69649 Bacillus subtilis 1423 -11529098 1500694056 lacr transcriptional regulator laci family (fn:negative regulation of the beta-galactosidase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvfj) (le:108172) (re:109164) (di:complement) BSUB0018 Z99121 g2635930 Bacillus subtilis 1423 -11529098 7500965362 yvfj hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable transcriptional regulator (laci family)) (le:72507) (re:73499) (di:direct) BSZ94043 Z94043 g1945710 Bacillus subtilis 1423 -11529098

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745189	1224	23380	243	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745205	1225	23381	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745209	1226	23382	855	284

Description

6500725241 yvej:slr transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) slr slr Bacillus subtilis 1423 -11529099 7000694701 slr transcription activator of competence development and sporula slr (db:pir2.dat) E69708 E69708 Bacillus subtilis 1423 -11529099 220021 slr putative transcriptional regulator (db:genpept-bct1) (de:bacillus subtilis putative orf1 unknown protein, putativetranscriptional regulator (slr), and intracellular esterase b(estb) genes, complete cds.) (nt:slr; positive regulator of competence development) (le:501) (re:959) (di:direct) BSU46134 U46134 g1762125 Bacillus subtilis 1423 -11529099 220251 slr transcriptional regulator (fn:positive regulation of competence development) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvej) (le:129611) (re:130069) (di:direct) BSUB0018 Z99121 g2635951 Bacillus subtilis 1423 -11529099 1500689778 yvej hypothetical protein (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (nt:similar to sinr of b.subtilis) (le:1677) (re:2135) (di:complement) BSYVEFGNS Z71928 g1495278 Bacillus subtilis 1423 -11529099 7500965277 yvej hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:probable transcriptional regulator (sinr family)) (le:51602) (re:52060) (di:complement) BSZ94043 Z94043 g1945689 Bacillus subtilis 1423 -11529099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745230	1227	23383	501	166

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745250	1228	23384	558	186

Description

GTC ORF with score 144 to: (db:genpept-bct2) (ec:3.1.1.24:4.1.1.44) (de:rhodococcus opacus succinyl coa:3-oxoadipate coa transferasesubunit homolog (pcai') gene, partial cds, protocatechuatedioxygenase beta subunit (pcah), protocatechuate dioxygenase ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745350	1229	23385	573	190

Description

6500725242 yvig:csra carbon storage regulator:carbon storage regulator homolog (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) csrA csrA Bacillus subtilis 1423 -11529100 66693 csra (de:carbon storage regulator homolog) (db:swissprot) CSRA_BACSU P33911 BACILLUS SUBTILIS 1423 -11529100 7000684929 csra carbon storage regulator csra (cl:glycogen biosynthesis inhibitor) (db:pir2.dat) H69608 H69608 Bacillus subtilis 1423 -11529100 220123 csra carbon storage regulator (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvig) (le:38016) (re:38240) (di:complement) BSUB0019 Z99122 g2636063 Bacillus subtilis 1423 -11529100 298106 csra (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762342 Bacillus subtilis 1423 -11529100 5000688886 (de:(csra) (pn:carbon storage regulator homolog) (gtcfc:12.13) (ec:) (csra_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) csrA csrA Bacillus subtilis 1423 10009311

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745351	1230	23386	255	84

Description

6500725243 transcriptional regulator:laci family:ribose operon repressor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) rbsR rbsR Bacillus subtilis 1423 -11529101 307934 rbsr (de:ribose operon repressor) (db:swissprot) RBSR_BACSU P36944 BACILLUS SUBTILIS 1423 -11529101 7000694808 rbsr transcription repressor of ribose operon (cl:lac repressor) (db:pir2.dat) E69690 E69690 Bacillus subtilis 1423 -11529101 7500889485 rbsr transcriptional regulator laci family (fn:negative regulation of the ribose operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:103378) (re:104358) (di:direct) BSUB0019 Z99122 g2636116 Bacillus subtilis 1423 -11529101 7502851581 rbsr repressor (db:genpept-bct1) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (nt:part of the ribose transport operon) (le:5660) (re:6640) (di:complement) BSZ92953 Z92953 g1894762 Bacillus subtilis 1423 -11529101 7500889483 rbsr (de:ribose operon repressor) (db:swissprot) RBSR_BACSU P36944 BACILLUS SUBTILIS 1423 -11529101

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745374	1231	23387	519	172

Description

5000688878 transcriptional regulator:lysr family:als operon regulatory protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) alsR alsR Bacillus subtilis 1423 -11529102 1500685064 alsr (de:als operon regulatory protein) (db:swissprot) ALSR_BACSU Q04778 BACILLUS SUBTILIS 1423 -11529102 7000684565 alsr alssd operon activator alsr:alpha-acetolactate operon transcriptional regulator alsr (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) A47126 A47126 Bacillus subtilis 1423 -11529102 7500876782 alsr als operom regulatory protein (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis als operon regulatory protein (alsr), ph6acetolactate synthase (alss) and acetolactate decarboxylase (alsd)genes, complete cds.) (nt:alsr is trancribed divergently from the alssd) (le:7... BACALSRD L04470 g142469 Bacillus subtilis 1423 -11529102 215156 alsr transcriptional regulator lysr family (fn:regulation of the alpha-acetolactate operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:113465) (re:114373) (di:direct) BSUB0019 Z99122 g2636127 Bacillus subtilis 1423 -11529102 7502851582 alsr transcriptional regulatory protein of the (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:10798) (re:11706) (di:complement) BSZ93767 Z93767 g1929339 Bacillus subtilis 1423 -11529102 59235 alsr (de:als operon regulatory protein) (db:swissprot) ALSR_BACSU Q04778 BACILLUS SUBTILIS 1423 -11529102 169857 alsr alssd operon activator alsr:alpha-acetolactate operon transcriptional regulator alsr (db:pir) A47126 A47126 Bacillus subtilis 1423 -11529102 6500725244 transcriptional regulator:lysr family:als operon regulatory protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) alsR alsR Bacillus subtilis 1423 -11529102

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745378	1232	23388	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745379	1233	23389	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745399	1234	23390	453	150

Description

6500725245 ywpi:glcr transcriptional regulator:deor family (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) glcR glcR Bacillus subtilis 1423 -11529103 7000694799 glcr transcription repressor glcr (db:pir2.dat) C69632 C69632 Bacillus subtilis 1423 -11529103 220411 glcr transcriptional regulator deor family (fn:negative regulation of the phosphotransferase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ywpi) (le:141173) (re:141949) (di:complement) BSUB0019 Z99122 g2636155 Bacillus subtilis 1423 -11529103 7500965358 ywpi (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:highly similar to phosphotransferase system) (le:7372) (re:8148) (di:direct) BSZ83337 Z83337 g1763710 Bacillus subtilis 1423 -11529103

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745494	1235	23391	264	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745511	1236	23392	240	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745516	1237	23393	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745520	1238	23394	909	303

Description

5000688905 ammonium transporter:probable ammonium transporter:membrane protein nrga (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) nrgA nrgA Bacillus subtilis 1423 -11529104 220390 nrga (de:probable ammonium transporter (membrane protein nrga)) (db:swissprot) NRGA_BACSU Q07429 BACILLUS SUBTILIS 1423 -11529104 7000685984 nrga ammonium transporter nrga (cl:ammonium transporter nrga) (db:pir2.dat) A36865 A36865 Bacillus subtilis 1423 -11529104 7500886593 nrga membrane-associated protein (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis operon membrane-associated protein (nrga), andpii-like protein (nrgb) genes, complete cds.) (nt:putative) (le:126) (re:1340) (di:direct) BACNRGABO L03216 g143264 Bacillus subtilis 1423 -11529104 216401 nrga ammonium transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:158754) (re:159968) (di:direct) BSUB0019 Z99122 g2636176 Bacillus subtilis 1423 -11529104 7502851583 nrga unknown (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mb1 genes.) (le:1335) (re:2549) (di:complement) BSZ82987 Z82987 g1684645 Bacillus subtilis 1423 -11529104 86512 nrga (de:probable ammonium transporter (membrane protein nrga)) (db:swissprot) NRGA_BACSU Q07429 BACILLUS SUBTILIS 1423 -11529104 170381 nrga ammonium transporter nrga (db:pir) A36865 A36865 Bacillus subtilis 1423 -11529104 6500725246 ammonium transporter:probable ammonium transporter:membrane protein nrga (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) nrgA nrgA Bacillus subtilis 1423 -11529104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745531	1239	23395	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745532	1240	23396	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745538	1241	23397	684	228

Description

6500725247 ywnd:mta transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) mta mta Bacillus subtilis 1423 -11529105 7000694702 mta transcription activator of multidrug-efflux transporter genes mta (cl:tipa protein) (db:pir2.dat) C69661 C69661 Bacillus subtilis 1423 -11529105 220223 mta transcriptional regulator (fn:positive regulation of multidrug-efflux) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ywnd) (le:166097) (re:166870) (di:complement) BSUB0019 Z99122 g2636185 Bacillus subtilis 1423 -11529105 7500955858 ywnd unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (nt:product similar to streptomyces lividans) (le:4361) (re:5134) (di:direct) BSUEROP Y08559 g1592700 Bacillus subtilis 1423 -11529105

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745540	1242	23398	870	289

Description

5000688570 transcriptional terminator rho:transcription termination factor rho (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) rho rho Bacillus subtilis 1423 -11529106 304118 rho (de:transcription termination factor rho) (db:swissprot) RHO_BACSU Q03222 BACILLUS SUBTILIS 1423 -11529106 7000686321 rho transcription terminator factor rho (cl:transcription termination factor rho) (db:pir2.dat) A47051 A47051 Bacillus subtilis 1423 -11529106 6500725248 rho transcriptional terminator rho (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:17095) (re:18378) (di:direct) BSDNA320D Z49782 g853769 Bacillus subtilis 1423 -11529106 7500889756 rho transcriptional terminator rho (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:205365) (re:206648) (di:complement) BSUB0019 Z99122 g2636233 Bacillus subtilis 1423 -11529106 6000685088 rho transcriptional terminator rho (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:4055) (re:5338) (di:complement) BSUB0020 Z99123 g2636245 Bacillus subtilis 1423 -11529106 94304 rho (de:transcription termination factor rho) (db:swissprot) RHO_BACSU Q03222 BACILLUS SUBTILIS 1423 -11529106 154393 rho transcription terminator factor rho (cl:transcription termination factor rho) (db:pir) A47051 A47051 Bacillus subtilis 1423 -11529106 219146 rho transcriptional terminator rho (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:4055) (re:5338) (di:complement) BSUB0020 Z99123 g2636245 Bacillus subtilis 1423 -11529106

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745541	1243	23399	420	139

Description

5000688892 transcriptional regulator:fnr/crp family:anaerobic regulatory protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) fnr fnr Bacillus subtilis 1423 -11529107 219413 fnr (de:anaerobic regulatory protein) (db:swissprot) FNR_BACSU P46908 BACILLUS SUBTILIS 1423 -11529107 7000685311 fnr transcription regulator of anaerobic genes fnr (db:pir2.dat) S60081 S60081 Bacillus subtilis 1423 -11529107 6500725249 fnr anaerobic regulatory protein (db:genpept-bct1) (de:b.subtilis nar(g,h,i,j,k), ywi(c,d,e) and args genes.) (le:1772) (re:2488) (di:direct) BSNARYWI Z49884 g971338 Bacillus subtilis 1423 -11529107 7500881690 fnr transcriptional regulator fnr/crp family (fn:regulation of anaerobic genes (nark, narghji)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:32165) (re:32881) (di:complement) BSUB0020 Z99123 g2636268 Bacillus subtilis 1423 -11529107 72212 fnr (de:anaerobic regulatory protein) (db:swissprot) FNR_BACSU P46908 BACILLUS SUBTILIS 1423 -11529107 169861 fnr anaerobic genes transcriptional regulator fnr (db:pir) S60081 S60081 Bacillus subtilis 1423 -11529107

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745551	1244	23400	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745554	1245	23401	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745559	1246	23402	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745560	1247	23403	1179	392

Description

6500725250 ywhi:phrf regulator of the activity of phosphatase rapf (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) phrF phrF Bacillus subtilis 1423 -11529108 7000694395 phrf phosphatase rapf regulator phrf (cl:phosphatase regulator) (db:pir2.dat) C69677 C69677 Bacillus subtilis 1423 -11529108 7500955860 phrf unknown:similar to phra phosphate regulator (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:8812) (re:8931) (di:complement) BSTHRZ Z80360 g1565244 Bacillus subtilis 1423 -11529108 219709 phrf regulator of the activity of phosphatase rapf (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ywhi) (le:47783) (re:47902) (di:direct) BSUB0020 Z99123 g2636283 Bacillus subtilis 1423 -11529108

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745572	1248	23404	495	165

Description

6500725251 ipa-47d:sact transcriptional antiterminator:sacpa operon antiterminator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sacT sacT Bacillus subtilis 1423 -11529109 7500891279 sact:ipa-47d (de:sacpa operon antiterminator) (db:swissprot) SACT_BACSU P26212 BACILLUS SUBTILIS 1423 -11529109 7000686548 sact transcription antiterminator of saca/sacp sact (cl:bacillus subtilis transcription antiterminator lict) (db:pir2.dat) S39702 S39702 Bacillus subtilis 1423 -11529109 5000688915 ipa-47d::sact (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:50594) (re:51424) (di:direct) BSGENR X73124 g580872 Bacillus subtilis 1423 -11529109 219284 sact transcriptional antiterminator (fn:positive regulation of saca and sacp) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-47d) (le:106538) (re:107368) (di:complement) BSUB0020 Z99123 g2636342 Bacillus subtilis 1423 -11529109 97842 sact:ipa-47d (de:sacpa operon antiterminator) (db:swissprot) SACT_BACSU P26212 BACILLUS SUBTILIS 1423 -11529109 170449 sact saca/sacp transcriptional antiterminator sact (db:pir) S39702 S39702 Bacillus subtilis 1423 -11529109

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745573	1249	23405	459	152

Description

6500725252 ipa-14r:sacs:sacx negative regulatory protein of sacy (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sacX sacX Bacillus subtilis 1423 -11529110 216672 sacx:sacs:ipa-14r (de:negative regulatory protein of sacy) (db:swissprot) SACX_BACSU P15400 BACILLUS SUBTILIS 1423 -11529110 7000686549 sacx levansucrase synthesis regulatory protein sacx:phosphotransferase system sucrose-specific permease homolog (cl:phosphotransferase system sucrose-specific enzyme ii, factor ii) (db:pir2.dat) JU0293 JU0293 Bacillus subtilis 1423 -11529110 7500891280 sacx regulatory protein (sr:bacillus subtilis (strain qb1072) (clone: psl(42,43)) dna) (db:genpept-bct1) (de:b.subtilis positive levansucrase and sucrase synthesis regulatoryprotein (sacy) and negative regulatory protein of sacy (sacx)genes, complete cds.) (nt:start codon, pu... BACSACXY M29333 g143504 Bacillus subtilis 1423 -11529110 5000688916 ipa-14r::sacx (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:13952) (re:15331) (di:complement) BSGENR X73124 g580867 Bacillus subtilis 1423 -11529110 219251 sacx negative regulatory protein of sacy (fn:sucrase regulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-14r, sacs) (le:142628) (re:144007) (di:direct) BSUB0020 Z99123 g2636376 Bacillus subtilis 1423 -11529110 97843 sacx:sacs:ipa-14r (de:negative regulatory protein of sacy) (db:swissprot) SACX_BACSU P15400 BACILLUS SUBTILIS 1423 -11529110 138893 sacx levansucrase synthesis regulatory protein sacx:phosphotransferase system sucrose-specific permease homolog (cl:phosphotransferase system sucrose-specific enzyme ii, factor ii) (db:pir) JU0293 JU0293 Bacillus subtilis 1423 -11529110

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745704	1250	23406	897	299

Description

6500725253 ipa-13r:sacs:sacy transcriptional antiterminator:levansucrase and sucrase synthesis operon antiterminator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) sacY sacY Bacillus subtilis 1423 -11529111 219250 sacy:sacs:ipa-13r (de:levansucrase and sucrase synthesis operon antiterminator) (db:swissprot) SACY_BACSU P15401 BACILLUS SUBTILIS 1423 -11529111 7000686550 sacy levansucrase gene transcription antiterminator sacy (cl:bacillus subtilis transcription antiterminator lict) (db:pir2.dat) JU0294 JU0294 Bacillus subtilis 1423 -11529111 7500891281 sacy regulatory protein (sr:bacillus subtilis (strain qb1072) (clone: psl(42,43)) dna) (db:genpept-bct1) (de:b.subtilis positive levansucrase and sucrase synthesis regulatoryprotein (sacy) and negative regulatory protein of sacy (sacx)genes, complete cds.) (le:1557) (re:2399)... BACSACXY M29333 g143505 Bacillus subtilis 1423 -11529111 216673 ipa-13r::sacy (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:13056) (re:13898) (di:complement) BSGENR X73124 g413937 Bacillus subtilis 1423 -11529111 5000688917 sacy sacy gene product (db:genpept-bct1) (de:bacillus subtilis tyrs1 gene for tyrosine trna synthetase, sacx andsacy genes, and three orfs.) (le:393) (re:1235) (di:direct) BSTYRS1G X52480 g40238 Bacillus subtilis 1423 -11529111 219752 sacy transcriptional antiterminator (fn:positive regulation of levansucrase and sucrase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-13r, sacs) (le:144061) (re:144903) (di:direct) BSUB0020 Z99123 g2636377 Bacillus subtilis 1423 -11529111 97844 sacy:sacs:ipa-13r (de:levansucrase and sucrase synthesis operon antiterminator) (db:swissprot) SACY_BACSU P15401 BACILLUS SUBTILIS 1423 -11529111 170317 sacy levansucrase gene transcription antiterminator sacy (db:pir) JU0294 JU0294 Bacillus subtilis 1423 -11529111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745706	1251	23407	510	169

Description

5000688884 celr:licr transcriptional regulator:antiterminator:putative cel operon regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) licR licR Bacillus subtilis 1423 -11529112 7500878523 celr:licr (de:putative cel operon regulator) (db:swissprot) CELR_BACSU P46321 BACILLUS SUBTILIS 1423 -11529112 7000684792 licr lichenan operon transcription antiterminator licr:cel operon regulator (db:pir2.dat) H69651 H69651 Bacillus subtilis 1423 -11529112 6500725254 celr putative cel operon regulator (db:genpept-bct1) (de:b.subtilis cela, celb, celc, celd and ywaa genes.) (le:187) (re:2112) (di:direct) BSCELABCD Z49992 g895747 Bacillus subtilis 1423 -11529112 219048 licr transcriptional regulator antiterminator (fn:regulation of the lichenan operon (licbcah)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: celr) (le:162396) (re:164321) (di:complement) BSUB0020 Z99123 g2636395 Bacillus subtilis 1423 -11529112 301558 celr cel operon regulator (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:60144) (re:62069) (di:direct) D83026 D83026 g1783265 Bacillus subtilis 1423 -11529112 63815 celr:licr (de:putative cel operon regulator) (db:swissprot) CELR_BACSU P46321 BACILLUS SUBTILIS 1423 -11529112 170450 licr lichenan operon transcription antiterminator licr:cel operon regulator (db:pir) H69651 H69651 Bacillus subtilis 1423 -11529112 222891 celr cel operon regulator (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:60144) (re:62069) (di:direct) D83026 D83026 g1783265 Bacillus subtilis 1423 -11529112

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745727	1252	23408	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745730	1253	23409	570	189

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745736	1254	23410	543	180

Description

6500725255 n15a:lict transcriptional antiterminator:bglg family:transcription antiterminator lict (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) licT licT Bacillus subtilis 1423 -11529113 222845 lict transcriptional antiterminator bglg family (fn:required for substrate-dependent induction and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:12375) (re:13208) (di:complement) BSUB0021 Z99124 g2636454 Bacillus subtilis 1423 -11529113 301512 lict lict antiterminator (fn:regulation of the lics gene) (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (le:10377) (re:11210) (di:direct) D83026 D83026 g665992 Bacillus subtilis 1423 -11529113 7000694709 lict transcriptional antiterminator required for substrate-dependen lict (db:pir) A69652 A69652 Bacillus subtilis 1423 -11529113

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745737	1255	23411	270	90

Description

6500725256 hutp1:hutp transcriptional regulator:hut operon positive regulatory protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) hutP hutP Bacillus subtilis 1423 -11529114 78096 hutp (de:hut operon positive regulatory protein) (db:swissprot) HUTP_BACSU P10943 BACILLUS SUBTILIS 1423 -11529114 131475 hutp regulatory protein hutp:histidine utilization operon transcriptional activator hutp (cl:regulatory protein hutp) (db:pir1.dat) RGBSHP S18809 Bacillus subtilis 1423 -11529114 215858 (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis huth and hutp genes, encoding histidase and a positiveregulatory protein, complete cds.) (nt:hut operon positive regulatory protein) (le:1121) (re:1576) (di:direct) BACHUT M20659 g143075 Bacillus subtilis 1423 -11529114 215865 hutp hutp protein:a positive regulator of the hut (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:7388) (re:7843) (di:complement) BACHUTWAPA D31856 g603771 Bacillus subtilis 1423 -11529114 7500883635 hutp transcriptional regulator (fn:positive regulation of the histidine) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: hutp1) (le:40992) (re:41447) (di:direct) BSUB0021 Z99124 g2636480 Bacillus subtilis 1423 -11529114 5000688899 (de:(hutp) (pn:hut operon positive regulatory protein) (gtcfc:12.13) (ec:) (hutp_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) hutP hutP Bacillus subtilis 1423 10020435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745739	1256	23412	624	208

Description

6500725257 yxxc:deor transcriptional regulator:deoxyribonucleoside regulator (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) deoR deoR Bacillus subtilis 1423 -11529115 7500880180 deor (de:deoxyribonucleoside regulator) (db:swissprot) DEOR_BACSU P39140 BACILLUS SUBTILIS 1423 -11529115 7000685012 deor transcription repressor of dra/nupc/pdp operon deor:dna binding protein deor (db:pir2.dat) S49454 S49454 Bacillus subtilis 1423 -11529115 5000689073 dna binding protein (db:genpept-bct1) (de:b.subtilis operon contg. dra, nupc and pdp genes.) (le:424) (re:1365) (di:direct) BSDNPOP X82174 g558556 Bacillus subtilis 1423 -11529115 219173 deor transcriptional regulator (fn:negative regulation of the dra-nupc-pdp operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxxc) (le:51890) (re:52831) (di:complement) BSUB0021 Z99124 g2636489 Bacillus subtilis 1423 -11529115 222537 deor hypothetical dna-binding protein (sr:bacillus subtilis (strain:bgsc 1a1 (marburg 168; trpc2)) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.) (nt:homologous to sorbitol operon regulator of) (le:18645) (re:19586) (d... D45912 D45912 g1408505 Bacillus subtilis 1423 -11529115 7502851584 dna binding protein (db:genpept) (de:b.subtilis operon contg. dra, nupc and pdp genes.) (le:424) (re:1365) (di:direct) BSDNPOP X82174 g558556 Bacillus subtilis 1423 -11529115 68268 deor (de:deoxyribonucleoside regulator) (db:swissprot) DEOR_BACSU P39140 BACILLUS SUBTILIS 1423 -11529115 169966 deor dra/nupc/pdp operon transcriptional repressor deor:dna binding protein deor (db:pir) S49454 S49454 Bacillus subtilis 1423 -11529115

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745742	1257	23413	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745752	1258	23414	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745753	1259	23415	768	255

Description

6500725258 ss92fr:iolr transcriptional regulator:deor family:dna-binding protein iolr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) iolR iolR Bacillus subtilis 1423 -11529116 79608 iolr:ss92fr (de:dna-binding protein iolr) (db:swissprot) IOLR_BACSU P46337 BACILLUS SUBTILIS 1423 -11529116 7000685639 iolr transcription repressor of myo-inositol catabolism operon iolr (db:pir2.dat) C69646 C69646 Bacillus subtilis 1423 -11529116 215757 iolr inositol operon repressor (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:prosite; ps00894; hth_deor_family; see swiss_prot) (le:33525) (re:34280) (di:complement) AB005554 AB005554 g904206 Bacillus subtilis 1423 -11529116 7500884196 iolr transcriptional regulator deor family (fn:negative regulation of the myo-inositol) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:84312) (re:85067) (di:direct) BSUB0021 Z99124 g2636523 Bacillus subtilis 1423 -11529116 5000688900 (de:(iolr) (pn:dna-binding protein iolr) (gn:ss92fr) (gtcfc:12.13) (ec:) (iolr_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) iolR iolR Bacillus subtilis 1423 10021923

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745765	1260	23416	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745780	1261	23417	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745787	1262	23418	462	153

Description

5000688896 transcriptional regulator:gntr family:gluconate operon transcriptional repressor:p28 protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) gntR gntR Bacillus subtilis 1423 -11529117 74255 gntr (de:gluconate operon transcriptional repressor (p28 protein)) (db:swissprot) GNTR_BACSU P10585 BACILLUS SUBTILIS 1423 -11529117 7000685437 gntr transcription repressor of gluconate operon gntr:gnt operon regulatory protein (db:pir2.dat) C26190 C26190 Bacillus subtilis 1423 -11529117 7500882620 gntr gluconate operon repressor (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:prosite; ps00043; hth_gntr_family; see swiss_prot) (le:4516) (re:5247) (di:complement) AB005554 AB005554 g563933 Bacillus subtilis 1423 -11529117 215717 gnt repressor (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:b.subtilis (gluconate operon) gntr, gntk and gntp genes encodinggnt repressor, gluconate kinase and permease, and gntz gene.) (le:236) (re:967) (di:direct) BACGNT J02584 g143014 Bacillus subtilis 1423 -11529117 215729 gntr transcriptional regulator gntr family (fn:negative regulation of the gluconate operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:113345) (re:114076) (di:direct) BSUB0021 Z99124 g2636552 Bacillus subtilis 1423 -11529117 170644 gntr gluconate operon transcriptional repressor gntr:gnt operon regulatory protein (db:pir) C26190 C26190 Bacillus subtilis 1423 -11529117 6500725259 transcriptional regulator:gntr family:gluconate operon transcriptional repressor:p28 protein (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) gntR gntR Bacillus subtilis 1423 -11529117

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745788	1263	23419	231	76

Description

6500725260 transcriptional regulator:ntrc/nifa family:arginine utilization regulatory protein rocr (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis) rocR rocR Bacillus subtilis 1423 -11529118 7000694700 rocr transcription activator of arginine utilization operons rocr (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) C69694 C69694 Bacillus subtilis 1423 -11529118 215787 rocr positive regulatory protein (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:27291) (re:28676) (di:direct) BACGNTZA D78193 g1064808 Bacillus subtilis 1423 -11529118 302083 rocr transcriptional regulator ntrc/nifa family (fn:positive regulation of arginine utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:145675) (re:147060) (di:direct) BSUB0021 Z99124 g2636582 Bacillus subtilis 1423 -11529118

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745789	1264	23420	462	153

Description

6500725261 spo0h:sigh rna polymerase sigma-30 factor:sigma-h:rna polymerase sigma-h factor:sigma-30 (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigH sigH Bacillus subtilis 1423 -11529119 96355 sigh:spo0h (de:rna polymerase sigma-h factor (sigma-30)) (db:swissprot) RPSH_BACSU P17869 BACILLUS SUBTILIS 1423 -11529119 7000686471 sigh:spo0h transcription initiation sigma factor sigh:rna polymerase sigma h factor:sigma-30:stage 0 sporulation protein spo0h:vegetative and early stationary-phase sigma factor sigh (cl:transcription initiation factor sigma h) (db:pir2.dat) A28625 A28625 Bacillus subtilis 1423 -11529119 7500890694 (sr:b.subtilis dna) (db:genpept-bct1) (de:b.subtilis rna polymerase sigma-30 factor (spooh) gene, completecds.) (nt:rna polymerase sigma-30 factor) (le:216) (re:872) (di:direct) BACSIGHA M29693 g143544 Bacillus subtilis 1423 -11529119 216746 sigh rna polymerase sigma-30 factor sigma-h (fn:expression of vegetative and early) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: spo0h) (le:116597) (re:117253) (di:direct) BSUB0001 Z99104 g2632365 Bacillus subtilis 1423 -11529119 153817 sigh:spo0h transcription initiation sigma factor sigh:rna polymerase sigma h factor:sigma-30:stage 0 sporulation protein spo0h:vegetative and early stationary-phase sigma factor sigh (cl:transcription initiation factor sigma h) (db:pir) A28625 A28625 Bacillus subtilis 1423 -11529119 5000688873 (de:(sigh) (pn:rna polymerase sigma-h factor:rna polymerase sigma-h factor:sigma-30) (gn:spo0h) (gtcfc:12.13) (ec:) (rpsh_bacsu) (keggfc:11.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis)) sigH sigH Bacillus subtilis 1423 10038298

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745902	1265	23421	660	219

Description

6500725262 ybbl:sigw rna polymerase ecf-type sigma factor:sigma-w (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigW sigW Bacillus subtilis 1423 -11529120 7000694557 sigw rna polymerase ecf-type sigma factor sigw (cl:transcription initiation factor sigma e) (db:pir2.dat) H69706 H69706 Bacillus subtilis 1423 -11529120 215710 ybbl (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (nt:putative ecf sigma factor sigw) (le:13496) (re:14059) (d... AB002150 AB002150 g1256141 Bacillus subtilis 1423 -11529120 3500684458 sigw rna polymerase ecf-type sigma factor sigma-w (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybbl) (le:194838) (re:195401) (di:direct) BSUB0001 Z99104 g2632440 Bacillus subtilis 1423 -11529120 6000686399 sigw rna polymerase ecf-type sigma factor sigma-w (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ybbl) (le:188) (re:751) (di:direct) BSUB0002 Z99105 g2632458 Bacillus subtilis 1423 -11529120

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745908	1266	23422	741	246

Description

5000688864 anti-anti-sigma factor:antagonist of rsbw:anti-sigma b factor antagonist (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) rsbV rsbV Bacillus subtilis 1423 -11529121 97453 rsbv (de:anti-sigma b factor antagonist) (db:swissprot) RSBV_BACSU P17903 BACILLUS SUBTILIS 1423 -11529121 7000686522 rsbv positive regulator of sigma-b activity anti-anti-sigma factor rsbv (cl:sporulation protein stage ii) (db:pir2.dat) A36131 A36131 Bacillus subtilis 1423 -11529121 7500891139 rsbv anti-sigma b factor rsbw antagonist (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar product in synechocystis.) (le:55151) (re:55480) (di:direct) AB001488 AB001488 g1881281 Bacillus subtilis 1423 -11529121 216641 (sr:b.subtilis (strains 168 and marburg), clone) (db:genpept-bct1) (de:b.subtilis minor sigma-37 factor of rna polymerase (rpof, sigb),complete cds.) (nt:orf v) (le:200) (re:529) (di:direct) BACRPOF M34995 g143458 Bacillus subtilis 1423 -11529121 302726 rsbv anti-anti-sigma factor antagonist of rsbw (fn:positive regulation of sigma-b-dependent gene) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:118895) (re:119224) (di:direct) BSUB0003 Z99106 g2632771 Bacillus subtilis 1423 -11529121 170254 rsbv positive regulator of sigma-b activity anti-anti-sigma factor rsbv (cl:sporulation protein stage ii) (db:pir) A36131 A36131 Bacillus subtilis 1423 -11529121 6500725263 anti-anti-sigma factor:antagonist of rsbw:anti-sigma b factor antagonist (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) rsbV rsbV Bacillus subtilis 1423 -11529121

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745921	1267	23423	396	131

Description

5000688865 switch protein/serine kinase and anti-sigma factor:inhibitory sigma-b binding protein:anti-sigma b factor:sigma-b negative effector rsbw (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) rsbW rsbW Bacillus subtilis 1423 -11529122 97454 rsbw (de:anti-sigma b factor (sigma-b negative effector rsbw)) (db:swissprot) RSBW_BACSU P17904 BACILLUS SUBTILIS 1423 -11529122 7000686523 rsbw sigma-b activity negative regulator rsbw:anti-sigma factor rsbw:switch protein / serine kinase rsbw (db:pir2.dat) B36131 B36131 Bacillus subtilis 1423 -11529122 7500891140 rsbw anti-sigma b factor sigma-b negative effector (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:55477) (re:55959) (di:direct) AB001488 AB001488 g1881282 Bacillus subtilis 1423 -11529122 216642 (sr:b.subtilis (strains 168 and marburg), clone) (db:genpept-bct1) (de:b.subtilis minor sigma-37 factor of rna polymerase (rpof, sigb),complete cds.) (nt:orf w) (le:526) (re:1008) (di:direct) BACRPOF M34995 g143459 Bacillus subtilis 1423 -11529122 302727 rsbw switch protein/serine kinase and anti-sigma (fn:negative regulation of sigma-b-dependent gene) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:119221) (re:119703) (di:direct) BSUB0003 Z99106 g2632772 Bacillus subtilis 1423 -11529122 170255 rsbw sigma-b activity negative regulator rsbw:anti-sigma factor rsbw:switch protein / serine kinase rsbw (db:pir) B36131 B36131 Bacillus subtilis 1423 -11529122 6500725264 switch protein/serine kinase and anti-sigma factor:inhibitory sigma-b binding protein:anti-sigma b factor:sigma-b negative effector rsbw (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) rsbW rsbW Bacillus subtilis 1423 -11529122

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745939	1268	23424	855	285

Description

6500725265 rpof:sigb rna polymerase sigma-37 factor:sigma-b:rna polymerase sigma-b factor:sigma-37 (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigB sigB Bacillus subtilis 1423 -11529123 7000694560 sigb:rpof transcription initiation factor sigma b:37k minor sigma factor rpof:rna polymerase chain sigma-37:rna polymerase general stress sigma factor sigb (cl:transcription sigma factor g:transcription initiation factor sigma katf homology) (db:pir1.dat) A25944 A27762 Bacillus subtilis 1423 -11529123 216643 sigb rna polymerase sigma-b factor sigma-37 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:55919) (re:56713) (di:direct) AB001488 AB001488 g1881283 Bacillus subtilis 1423 -11529123 216645 (sr:b.subtilis (strains 168 and marburg), clone) (db:genpept-bct1) (de:b.subtilis minor sigma-37 factor of rna polymerase (rpof, sigb),complete cds.) (nt:37 kd minor sigma factor (rpof, sigb; ttg start) (le:968) (re:1762) (di:direct) BACRPOF M34995 g143460 Bacillus subtilis 1423 -11529123 302728 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis rpof gene encoding minor sigma-37 factor of rnapolymerase, complete cds.) (nt:37 kd minor sigma factor (ttg start codon)) (le:601) (re:1395) (di:direct) BACRPOG M14508 g143463 Bacillus subtilis 1423 -11529123 7500954155 sigb rna polymerase sigma-37 factor sigma-b (fn:general stress sigma factor (class ii genes)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: rpof) (le:119663) (re:120457) (di:direct) BSUB0003 Z99106 g2632773 Bacillus subtilis 1423 -11529123

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745956	1269	23425	705	235

Description

6500725266 pcf:ykxe:xpf rna polymerase pbsx sigma factor-like:positive control factor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) xpf xpf Bacillus subtilis 1423 -11529124 7500887721 xpf:pcf (de:positive control factor) (db:swissprot) PCF_BACSU P39784 BACILLUS SUBTILIS 1423 -11529124 7000686102 xpf positive control factor xre region xpf:hypothetical protein 7:rna polymerase pbsx sigma factor-like xpf (db:pir2.dat) I40413 I40413 Bacillus subtilis 1423 -11529124 5000689136 (fn:positive control factor) (db:genpept-bct1) (de:b.subtilis (so113) genomic dna (5425bp).) (nt:orf7; homology to regions 4.1 and 4.2 of sigma) (le:3600) (re:4109) (di:direct) BSGENDNA Z34287 g498816 Bacillus subtilis 1423 -11529124 219234 xpf sigma factor-like positive control protein (fn:required for expression of the pbsx late) (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqaq of the skin element) (le:3599) (re:4108) (di:direct) BSPBSXSE Z70177 g1225941 Bacillus subtilis 1423 -11529124 219483 xpf rna polymerase pbsx sigma factor-like (fn:required for expression of the pbsx late) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: pcf, ykxe) (le:129548) (re:130057) (di:direct) BSUB0007 Z99110 g2633610 Bacillus subtilis 1423 -11529124 88799 xpf:pcf (de:positive control factor) (db:swissprot) PCF_BACSU P39784 BACILLUS SUBTILIS 1423 -11529124 170444 xpf positive control factor xre region xpf:hypothetical protein 7:rna polymerase pbsx sigma factor-like xpf (db:pir) I40413 I40413 Bacillus subtilis 1423 -11529124

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745963	1270	23426	762	254

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745966	1271	23427	660	219

Description

GTC ORF with score 317 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745983	1272	23428	315	104

Description

6500725267 spoiigb:sige rna polymerase sporulation-specific sigma-29 factor:sigma-e:rna polymerase sigma-e factor precursor:sigma-29:p31:stage ii sporulation protein gb (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigE sigE Bacillus subtilis 1423 -11529125 216870 spoiig sporulation protein (sr:b.subtilis dna) (db:genpept-bct1) (de:b.subtilis sporulation protein gene, complete cds.) (le:352) (re:1071) (di:direct) BACSPOII M57606 g143621 Bacillus subtilis 1423 -11529125 7500954158 sige rna polymerase sporulation-specific sigma-29 (fn:early mother cell-specific gene expression) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: spoiigb) (le:5746) (re:6465) (di:direct) BSUB0009 Z99112 g2633905 Bacillus subtilis 1423 -11529125 7000694564 sige rna polymerase sporulation mother cell-specific early sigma sige (cl:transcription initiation factor sigma k) (db:pir) B69706 B69706 Bacillus subtilis 1423 -11529125

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501745989	1273	23429	972	324

Description

6500725268 spoiiig:sigg rna polymerase sporulation-specific sigma factor:sigma-g:rna polymerase sigma-g factor:stage iii sporulation protein g (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigG sigG Bacillus subtilis 1423 -11529126 216587 sigg:spoiiig (de:rna polymerase sigma-g factor (stage iii sporulation protein g)) (db:swissprot) RPSG_BACSU P19940 BACILLUS SUBTILIS 1423 -11529126 139172 sigg:spoiiig transcription initiation sigma factor sigg:rna polymerase sporulation forespore-specific late sigma factor sigg (cl:transcription sigma factor g:transcription initiation factor sigma katf homology) (db:pir2.dat) A30202 A30171 Bacillus subtilis 1423 -11529126 7500890693 (sr:b.subtilis (strain 168tt) is60sigma12spoiig-5 cell line dna, clone) (db:genpept-bct1) (de:b.subtilis sporulation-specific sigma factor (spoiig) gene, 3' end,sporulation-specific sigma factor homolog (orf3), complete cds, andorf4, 5' end.) (nt:sporu... BACRHO J04077 g143430 Bacillus subtilis 1423 -11529126 5000688872 spoiiig sigma-g factor (db:genpept-bct1) (de:b. subtilis spoiiig gene for sigma-g factor.) (le:143) (re:925) (di:direct) BCSPOIII X57547 g580764 Bacillus subtilis 1423 -11529126 217960 sigg rna polymerase sporulation-specific sigma factor (fn:late forespore-specific gene expression) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: spoiiig) (le:6605) (re:7387) (di:direct) BSUB0009 Z99112 g2633906 Bacillus subtilis 1423 -11529126 96352 sigg:spoiiig (de:rna polymerase sigma-g factor (stage iii sporulation protein g)) (db:swissprot) RPSG_BACSU P19940 BACILLUS SUBTILIS 1423 -11529126 7000686470 sigg:spoiiig transcription initiation sigma factor sigg:rna polymerase sporulation forespore-specific late sigma factor sigg (cl:transcription sigma factor g:transcription initiation factor sigma katf homology) (db:pir) A30202 A30202 Bacillus subtilis 1423 -11529126

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746079	1274	23430	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746080	1275	23431	813	270

Description

6500725269 flab:sigd rna polymerase sigma-28 factor:sigma-d:rna polymerase sigma-d factor:sigma-28 (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigD sigD Bacillus subtilis 1423 -11529127 96320 sigd:flab (de:rna polymerase sigma-d factor (sigma-28)) (db:swissprot) RPSD_BACSU P10726 BACILLUS SUBTILIS 1423 -11529127 7000686466 sigd transcription initiation factor sigmad:rna polymerase sigma factor sigd:flagella/motility/chemotaxis/autolysis-specific (cl:transcription initiation factor sigmad:transcription initiation factor sigma katf homology) (db:pir2.dat) C55216 C55216 Bacillus subtilis 1423 -11529127 7500890680 sigd sigma factor 28 (sr:b.subtilis (strain w168) dna, clones pjh(1-1,6-2)) (db:genpept-bct1) (de:b.subtilis distal fla/che region; complete orfa, orfb and sigma-28factor (sigd) gene; orfc, 5' end.) (le:1176) (re:1940) (di:direct) BACSIGD M20144 g289304 Bacillus subtilis 1423 -11529127 216744 sigd rna polymerase sigma-28 factor sigma-d (fn:regulon includes genes involved in flagellar) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: flab) (le:117465) (re:118229) (di:direct) BSUB0009 Z99112 g2634019 Bacillus subtilis 1423 -11529127 170636 sigd transcription initiation factor sigmad:rna polymerase sigma factor sigd:flagella/motility/chemotaxis/autolysis-specific (cl:transcription initiation factor sigma katf homology) (db:pir) C55216 C55216 Bacillus subtilis 1423 -11529127 5000688869 (de:(sigd) (pn:rna polymerase sigma-d factor:rna polymerase sigma-d factor:sigma-28) (gn:flab) (gtcfc:12.13) (ec:) (rpsd_bacsu) (keggfc:11.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis)) sigD sigD Bacillus subtilis 1423 10038263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746085	1276	23432	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746092	1277	23433	663	221

Description

5000688875 ypum:sigx rna polymerase ecf-type sigma factor:sigma-x:probable rna polymerase sigma factor in dacb-aroc intergenic region:orfx20 (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigX sigX Bacillus subtilis 1423 -11529128 98521 sigx (de:rna polymerase sigma factor sigx) (db:swissprot) SIGX_BACSU P35165 BACILLUS SUBTILIS 1423 -11529128 7000686600 sigx rna polymerase ecf-type sigma factor sigx (db:pir2.dat) S45561 S45561 Bacillus subtilis 1423 -11529128 7500891624 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx20) (le:24398) (re:24982) (di:direct) BACDIA L09228 g410143 Bacillus subtilis 1423 -11529128 215522 sigx rna polymerase ecf-type sigma factor sigma-x (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypum) (le:18601) (re:19185) (di:complement) BSUB0013 Z99116 g2634745 Bacillus subtilis 1423 -11529128 170276 sigx rna polymerase ecf-type sigma factor sigx (db:pir) S45561 S45561 Bacillus subtilis 1423 -11529128 6500725270 ypum rna polymerase ecf-type sigma factor:sigma-x:probable rna polymerase sigma factor in dacb-aroc intergenic region:orfx20 (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigX sigX Bacillus subtilis 1423 -11529128

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746104	1278	23434	738	245

Description

6500725271 spoiiac:sigf rna polymerase sporulation-specific sigma factor:sigma-f:rna polymerase sigma-f factor:stage ii sporulation protein ac:sporulation sigma factor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigF sigF Bacillus subtilis 1423 -11529129 96351 sigf:spoiiac (de:(sporulation sigma factor)) (db:swissprot) RPSF_BACSU P07860 BACILLUS SUBTILIS 1423 -11529129 7000686469 sigf:spoiiac transcription initiation sigma factor sigf:stage ii sporulation protein spoiiac (cl:transcription sigma factor g:transcription initiation factor sigma katf homology) (db:pir2.dat) A28567 A28567 Bacillus subtilis 1423 -11529129 7500890692 spoiiac (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:275454) (re:276221) (di:direct) BACJH642 D84432 g1304000 Bacillus subtilis 1423 -11529129 216244 (sr:b.subtilis (strain 168) dna, clone bglii/psti) (db:genpept-bct1) (de:b.subtilis spoiia gene encoding a sporulation-specific sigmafactor, complete cds.) (nt:sporulation-specific sigma factor) (le:90) (re:857) (di:direct) BACSPO2A M15744 g143611 Bacillus subtilis 1423 -11529129 216864 sigf rna polymerase sporulation-specific sigma factor (fn:early forespore-specific gene expression) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: spoiiac) (le:47398) (re:48165) (di:complement) BSUB0013 Z99116 g2634780 Bacillus subtilis 1423 -11529129 139170 sigf:spoiiac transcription initiation sigma factor sigf:stage ii sporulation protein spoiiac (cl:transcription sigma factor g:transcription initiation factor sigma katf homology) (db:pir) A28567 A28567 Bacillus subtilis 1423 -11529129 5000688871 (de:(sigf) (pn:rna polymerase sigma-f factor:rna polymerase sigma-f factor:stage ii sporulation protein ac:sporulation sigma factor) (gn:spoiiac) (gtcfc:12.13) (ec:) (rpsf_bacsu) (keggfc:11.2) (bsorffc:6.1.1) (db:gtc-bacillus su) sigF sigF Bacillus subtilis 1423 10038294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746122	1279	23435	1227	409

Description

6500725272 rpod:crsa:siga rna polymerase major sigma-43 factor:rna polymerase sigma factor rpod:sigma-a:sigma-43 (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigA sigA Bacillus subtilis 1423 -11529130 219624 siga:rpod (de:rna polymerase sigma factor rpod (sigma-a) (sigma-43)) (db:swissprot) RPSA_BACSU P06224 BACILLUS SUBTILIS 1423 -11529130 123960 siga:rpod transcription initiation factor sigma a:rna polymerase major sigma factor siga:rna polymerase sigma factor 43:sigma factor a (cl:transcription initiation factor sigma 43:transcription initiation factor sigma katf homology:transcription initiation factor sigma region 1 homology) (db:pir1.dat) (mp:224 (degrees)) RNBS43 A22626 Bacillus subtilis 1423 -11529130 216077 rpod (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:118275) (re:119390) (di:direct) BACJH642 D84432 g1303833 Bacillus subtilis 1423 -11529130 216639 (sr:b.subtilis dna, clone pcps7) (db:genpept-bct1) (de:b.subtilis rpod gene encoding rna polymerase sigma-43 factor,complete cds.) (nt:rna polymerase sigma-43 factor.) (le:36) (re:1151) (di:direct) BACRPOD M10089 g143454 Bacillus subtilis 1423 -11529130 5000688867 (db:genpept-bct1) (de:bacillus subtilis sigma 43 operon with p23-dnae-rpod genes (dnaefor dna primase, rpod for rna polymerase).) (nt:rpod (aa 1-311)) (le:3489) (re:4604) (di:direct) BSSIG43 X03897 g40143 Bacillus subtilis 1423 -11529130 6000685133 siga rna polymerase major sigma-43 factor sigma-a (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: rpod, crsa) (le:204230) (re:205345) (di:complement) BSUB0013 Z99116 g2634953 Bacillus subtilis 1423 -11529130 7500890676 siga rna polymerase major sigma-43 factor sigma-a (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: rpod, crsa) (le:40) (re:1155) (di:complement) BSUB0014 Z99117 g2634967 Bacillus subtilis 1423 -11529130 96311 siga:rpod (de:rna polymerase sigma factor rpod (sigma-a) (sigma-43)) (db:swissprot) RPSA_BACSU P06224 BACILLUS SUBTILIS 1423 -11529130

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746125	1280	23436	582	193

Description

6500725273 rna polymerase ecf-type sigma factor:sigma-z (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigZ sigZ Bacillus subtilis 1423 -11529131 7500891628 sigz (de:rna polymerase sigma factor sigz) (db:swissprot) SIGZ_BACSU O05409 BACILLUS SUBTILIS 1423 -11529131 7000694559 sigz rna polymerase ecf-type sigma factor sigz (db:pir2.dat) C69707 C69707 Bacillus subtilis 1423 -11529131 1500692673 sigz rna polymerase sigma factor sigz (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934635 Bacillus subtilis 1423 -11529131 7500891631 sigz rna polymerase ecf-type sigma factor sigma-z (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:142063) (re:142593) (di:complement) BSUB0014 Z99117 g2635129 Bacillus subtilis 1423 -11529131

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746126	1281	23437	237	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746130	1282	23438	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746138	1283	23439	441	146

Description

6500725274 rna polymerase ecf-type sigma factor:sigma-v (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigV sigV Bacillus subtilis 1423 -11529132 7500891620 sigv (de:rna polymerase sigma factor sigv) (db:swissprot) SIGV_BACSU O05404 BACILLUS SUBTILIS 1423 -11529132 7000694556 sigv rna polymerase ecf-type sigma factor sigv (db:pir2.dat) G69706 G69706 Bacillus subtilis 1423 -11529132 1500692647 sigv rna polymerase sigma factor sigv (db:genpept-bct1) (de:bacillus subtilis cysteine synthase (yrha), cystathioninegamma-lyase (yrhb), yrhc (yrhc), yrhd (yrhd), formate dehydrogenasechain a (yrhe), yrhf (yrhf), formate dehydrogenase (yrhg), yrhh(yrhh), regulatory protein (yrhi), cytochro... BSU93874 U93874 g1934618 Bacillus subtilis 1423 -11529132 7500891623 sigv rna polymerase ecf-type sigma factor sigma-v (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:169670) (re:170170) (di:direct) BSUB0014 Z99117 g2635158 Bacillus subtilis 1423 -11529132

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746146	1284	23440	207	68

Description

5000688874 sigma-l:rna polymerase sigma-54 factor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigL sigL Bacillus subtilis 1423 -11529133 95959 sigl (de:rna polymerase sigma-54 factor) (db:swissprot) RP54_BACSU P24219 BACILLUS SUBTILIS 1423 -11529133 7000686442 sigl transcription initiation factor sigma 54 sigl:rna polymerase sigma factor sigl (db:pir2.dat) A41229 A41229 Bacillus subtilis 1423 -11529133 7500890506 sigl sigma factor 54 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:b.subtillis sigma factor 54 (sigl) gene, complete cds.) (le:148) (re:1458) (di:direct) BACSIG54A M73443 g143536 Bacillus subtilis 1423 -11529133 216740 sigl rna polymerase sigma-54 factor sigma-l (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:112011) (re:113321) (di:complement) BSUB0018 Z99121 g2635933 Bacillus subtilis 1423 -11529133 220269 sigl rna polymerase sigma-54 factor (db:genpept-bct1) (de:b.subtilis pnba, sigl, yve(j,k,l,m,n,o,p,q,r,s,t) andyvf(a,b,c,d,e,f,g,h) genes.) (le:18425) (re:19735) (di:direct) BSYVEFGNS Z71928 g1495296 Bacillus subtilis 1423 -11529133 1500685497 sigl sigma factor 54 (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (le:68350) (re:69660) (di:direct) BSZ94043 Z94043 g1945707 Bacillus subtilis 1423 -11529133 170635 sigl transcription initiation factor sigma 54 sigl:rna polymerase sigma factor sigl (db:pir) A41229 A41229 Bacillus subtilis 1423 -11529133 6500725275 sigma-l:rna polymerase sigma-54 factor (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigL sigL Bacillus subtilis 1423 -11529133

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746253	1285	23441	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746254	1286	23442	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746255	1287	23443	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746256	1288	23444	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746277	1289	23445	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746282	1290	23446	903	301

Description

6500725276 yxlb:sigy rna polymerase ecf-type sigma factor:sigma-y (gtcfc:10.2) (keggfc:14.2) (bsorffc:6.1.1) (db:gtc-bacillus subtilis) sigY sigY Bacillus subtilis 1423 -11529134 7500891625 sigy (de:rna polymerase sigma factor sigy) (db:swissprot) SIGY_BACSU P94370 BACILLUS SUBTILIS 1423 -11529134 7000694558 sigy rna polymerase ecf-type sigma factor sigy (db:pir2.dat) B69707 B69707 Bacillus subtilis 1423 -11529134 301549 sigy rna polymerase ecf-type sigma factor sigma-y (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxlb) (le:170704) (re:171240) (di:complement) BSUB0020 Z99123 g2636405 Bacillus subtilis 1423 -11529134 222882 sigy sigma factor (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to rna polymerase sigma factors;) (le:53225) (re:53761) (di:direct) D83026 D83026 g1783256 Bacillus subtilis 1423 -11529134

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746297	1291	23447	384	127

Description

6500725277 ygar:cspr rrna methylase homolog (gtcfc:10.3) (keggfc:14.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) cspR cspR Bacillus subtilis 1423 -11529135 7000694567 cspr rrna methylase homolog cspr (db:pir2.dat) G69608 G69608 Bacillus subtilis 1423 -11529135 7500965169 cspr rrna methylase homolog (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: ygar) (le:166824) (re:167306) (di:direct) BSUB0005 Z99108 g2633216 Bacillus subtilis 1423 -11529135

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746313	1292	23448	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746325	1293	23449	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746420	1294	23450	906	302

Description

6500725278 rnc:rncs ribonuclease iii (gtcfc:10.3) (ec:3.1.26.3) (keggfc:14.1) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rncS rncS Bacillus subtilis 1423 -11529136 7000694515 rncs:srb ribonuclease iii::rnase d:rnase o (cl:ribonuclease iii:double-stranded rna-binding repeat homology) (ec:3.1.26.3) (db:pir2.dat) B69693 B69693 Bacillus subtilis 1423 -11529136 7500965148 rncs ribonuclease iii (db:genpept-bct1) (ec:3.1.26.3) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: rnc) (le:66689) (re:67438) (di:direct) BSUB0009 Z99112 g2633965 Bacillus subtilis 1423 -11529136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746424	1295	23451	453	150

Description

6500725279 ribonuclease h (gtcfc:10.3) (ec:3.1.26.4) (keggfc:14.1) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rnh rnh Bacillus subtilis 1423 -11529137 7000694513 rnh ribonuclease h rnh (cl:ribonuclease hii) (db:pir2.dat) C69693 C69693 Bacillus subtilis 1423 -11529137 7500965146 rnh ribonuclease h (db:genpept-bct1) (ec:3.1.26.4) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:78430) (re:79197) (di:direct) BSUB0009 Z99112 g2633978 Bacillus subtilis 1423 -11529137

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746427	1296	23452	414	138

Description

6500725280 ribosome recycling factor (gtcfc:10.3) (keggfc:14.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) frr frr Bacillus subtilis 1423 -11529138 7000694546 frr ribosome recycling factor frr (cl:ribosome releasing factor) (db:pir2.dat) G69626 G69626 Bacillus subtilis 1423 -11529138 7500955449 frr ribosome recycling factor (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:121498) (re:122055) (di:direct) BSUB0009 Z99112 g2634024 Bacillus subtilis 1423 -11529138

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746440	1297	23453	660	219

Description

GTC ORF with score 187 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.).) (nt:similar to (swissprot accession number p39643)) (le:5534) (re:6772) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746441	1298	23454	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746442	1299	23455	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746453	1300	23456	825	274

Description

6500725281 ypji:paps poly:a polymerase:pap (gtcfc:10.3) (ec:2.7.7.19) (keggfc:14.1) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) papS papS Bacillus subtilis 1423 -11529139 88627 paps (ec:2.7.7.19) (de:poly(a) polymerase, (pap)) (db:swissprot) PAPS_BACSU P42977 BACILLUS SUBTILIS 1423 -11529139 7000686086 paps poly a polymerase paps (db:pir2.dat) B69672 B69672 Bacillus subtilis 1423 -11529139 217160 ypji poly a polymerase (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:38.9% of identical aminoa... BACYPIA L47709 g1146238 Bacillus subtilis 1423 -11529139 7500887655 paps poly a polymerase (db:genpept-bct1) (ec:2.7.7.19) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: ypji) (le:159582) (re:160775) (di:complement) BSUB0012 Z99115 g2634663 Bacillus subtilis 1423 -11529139 5000688569 (de:(paps) (pn:a polymerase:pap:poly:a polymerase :pap) (gtcfc:10.02:10.03) (ec:2.7.7.19) (paps_bacsu) (keggfc:11.1) (bsorffc:4.2.0) (db:gtc-bacillus subtilis)) papS papS Bacillus subtilis 1423 10030754

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746473	1301	23457	810	270

Description

GTC ORF with score 1282 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completecds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746576	1302	23458	513	171

Description

GTC ORF with score 369 to: (sr:neurospora crassa (individual_isolate ic3, strain 74a) (library) (db:genpept-pln1) (ec:4.1.1.17) (de:neurospora crassa ornithine decarboxylase gene, complete cds.) (nt:putative) (le:2577:2981) (re:2910:4101) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746594	1303	23459	486	162

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746602	1304	23460	864	287

Description

6500725282 ribonuclease ph:rnase ph:trna nucleotidyltransferase (gtcfc:10.3:10.6) (ec:2.7.7.56) (keggfc:14.1) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rph rph Bacillus subtilis 1423 -11529140 95773 rph (ec:2.7.7.56) (de:nucleotidyltransferase)) (db:swissprot) RNPH_BACSU P28619 BACILLUS SUBTILIS 1423 -11529140 216596 rph rnase ph (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis rnase ph (rph) gene, complete cds.) (le:1258) (re:1995) (di:direct) BACRPHA M85163 g143444 Bacillus subtilis 1423 -11529140 220335 rph ribonuclease ph (db:genpept-bct1) (ec:2.7.7.56) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:105124) (re:105861) (di:complement) BSUB0015 Z99118 g2635302 Bacillus subtilis 1423 -11529140 304208 rph rnase ph (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:suppression of cold sensitive mutations in) (le:64046) (re:64783) (di:direct) BSZ75208 Z75208 g1770059 Bacillus subtilis 1423 -11529140 7000686430 rph ribonuclease ph rph (cl:trna nucleotidyltransferase) (db:pir) D69694 D69694 Bacillus subtilis 1423 -11529140 5000688572 (de:(rph) (pn:ribonuclease ph:rnase ph:ribonuclease ph :rnase ph:trna nucleotidyltransferase) (gtcfc:10.02:10.03) (ec:2.7.7.56) (rnph_bacsu) (keggfc:11.1) (bsorffc:4.2.0) (db:gtc-bacillus subtilis)) rph rph Bacillus subtilis 1423 10037722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746607	1305	23461	198	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746621	1306	23462	318	105

Description

GTC ORF with score 93 to: (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (nt:similarity to arsenic efflux pump protein ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746634	1307	23463	972	324

Description

5000689830 yxin:ss8e:dead atp-dependent rna helicase:probable rna helicase in wapa-lict intergenic region (gtcfc:10.3) (keggfc:14.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) deaD deaD Bacillus subtilis 1423 -11529141 116832 dead:ss8e (de:probable atp-dependent rna helicase dead) (db:swissprot) DEAD_BACSU P42305 BACILLUS SUBTILIS 1423 -11529141 7000688768 dead atp-dependent rna helicase dead (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) E69613 E69613 Bacillus subtilis 1423 -11529141 222842 dead atp-dependent rna helicase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxin) (le:15496) (re:16935) (di:complement) BSUB0021 Z99124 g2636457 Bacillus subtilis 1423 -11529141 301509 dead (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to atp dependent rna helicase dead of e.) (le:6650) (re:8089) (di:direct) D83026 D83026 g665989 Bacillus subtilis 1423 -11529141 6500725283 yxin:ss8e atp-dependent rna helicase:probable rna helicase in wapa-lict intergenic region (gtcfc:10.3) (keggfc:14.2) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) deaD deaD Bacillus subtilis 1423 -11529141

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746637	1308	23464	723	241

Description

6500725284 ribonuclease p:protein component:ribonuclease p protein component:protein c5:rnase p (gtcfc:10.3) (ec:3.1.26.5) (keggfc:14.1) (bsorffc:4.2.1) (db:gtc-bacillus subtilis) rnpA rnpA Bacillus subtilis 1423 -11529142 95755 rnpa (ec:3.1.26.5) (de:ribonuclease p protein component, (protein c5) (rnase p)) (db:swissprot) RNPA_BACSU P25814 BACILLUS SUBTILIS 1423 -11529142 7000686426 rnpa ribonuclease p protein component rnpa (cl:ribonuclease p, protein component) (db:pir2.dat) S66029 S66029 Bacillus subtilis 1423 -11529142 7500890462 rnpa protein component of ribonuclease p (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:62749) (re:63099) (di:complement) BAC180K D26185 g467389 Bacillus subtilis 1423 -11529142 214989 rnpa ribonuclease p protein component (db:genpept-bct1) (ec:3.1.26.5) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:214681) (re:215031) (di:complement) BSUB0021 Z99124 g2636652 Bacillus subtilis 1423 -11529142 206275 rnpa ribonuclease p protein component rnpa (db:pir) S66029 S66029 Bacillus subtilis 1423 -11529142 5000688571 (de:(rnpa) (pn:ribonuclease p protein component:rnase p:ribonuclease p protein component :protein c5:rnase p) (gtcfc:10.02:10.03) (ec:3.1.26.5) (rnpa_bacsu) (keggfc:11.1) (bsorffc:4.2.0) (db:gtc-bacillus subtilis)) rnpA rnpA Bacillus subtilis 1423 10037704

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746639	1309	23465	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746652	1310	23466	543	180

Description

5000688597 ribosomal protein l33:50s ribosomal protein l33 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmG rpmG Bacillus subtilis 1423 -11529143 95181 rpmg (de:50s ribosomal protein l33) (db:swissprot) RL33_BACSU Q06798 BACILLUS SUBTILIS 1423 -11529143 7000686390 rpmg ribosomal protein l33 rpmg (cl:escherichia coli ribosomal protein l33) (db:pir2.dat) S39857 S39857 Bacillus subtilis 1423 -11529143 7500890209 rpmg ribosomal protein l33 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis genes for sigma factor h and ribosomal proteins.) (le:412) (re:561) (di:direct) BACSHRBPNS D13303 g285626 Bacillus subtilis 1423 -11529143 216735 rpmg ribosomal protein l33 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:117346) (re:117495) (di:direct) BSUB0001 Z99104 g2632366 Bacillus subtilis 1423 -11529143 149043 rpmg ribosomal protein l33 rpmg (cl:escherichia coli ribosomal protein l33) (db:pir) S39857 S39857 Bacillus subtilis 1423 -11529143 6500725285 ribosomal protein l33:50s ribosomal protein l33 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmG rpmG Bacillus subtilis 1423 -11529143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746653	1311	23467	402	133

Description

6500725286 relc:tsp:rplk ribosomal protein l11:50s ribosomal protein l11:bl11 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplK rplK Bacillus subtilis 1423 -11529144 7000689317 rplk ribosomal protein l11 bl11 rplk (cl:escherichia coli ribosomal protein l11) (db:pir2.dat) S39860 S39860 Bacillus subtilis 1423 -11529144 7500954916 rplk ribosomal protein l11 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis genes for sigma factor h and ribosomal proteins.) (le:1654) (re:2079) (di:direct) BACSHRBPNS D13303 g285629 Bacillus subtilis 1423 -11529144 216738 rplk ribosomal protein l11 bl11 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: relc, tsp) (le:118588) (re:119013) (di:direct) BSUB0001 Z99104 g2632369 Bacillus subtilis 1423 -11529144 148857 rplk ribosomal protein l11 bl11 rplk (cl:escherichia coli ribosomal protein l11) (db:pir) S39860 S39860 Bacillus subtilis 1423 -11529144

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746654	1312	23468	459	152

Description

6500725287 ribosomal protein l1:50s ribosomal protein l1:bl1 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplA rplA Bacillus subtilis 1423 -11529145 7000694523 rpla ribosomal protein l1 (cl:escherichia coli ribosomal protein l1) (db:pir2.dat) E69694 E69694 Bacillus subtilis 1423 -11529145 7500965153 rpla ribosomal protein l1 bl1 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:119107) (re:119805) (di:direct) BSUB0001 Z99104 g2632370 Bacillus subtilis 1423 -11529145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746657	1313	23469	252	83

Description

5000688580 ribosomal protein l10:50s ribosomal protein l10:bl5 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplJ rplJ Bacillus subtilis 1423 -11529146 7000686347 rplj ribosomal protein l10 bl5 rplj (cl:escherichia coli ribosomal protein l10) (db:pir2.dat) D69695 D69695 Bacillus subtilis 1423 -11529146 7500965155 rplj ribosomal protein l10 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l1, l10 and l12,partial and complete cds.) (le:347) (re:847) (di:direct) BACRPL2 D50303 g786163 Bacillus subtilis 1423 -11529146 216606 rplj ribosomal protein l10 bl5 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:120057) (re:120557) (di:direct) BSUB0001 Z99104 g2632371 Bacillus subtilis 1423 -11529146 6500725288 ribosomal protein l10:50s ribosomal protein l10:bl5 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplJ rplJ Bacillus subtilis 1423 -11529146 94706 rl10_bacsu (de:50s ribosomal protein l10 (bl5).) P42923 P42923 Bacillus subtilis 1423 -11529146

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746658	1314	23470	246	81

Description

6500725289 ribosomal protein l12:50s ribosomal protein l7/l12:bl9:a type (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplL rplL Bacillus subtilis 1423 -11529147 7000694524 rpll ribosomal protein l7/l12:ribosomal protein bl9 (cl:escherichia coli ribosomal protein l12) (db:pir1.dat) R5BS9 F69695 Bacillus subtilis 1423 -11529147 7500953532 rpll ribosomal protein l12 bl9 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:120604) (re:120975) (di:direct) BSUB0001 Z99104 g2632372 Bacillus subtilis 1423 -11529147

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746660	1315	23471	195	64

Description

6500725290 stra:fun:rpsl ribosomal protein s12:30s ribosomal protein s12:bs12 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsL rpsL Bacillus subtilis 1423 -11529148 7000694533 rpsl ribosomal protein s12 rpsl:ribosomal protein bs12 (cl:escherichia coli ribosomal protein s12) (db:pir2.dat) C69700 C69700 Bacillus subtilis 1423 -11529148 222750 rpsl ribosomal protein s12 bs12 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: stra, fun) (le:129701) (re:130117) (di:direct) BSUB0001 Z99104 g2632377 Bacillus subtilis 1423 -11529148 7500954828 rpsl ribosomal protein l12 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for rna polymerase beta subunit, ribosomalproteins l12 and s7, elongation factors g and tu and ribosomalproteins s10 and l3, partial and complete cds.) (le:2789) (re:... D64127 D64127 g1644221 Bacillus subtilis 1423 -11529148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746661	1316	23472	183	60

Description

6500725291 ribosomal protein s7:30s ribosomal protein s7:bs7 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsG rpsG Bacillus subtilis 1423 -11529149 7000694541 rpsg ribosomal protein s7 rpsg:ribosomal protein bs7 (cl:escherichia coli ribosomal protein s7) (db:pir2.dat) F69699 F69699 Bacillus subtilis 1423 -11529149 222751 rpsg ribosomal protein s7 bs7 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:130159) (re:130629) (di:direct) BSUB0001 Z99104 g2632378 Bacillus subtilis 1423 -11529149 7500954805 rpsg ribosomal protein s7 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for rna polymerase beta subunit, ribosomalproteins l12 and s7, elongation factors g and tu and ribosomalproteins s10 and l3, partial and complete cds.) (le:3247) (re:... D64127 D64127 g1644222 Bacillus subtilis 1423 -11529149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746753	1317	23473	666	222

Description

6500725292 teta:rpsj ribosomal protein s10:30s ribosomal protein s10:bs13 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsJ rpsJ Bacillus subtilis 1423 -11529150 7000694532 rpsj ribosomal protein s10 rpsj:ribosomal protein bs13 (cl:escherichia coli ribosomal protein s10) (db:pir2.dat) A69700 A69700 Bacillus subtilis 1423 -11529150 222755 rpsj ribosomal protein s10 bs13 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: teta) (le:135362) (re:135670) (di:direct) BSUB0001 Z99104 g2632382 Bacillus subtilis 1423 -11529150 7500954816 rpsj ribosomal protein s10 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for rna polymerase beta subunit, ribosomalproteins l12 and s7, elongation factors g and tu and ribosomalproteins s10 and l3, partial and complete cds.) (le:8450) (re:... D64127 D64127 g1644226 Bacillus subtilis 1423 -11529150

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746755	1318	23474	333	110

Description

5000688575 ribosomal protein l3:50s ribosomal protein l3:bl3 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplC rplC Bacillus subtilis 1423 -11529151 95287 rplc (de:50s ribosomal protein l3 (bl3)) (db:swissprot) RL3_BACSU P42920 BACILLUS SUBTILIS 1423 -11529151 7000686400 rplc ribosomal protein l3 bl3 rplc (cl:escherichia coli ribosomal protein l3) (db:pir2.dat) G69694 G69694 Bacillus subtilis 1423 -11529151 220010 rplc ribosomal protein l3 bl3 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:135710) (re:136339) (di:direct) BSUB0001 Z99104 g2632383 Bacillus subtilis 1423 -11529151 7500890267 rplc l3 (db:genpept-bct2) (de:bacillus subtilis ribosomal protein gene cluster, rpsj, rplc, rpld,rplw, rplb, rpss, rplv and rpsc genes, complete cds, and rplp gene,partial cds.) (nt:ribosomal protein) (le:667) (re:1296) (di:direct) BSU43929 U43929 g1165303 Bacillus subtilis 1423 -11529151 6500725293 ribosomal protein l3:50s ribosomal protein l3:bl3 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplC rplC Bacillus subtilis 1423 -11529151

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746756	1319	23475	402	134

Description

5000688576 ribosomal protein l4:50s ribosomal protein l4 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplD rplD Bacillus subtilis 1423 -11529152 95360 rpld (de:50s ribosomal protein l4) (db:swissprot) RL4_BACSU P42921 BACILLUS SUBTILIS 1423 -11529152 7000686404 rpld ribosomal protein l4 rpld (cl:escherichia coli ribosomal protein l4) (db:pir2.dat) H69694 H69694 Bacillus subtilis 1423 -11529152 216598 rpld ribosomal protein l4 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13, l4, l23, l2,s19, l22, s3 and l16, partial and complete cds.) (le:517) (re:1140) (di:direct) BACRPL1 D50302 g786154 Bacillus subtilis 1423 -11529152 220011 rpld ribosomal protein l4 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:136367) (re:136990) (di:direct) BSUB0001 Z99104 g2632384 Bacillus subtilis 1423 -11529152 7500890308 rpld l4 (db:genpept-bct2) (de:bacillus subtilis ribosomal protein gene cluster, rpsj, rplc, rpld,rplw, rplb, rpss, rplv and rpsc genes, complete cds, and rplp gene,partial cds.) (nt:ribosomal protein) (le:1324) (re:1947) (di:direct) BSU43929 U43929 g1165304 Bacillus subtilis 1423 -11529152 6500725294 ribosomal protein l4:50s ribosomal protein l4 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplD rplD Bacillus subtilis 1423 -11529152

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746761	1320	23476	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746767	1321	23477	360	120

Description

5000688590 ribosomal protein l23:50s ribosomal protein l23 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplW rplW Bacillus subtilis 1423 -11529153 94995 rplw (de:50s ribosomal protein l23) (db:swissprot) RL23_BACSU P42924 BACILLUS SUBTILIS 1423 -11529153 7000686369 rplw ribosomal protein l23 (cl:escherichia coli ribosomal protein l23) (db:pir1.dat) A69697 A69697 Bacillus subtilis 1423 -11529153 216599 rplw ribosomal protein l23 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13, l4, l23, l2,s19, l22, s3 and l16, partial and complete cds.) (le:1140) (re:1427) (di:direct) BACRPL1 D50302 g786155 Bacillus subtilis 1423 -11529153 220012 rplw ribosomal protein l23 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:136990) (re:137277) (di:direct) BSUB0001 Z99104 g2632385 Bacillus subtilis 1423 -11529153 7500890083 rplw l23 (db:genpept-bct2) (de:bacillus subtilis ribosomal protein gene cluster, rpsj, rplc, rpld,rplw, rplb, rpss, rplv and rpsc genes, complete cds, and rplp gene,partial cds.) (nt:ribosomal protein) (le:1947) (re:2234) (di:direct) BSU43929 U43929 g1165305 Bacillus subtilis 1423 -11529153 6500725295 ribosomal protein l23:50s ribosomal protein l23 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplW rplW Bacillus subtilis 1423 -11529153

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746774	1322	23478	342	114

Description

GTC ORF with score 96 to: (or:Human herpesvirus 4) (sr:epstein-barr virus (strain p3hr-1) dna) (db:genpept-vrl) (de:epstein-barr virus glycoprotein 340 (bllf1) and bllf2 genes,complete cds's, and bllfr3 gene, first exon.) (le:1) (re:2661) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746777	1323	23479	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746780	1324	23480	600	199

Description

6500725296 ribosomal protein l2:50s ribosomal protein l2:bl2 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplB rplB Bacillus subtilis 1423 -11529154 7000694527 rplb ribosomal protein l2 bl2 rplb (cl:escherichia coli ribosomal protein l2) (db:pir2.dat) F69694 F69694 Bacillus subtilis 1423 -11529154 216600 rplb ribosomal protein l2 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13, l4, l23, l2,s19, l22, s3 and l16, partial and complete cds.) (le:1459) (re:2292) (di:direct) BACRPL1 D50302 g786156 Bacillus subtilis 1423 -11529154 7500954884 rplb ribosomal protein l2 bl2 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:137309) (re:138142) (di:direct) BSUB0001 Z99104 g2632386 Bacillus subtilis 1423 -11529154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746787	1325	23481	642	213

Description

6500725297 ribosomal protein s19:30s ribosomal protein s19:bs19 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsS rpsS Bacillus subtilis 1423 -11529155 7000694536 rpss ribosomal protein s19 rpss:ribosomal protein bs19 (cl:escherichia coli ribosomal protein s19) (db:pir2.dat) B69701 B69701 Bacillus subtilis 1423 -11529155 216601 rpss ribosomal protein s19 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13, l4, l23, l2,s19, l22, s3 and l16, partial and complete cds.) (le:2350) (re:2628) (di:direct) BACRPL1 D50302 g786157 Bacillus subtilis 1423 -11529155 220014 rpss ribosomal protein s19 bs19 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:138200) (re:138478) (di:direct) BSUB0001 Z99104 g2632387 Bacillus subtilis 1423 -11529155 7500954856 rpss s19 (db:genpept-bct2) (de:bacillus subtilis ribosomal protein gene cluster, rpsj, rplc, rpld,rplw, rplb, rpss, rplv and rpsc genes, complete cds, and rplp gene,partial cds.) (nt:ribosomal protein) (le:3157) (re:3435) (di:direct) BSU43929 U43929 g1165307 Bacillus subtilis 1423 -11529155

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746817	1326	23482	411	136

Description

5000688589 ribosomal protein l22:bl17:50s ribosomal protein l22 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplV rplV Bacillus subtilis 1423 -11529156 94973 rplv (de:50s ribosomal protein l22) (db:swissprot) RL22_BACSU P42060 BACILLUS SUBTILIS 1423 -11529156 7000686367 rplv ribosomal protein l22 bl17 (cl:escherichia coli ribosomal protein l22) (db:pir2.dat) H69696 H69696 Bacillus subtilis 1423 -11529156 216602 rplv ribosomal protein l22 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13, l4, l23, l2,s19, l22, s3 and l16, partial and complete cds.) (le:2645) (re:2986) (di:direct) BACRPL1 D50302 g786158 Bacillus subtilis 1423 -11529156 220015 rplv ribosomal protein l22 bl17 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:138495) (re:138836) (di:direct) BSUB0001 Z99104 g2632388 Bacillus subtilis 1423 -11529156 7500890064 rplv l22 (db:genpept-bct2) (de:bacillus subtilis ribosomal protein gene cluster, rpsj, rplc, rpld,rplw, rplb, rpss, rplv and rpsc genes, complete cds, and rplp gene,partial cds.) (nt:ribosomal protein) (le:3452) (re:3793) (di:direct) BSU43929 U43929 g1165308 Bacillus subtilis 1423 -11529156 6500725298 ribosomal protein l22:bl17:50s ribosomal protein l22 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplV rplV Bacillus subtilis 1423 -11529156

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746819	1327	23483	1242	413

Description

GTC ORF with score 453 to: (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to cytochrome p450 / nadph-cytochrome p450) (le:173710) (re:176874) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746830	1328	23484	288	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746942	1329	23485	510	169

Description

6500725299 ribosomal protein s3:30s ribosomal protein s3:bs3:bs2 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsC rpsC Bacillus subtilis 1423 -11529157 7000694540 rpsc ribosomal protein s3 rpsc:ribosomal protein bs2:ribosomal protein bs3 (cl:escherichia coli ribosomal protein s3) (db:pir2.dat) B69699 B69699 Bacillus subtilis 1423 -11529157 216603 rpsc ribosomal protein s3 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13, l4, l23, l2,s19, l22, s3 and l16, partial and complete cds.) (le:2990) (re:3646) (di:direct) BACRPL1 D50302 g786159 Bacillus subtilis 1423 -11529157 7500954793 rpsc ribosomal protein s3 bs3 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:138840) (re:139496) (di:direct) BSUB0001 Z99104 g2632389 Bacillus subtilis 1423 -11529157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746959	1330	23486	333	110

Description

5000688585 ribosomal protein l16:50s ribosomal protein l16 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplP rplP Bacillus subtilis 1423 -11529158 94835 rplp (de:50s ribosomal protein l16) (db:swissprot) RL16_BACSU P14577 BACILLUS SUBTILIS 1423 -11529158 7000686357 rplp ribosomal protein l16 rplp (cl:escherichia coli ribosomal protein l16) (db:pir2.dat) B69696 B69696 Bacillus subtilis 1423 -11529158 7500889976 rplp ribosomal protein l16 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:139498) (re:139932) (di:direct) BSUB0001 Z99104 g2632390 Bacillus subtilis 1423 -11529158 6500725300 ribosomal protein l16:50s ribosomal protein l16 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplP rplP Bacillus subtilis 1423 -11529158

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746960	1331	23487	351	116

Description

GTC ORF with score 377 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c215.) (nt:spbc215.12, len:983, similarity:mus musculus,) (le:28413:28480:28878:29289) (re:28435:28839:29229:31505) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746971	1332	23488	564	188

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746974	1333	23489	384	127

Description

5000688594 ribosomal protein l29:50s ribosomal protein l29 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmC rpmC Bacillus subtilis 1423 -11529159 219628 rpmc (de:50s ribosomal protein l29) (db:swissprot) RL29_BACSU P12873 BACILLUS SUBTILIS 1423 -11529159 129141 rpmc ribosomal protein l29 (cl:escherichia coli ribosomal protein l29) (db:pir1.dat) R5BS2L S05990 Bacillus subtilis 1423 -11529159 216615 rpmc ribosomal protein l29 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044972 Bacillus subtilis 1423 -11529159 7500890143 (db:genpept-bct1) (de:b.subtilis s10/spc operon rpmc, rpsq, rpln, rplx, rple, rpsn genes.) (nt:l29 protein (aa 1-66)) (le:313) (re:513) (di:direct) BSSPC X15664 g40148 Bacillus subtilis 1423 -11529159 6500725301 rpmc ribosomal protein l29 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:139922) (re:140122) (di:direct) BSUB0001 Z99104 g2632391 Bacillus subtilis 1423 -11529159 95074 rpmc (de:50s ribosomal protein l29) (db:swissprot) RL29_BACSU P12873 BACILLUS SUBTILIS 1423 -11529159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746981	1334	23490	213	71

Description

6500725302 ribosomal protein s17:30s ribosomal protein s17:bs16 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsQ rpsQ Bacillus subtilis 1423 -11529160 128808 rpsq ribosomal protein s17:ribosomal protein bs16 (cl:escherichia coli ribosomal protein s17) (db:pir1.dat) R3BS17 S05991 Bacillus subtilis 1423 -11529160 219629 (db:genpept-bct1) (de:b.subtilis s10/spc operon rpmc, rpsq, rpln, rplx, rple, rpsn genes.) (nt:s17 protein (aa 1-87)) (le:536) (re:799) (di:direct) BSSPC X15664 g40149 Bacillus subtilis 1423 -11529160 7500953515 rpsq ribosomal protein s17 bs16 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:140145) (re:140408) (di:direct) BSUB0001 Z99104 g2632392 Bacillus subtilis 1423 -11529160

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746982	1335	23491	459	152

Description

5000688583 ribosomal protein l14:50s ribosomal protein l14 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplN rplN Bacillus subtilis 1423 -11529161 219630 rpln (de:50s ribosomal protein l14) (db:swissprot) RL14_BACSU P12875 BACILLUS SUBTILIS 1423 -11529161 129030 rpln ribosomal protein l14 (cl:escherichia coli ribosomal protein l14) (db:pir1.dat) R5BS4B S05992 Bacillus subtilis 1423 -11529161 216617 rpln ribosomal protein l14 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044974 Bacillus subtilis 1423 -11529161 7500889938 (db:genpept-bct1) (de:b.subtilis s10/spc operon rpmc, rpsq, rpln, rplx, rple, rpsn genes.) (nt:l14 protein (aa 1-122)) (le:840) (re:1208) (di:direct) BSSPC X15664 g40150 Bacillus subtilis 1423 -11529161 6500725303 rpln ribosomal protein l14 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:140449) (re:140817) (di:direct) BSUB0001 Z99104 g2632393 Bacillus subtilis 1423 -11529161 94790 rpln (de:50s ribosomal protein l14) (db:swissprot) RL14_BACSU P12875 BACILLUS SUBTILIS 1423 -11529161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746989	1336	23492	423	140

Description

5000688591 ribosomal protein l24:histone-like protein hpb12:50s ribosomal protein l24:bl23 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplX rplX Bacillus subtilis 1423 -11529162 219631 rplx (de:50s ribosomal protein l24 (bl23)) (db:swissprot) RL24_BACSU P12876 BACILLUS SUBTILIS 1423 -11529162 129122 rplx ribosomal protein l24:bl23:histone-like protein hpb12 (cl:escherichia coli ribosomal protein l24) (db:pir1.dat) R5BS2B S05993 Bacillus subtilis 1423 -11529162 216608 rplx ribosomal protein l24 (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis ribosomal protein l24 (rplx) gene, complete cds.) (le:38) (re:349) (di:direct) BACRPL24A M81748 g143446 Bacillus subtilis 1423 -11529162 216618 rplx ribosomal protein l24 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044975 Bacillus subtilis 1423 -11529162 7500890102 (db:genpept-bct1) (de:b.subtilis s10/spc operon rpmc, rpsq, rpln, rplx, rple, rpsn genes.) (nt:l24 protein (aa 1-103)) (le:1246) (re:1557) (di:direct) BSSPC X15664 g40151 Bacillus subtilis 1423 -11529162 7502851585 rplx ribosomal protein l24 bl23 histone-like (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:140855) (re:141166) (di:direct) BSUB0001 Z99104 g2632394 Bacillus subtilis 1423 -11529162 95014 rplx (de:50s ribosomal protein l24 (bl23)) (db:swissprot) RL24_BACSU P12876 BACILLUS SUBTILIS 1423 -11529162 6500725304 ribosomal protein l24:histone-like protein hpb12:50s ribosomal protein l24:bl23 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplX rplX Bacillus subtilis 1423 -11529162

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501746992	1337	23493	402	134

Description

5000688577 ribosomal protein l5:50s ribosomal protein l5:bl6 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplE rplE Bacillus subtilis 1423 -11529163 219632 rple (de:50s ribosomal protein l5 (bl6)) (db:swissprot) RL5_BACSU P12877 BACILLUS SUBTILIS 1423 -11529163 128904 rple ribosomal protein l5:bl6 (cl:escherichia coli ribosomal protein l5) (db:pir1.dat) R5BS5 S05994 Bacillus subtilis 1423 -11529163 216619 rple ribosomal protein l5 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044976 Bacillus subtilis 1423 -11529163 7500890326 (db:genpept-bct1) (de:b.subtilis s10/spc operon rpmc, rpsq, rpln, rplx, rple, rpsn genes.) (nt:l5 protein (aa 1-179)) (le:1584) (re:2123) (di:direct) BSSPC X15664 g40152 Bacillus subtilis 1423 -11529163 7502851586 rple ribosomal protein l5 bl6 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:141193) (re:141732) (di:direct) BSUB0001 Z99104 g2632395 Bacillus subtilis 1423 -11529163 95378 rple (de:50s ribosomal protein l5 (bl6)) (db:swissprot) RL5_BACSU P12877 BACILLUS SUBTILIS 1423 -11529163 6500725305 ribosomal protein l5:50s ribosomal protein l5:bl6 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplE rplE Bacillus subtilis 1423 -11529163

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747008	1338	23494	375	124

Description

GTC ORF with score 181 to: (sr:pyrococcus horikoshii (strain:ot3) dna) (db:genpept-bct2) (de:pyrococcus horikoshii ot3 genomic dna, 777001-994000 nt. position(4/7).) (nt:similar to pir:f64337 percent identity: 71.014 in) (le:5317) (re:6159) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747013	1339	23495	270	90

Description

6500725306 ribosomal protein s14:30s ribosomal protein s14:bs-a (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsN rpsN Bacillus subtilis 1423 -11529164 128776 rpsn ribosomal protein s14:ribosomal protein bs-a (cl:escherichia coli ribosomal protein s14) (db:pir1.dat) R3BS14 S05995 Bacillus subtilis 1423 -11529164 216620 rpsn ribosomal protein l14 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044977 Bacillus subtilis 1423 -11529164 219633 (db:genpept-bct1) (de:b.subtilis s10/spc operon rpmc, rpsq, rpln, rplx, rple, rpsn genes.) (nt:s14 protein (aa 1-61)) (le:2146) (re:2331) (di:direct) BSSPC X15664 g580930 Bacillus subtilis 1423 -11529164 7500953512 rpsn ribosomal protein s14 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:141755) (re:141940) (di:direct) BSUB0001 Z99104 g2632396 Bacillus subtilis 1423 -11529164

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747014	1340	23496	285	94

Description

6500725307 ribosomal protein s8:30s ribosomal protein s8:bs8 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsH rpsH Bacillus subtilis 1423 -11529165 7000694542 rpsh ribosomal protein s8:ribosomal protein bs8 (cl:escherichia coli ribosomal protein s8) (db:pir2.dat) G69699 G69699 Bacillus subtilis 1423 -11529165 222728 rpsh ribosomal protein s8 bs8 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:141972) (re:142370) (di:direct) BSUB0001 Z99104 g2632397 Bacillus subtilis 1423 -11529165 7500954811 rpsh ribosomal protein s8 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal protein s5, ribosomal proteinl18, ribosomal protein l6 and ribosomal protein s8, complete andpartial cds.) (le:1) (re:399) (di:direct) D64125 D64125 g1644197 Bacillus subtilis 1423 -11529165

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747015	1341	23497	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747018	1342	23498	861	287

Description

GTC ORF with score 413 to: (sr:bos taurus (library: cdna library) liver cdna to mrna) (db:genpept-mam) (ec:1.2.4.4) (de:bos taurus branched-chain alpha-ketoacid dehydrogenase e(1) betasubunit precursor (bckdh) mrna, complete cds.) (nt:precursor; e(1) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747025	1343	23499	558	185

Description

6500725308 ribosomal protein l6:bl8:50s ribosomal protein l6:bl10 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplF rplF Bacillus subtilis 1423 -11529166 7000694530 rplf ribosomal protein l6 bl8 rplf (cl:escherichia coli ribosomal protein l6) (db:pir2.dat) B69695 B69695 Bacillus subtilis 1423 -11529166 216622 rplf ribosomal protein l6 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,initiation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044979 Bacillus subtilis 1423 -11529166 222729 rplf ribosomal protein l6 bl8 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:142400) (re:142939) (di:direct) BSUB0001 Z99104 g2632398 Bacillus subtilis 1423 -11529166 7500965157 rplf ribosomal protein l6 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal protein s5, ribosomal proteinl18, ribosomal protein l6 and ribosomal protein s8, complete andpartial cds.) (le:429) (re:968) (di:direct) D64125 D64125 g1644198 Bacillus subtilis 1423 -11529166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747129	1344	23500	579	193

Description

6500725309 ribosomal protein l18:50s ribosomal protein l18 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplR rplR Bacillus subtilis 1423 -11529167 7000694525 rplr ribosomal protein l18 rplr (cl:escherichia coli ribosomal protein l18) (db:pir2.dat) D69696 D69696 Bacillus subtilis 1423 -11529167 222730 rplr ribosomal protein l18 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:142972) (re:143334) (di:direct) BSUB0001 Z99104 g2632399 Bacillus subtilis 1423 -11529167 7500965156 rplr ribosomal protein l18 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal protein s5, ribosomal proteinl18, ribosomal protein l6 and ribosomal protein s8, complete andpartial cds.) (le:1001) (re:1363) (di:direct) D64125 D64125 g1644199 Bacillus subtilis 1423 -11529167

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747139	1345	23501	549	182

Description

6500725310 spca:rpse ribosomal protein s5:30s ribosomal protein s5:bs5 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsE rpsE Bacillus subtilis 1423 -11529168 97337 rpse:spca (de:30s ribosomal protein s5 (bs5)) (db:swissprot) RS5_BACSU P21467 BACILLUS SUBTILIS 1423 -11529168 7000686510 rpse ribosomal protein s5 (cl:escherichia coli ribosomal protein s5) (db:pir1.dat) R3BS5S D69699 Bacillus subtilis 1423 -11529168 216624 rpse ribosomal protein s5 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044981 Bacillus subtilis 1423 -11529168 7500891058 rpse ribosomal protein s5 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:143359) (re:143859) (di:direct) BSUB0001 Z99104 g2632400 Bacillus subtilis 1423 -11529168 5000688603 (de:(rpse) (pn:30s ribosomal protein s5:bs5:30s ribosomal protein s5:bs5) (gn:spca) (gtcfc:10.04) (ec:) (rs5_bacsu) (keggfc:11.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis)) rpsE rpsE Bacillus subtilis 1423 10039234

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747145	1346	23502	744	247

Description

6500725311 ribosomal protein l30:50s ribosomal protein l30:bl27 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmD rpmD Bacillus subtilis 1423 -11529169 129146 rpmd ribosomal protein l30:bl27 (cl:escherichia coli ribosomal protein l30) (db:pir1.dat) R5BS30 S12681 Bacillus subtilis 1423 -11529169 216625 rpmd ribosomal protein l30 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044982 Bacillus subtilis 1423 -11529169 216839 (sr:bacillus subtilis (strain 1a241) dna) (db:genpept-bct1) (de:bacillus subtilis spectinomycin resistance (s5, l30, l15, secy andadk) genes, complete cds.) (nt:spc orf2; l30) (le:563) (re:742) (di:direct) BACSPCR M31102 g143576 Bacillus subtilis 1423 -11529169 7500953548 rpmd ribosomal protein l30 bl27 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:143873) (re:144052) (di:direct) BSUB0001 Z99104 g2632401 Bacillus subtilis 1423 -11529169 216694 l30 ribosomal protein (sr:bacillus subtilis (strain:207-21) dna) (db:genpept-bct2) (de:bacillus subtilis genes for ribosomal proteins, secy, adenylatekinase and methionine amino peptidase, complete cds.) (le:53) (re:232) (di:direct) BACSECY D00619 g216337 Bacillus subtilis 1423 -11529169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747154	1347	23503	504	168

Description

5000688584 ribosomal protein l15:50s ribosomal protein l15 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplO rplO Bacillus subtilis 1423 -11529170 94808 rplo (de:50s ribosomal protein l15) (db:swissprot) RL15_BACSU P19946 BACILLUS SUBTILIS 1423 -11529170 129053 rplo ribosomal protein l15 (cl:escherichia coli ribosomal protein l15) (db:pir1.dat) R5BSL5 S12682 Bacillus subtilis 1423 -11529170 216626 rplo ribosomal protein l15 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044983 Bacillus subtilis 1423 -11529170 216840 (sr:bacillus subtilis (strain 1a241) dna) (db:genpept-bct1) (de:bacillus subtilis spectinomycin resistance (s5, l30, l15, secy andadk) genes, complete cds.) (nt:spc orf3; l15) (le:773) (re:1213) (di:direct) BACSPCR M31102 g143577 Bacillus subtilis 1423 -11529170 7500889960 rplo ribosomal protein l15 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:144083) (re:144523) (di:direct) BSUB0001 Z99104 g2632402 Bacillus subtilis 1423 -11529170 216695 l15 ribosomal protein (sr:bacillus subtilis (strain:207-21) dna) (db:genpept-bct2) (de:bacillus subtilis genes for ribosomal proteins, secy, adenylatekinase and methionine amino peptidase, complete cds.) (le:263) (re:703) (di:direct) BACSECY D00619 g216338 Bacillus subtilis 1423 -11529170 6500725312 ribosomal protein l15:50s ribosomal protein l15 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplO rplO Bacillus subtilis 1423 -11529170

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747169	1348	23504	657	218

Description

6500725313 rpmx:rpmj ribosomal protein l36:50s ribosomal protein l36:ribosomal protein ii:ribosomal protein b:bl38 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmJ rpmJ Bacillus subtilis 1423 -11529171 95231 rpmj (de:(bl38)) (db:swissprot) RL36_BACSU P20278 BACILLUS SUBTILIS 1423 -11529171 149064 rpmj ribosomal protein l36:ribosomal protein b rpmj (cl:escherichia coli ribosomal protein l36) (db:pir2.dat) B32307 A32307 Bacillus subtilis 1423 -11529171 7500890240 rpmj ribosomal protein b (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis initiation factor 1, ribosomal proteins b, s13, s11, l17and rna polymerase alpha core protein genes, complete cds.) (le:487) (re:600) (di:direct) BACALPHA M26414 g142460 Bacillus subtilis 1423 -11529171 215149 rpmj ribosomal protein b (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044988 Bacillus subtilis 1423 -11529171 216631 rpmj ribosomal protein l36 ribosomal protein b (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: rpmx) (le:147835) (re:147948) (di:direct) BSUB0001 Z99104 g2632407 Bacillus subtilis 1423 -11529171 7000686398 rpmj ribosomal protein l36:ribosomal protein b rpmj (cl:escherichia coli ribosomal protein l36) (db:pir) B32307 D69698 Bacillus subtilis 1423 -11529171 5000688599 (de:(rpmj) (pn:50s ribosomal protein l36:ribosomal protein b:bl38:50s ribosomal protein l36:ribosomal protein ii:ribosomal protein b:bl38) (gtcfc:10.04) (ec:) (rl36_bacsu) (keggfc:11.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmJ rpmJ Bacillus subtilis 1423 10037194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747174	1349	23505	591	196

Description

6500725314 ribosomal protein s13:30s ribosomal protein s13:bs14 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsM rpsM Bacillus subtilis 1423 -11529172 128757 rpsm ribosomal protein s13:ribosomal protein bs14 (cl:escherichia coli ribosomal protein s13) (db:pir1.dat) R3BS13 C32307 Bacillus subtilis 1423 -11529172 215150 rpsm ribosomal protein s13 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis initiation factor 1, ribosomal proteins b, s13, s11, l17and rna polymerase alpha core protein genes, complete cds.) (le:623) (re:988) (di:direct) BACALPHA M26414 g142461 Bacillus subtilis 1423 -11529172 7500953510 rpsm ribosomal protein s13 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:147971) (re:148336) (di:direct) BSUB0001 Z99104 g2632408 Bacillus subtilis 1423 -11529172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747185	1350	23506	279	92

Description

5000688609 ribosomal protein s11:30s ribosomal protein s11:bs11 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsK rpsK Bacillus subtilis 1423 -11529173 96917 rpsk (de:30s ribosomal protein s11 (bs11)) (db:swissprot) RS11_BACSU P04969 BACILLUS SUBTILIS 1423 -11529173 128727 rpsk ribosomal protein s11:ribosomal protein bs11 (cl:escherichia coli ribosomal protein s11) (db:pir1.dat) R3BSS1 D32307 Bacillus subtilis 1423 -11529173 215151 rpsk ribosomal protein s11 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis initiation factor 1, ribosomal proteins b, s13, s11, l17and rna polymerase alpha core protein genes, complete cds.) (le:1009) (re:1404) (di:direct) BACALPHA M26414 g142462 Bacillus subtilis 1423 -11529173 216633 rpsk ribosomal protein s11 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044990 Bacillus subtilis 1423 -11529173 216637 (sr:b.subtilis (strain 168 marburg) dna clone lambda-gt11-11-1) (db:genpept-bct1) (de:b.subtilis dna sequence of the rpsm-rpoa interval.) (nt:ribosomal protein s11) (le:133) (re:528) (di:direct) BACRPOA M13957 g143451 Bacillus subtilis 1423 -11529173 7500890855 rpsk ribosomal protein s11 bs11 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:148357) (re:148752) (di:direct) BSUB0001 Z99104 g2632409 Bacillus subtilis 1423 -11529173 6500725315 ribosomal protein s11:30s ribosomal protein s11:bs11 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsK rpsK Bacillus subtilis 1423 -11529173

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747193	1351	23507	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747197	1352	23508	411	136

Description

6500725316 ribosomal protein l17:50s ribosomal protein l17:bl15:bl21 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplQ rplQ Bacillus subtilis 1423 -11529174 7000689318 rplq ribosomal protein l17:ribosomal protein bl15 rplq (cl:escherichia coli ribosomal protein l17) (db:pir2.dat) F32307 F32307 Bacillus subtilis 1423 -11529174 7500954935 rplq ribosomal protein l17 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis initiation factor 1, ribosomal proteins b, s13, s11, l17and rna polymerase alpha core protein genes, complete cds.) (le:2603) (re:2965) (di:direct) BACALPHA M26414 g142464 Bacillus subtilis 1423 -11529174 215153 rplq ribosomal protein l17 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044992 Bacillus subtilis 1423 -11529174 216635 rplq ribosomal protein l17 bl15 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:149951) (re:150313) (di:direct) BSUB0001 Z99104 g2632411 Bacillus subtilis 1423 -11529174 148912 rplq ribosomal protein l17:ribosomal protein bl15 rplq (cl:escherichia coli ribosomal protein l17) (db:pir) F32307 F32307 Bacillus subtilis 1423 -11529174

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747198	1353	23509	309	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747309	1354	23510	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747312	1355	23511	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747315	1356	23512	282	93

Description

6500725317 ribosomal protein l13:50s ribosomal protein l13 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplM rplM Bacillus subtilis 1423 -11529175 121108 rplm (de:50s ribosomal protein l13) (db:swissprot) RL13_BACSU P70974 BACILLUS SUBTILIS 1423 -11529175 7000686351 rplm ribosomal protein l13 rplm (cl:escherichia coli ribosomal protein l13) (db:pir2.dat) G69695 G69695 Bacillus subtilis 1423 -11529175 222737 rplm ribosomal protein l13 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:153841) (re:154278) (di:direct) BSUB0001 Z99104 g2632416 Bacillus subtilis 1423 -11529175 7500889928 rplm ribosomal protein l13 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:3402) (re:3839) (di:direct) D64126 D64126 g1644207 Bacillus subtilis 1423 -11529175

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747323	1357	23513	786	261

Description

6500725318 ribosomal protein s9:30s ribosomal protein s9:bs10 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsI rpsI Bacillus subtilis 1423 -11529176 7000694543 rpsi ribosomal protein s9 rpsi:ribosomal protein bs10 (cl:escherichia coli ribosomal protein s9) (db:pir2.dat) H69699 H69699 Bacillus subtilis 1423 -11529176 222738 rpsi ribosomal protein s9 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:154299) (re:154691) (di:direct) BSUB0001 Z99104 g2632417 Bacillus subtilis 1423 -11529176 7500954812 rpsi ribosomal protein s9 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:3860) (re:4252) (di:direct) D64126 D64126 g1644208 Bacillus subtilis 1423 -11529176

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747329	1358	23514	546	181

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747341	1359	23515	297	98

Description

6500725319 ribosomal protein l32 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmF rpmF Bacillus subtilis 1423 -11529177 7000694528 rpmf ribosomal protein l32 (cl:escherichia coli ribosomal protein l32) (db:pir1.dat) H69697 H69697 Bacillus subtilis 1423 -11529177 5500687767 rpmf ribosomal protein l32 (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:20933) (re:21112) (di:direct) BS16823KB Z98682 g2340011 Bacillus subtilis 1423 -11529177 7500954975 rpmf ribosomal protein l32 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:180416) (re:180595) (di:direct) BSUB0008 Z99111 g2633879 Bacillus subtilis 1423 -11529177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747355	1360	23516	567	189

Description

6500725320 ylot:rpmb ribosomal protein l28:50s ribosomal protein l28 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmB rpmB Bacillus subtilis 1423 -11529178 216890 rpmb (de:50s ribosomal protein l28) (db:swissprot) RL28_BACSU P37807 BACILLUS SUBTILIS 1423 -11529178 7000686376 rpmb ribosomal protein l28 rpmb (cl:escherichia coli ribosomal protein l28) (db:pir2.dat) S39982 S39982 Bacillus subtilis 1423 -11529178 7500890137 rpmb ribosomal protein l28 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylot) (le:56578) (re:56766) (di:complement) BSUB0009 Z99112 g2633954 Bacillus subtilis 1423 -11529178 5000688593 ylot putative rpmb protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:18350) (re:18538) (di:complement) BSY13937 Y13937 g2337811 Bacillus subtilis 1423 -11529178 5500684716 ribosomal protein l28 (sr:bacillus subtilis (sub_strain py79, strain w168) sporulation dna) (db:genpept-bct2) (de:bacillus subtilis sporulation factor (spovm) gene and ribosomalprotein l28 gene, complete cds's.) (le:297) (re:485) (di:complement) BACSPORLG L12244 g143648 Bacillus subtilis 1423 -11529178 95063 rpmb (de:50s ribosomal protein l28) (db:swissprot) RL28_BACSU P37807 BACILLUS SUBTILIS 1423 -11529178 170514 rpmb ribosomal protein l28 rpmb (db:pir) S39982 S39982 Bacillus subtilis 1423 -11529178

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747358	1361	23517	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747368	1362	23518	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747371	1363	23519	363	120

Description

6500725321 ribosomal protein s16:30s ribosomal protein s16:bs17 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsP rpsP Bacillus subtilis 1423 -11529179 7000689313 rpsp ribosomal protein s16 bs17 rpsp:ribosomal protein bs17 (cl:escherichia coli ribosomal protein s16) (db:pir2.dat) C47154 C47154 Bacillus subtilis 1423 -11529179 7500954845 rpsp ribosomal protein s16 bs17 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:74599) (re:74871) (di:direct) BSUB0009 Z99112 g2633971 Bacillus subtilis 1423 -11529179 4000710141 rpsp 30s ribosomal protein s16 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis orf1, ffh, rpsp genes for orf1, ffh and 30sribosomal protein s16, complete cds.) (le:2157) (re:2429) (di:direct) D14356 D14356 g2309081 Bacillus subtilis 1423 -11529179 148581 rpsp ribosomal protein s16 bs17 rpsp:ribosomal protein bs17 (cl:escherichia coli ribosomal protein s16) (db:pir) C47154 C47154 Bacillus subtilis 1423 -11529179

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747375	1364	23520	792	263

Description

6500725322 ribosomal protein l19 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplS rplS Bacillus subtilis 1423 -11529180 7500890019 rpls (de:50s ribosomal protein l19) (db:swissprot) RL19_BACSU O31742 BACILLUS SUBTILIS 1423 -11529180 7000694526 rpls ribosomal protein l19 rpls (cl:escherichia coli ribosomal protein l19) (db:pir2.dat) E69696 E69696 Bacillus subtilis 1423 -11529180 7500890021 rpls ribosomal protein l19 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:77012) (re:77368) (di:direct) BSUB0009 Z99112 g2633976 Bacillus subtilis 1423 -11529180

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747496	1365	23521	783	260

Description

6500725323 ribosomal protein s2 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsB rpsB Bacillus subtilis 1423 -11529181 7000694537 rpsb ribosomal protein s2 rpsb:ribosomal protein bs1 (cl:escherichia coli ribosomal protein s2) (db:pir2.dat) A69699 A69699 Bacillus subtilis 1423 -11529181 7500954787 rpsb ribosomal protein s2 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:118905) (re:119645) (di:direct) BSUB0009 Z99112 g2634021 Bacillus subtilis 1423 -11529181

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747503	1366	23522	552	184

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747521	1367	23523	336	112

Description

6500725324 ribosomal protein s15:30s ribosomal protein s15:bs18 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsO rpsO Bacillus subtilis 1423 -11529182 7000694535 rpso ribosomal protein s15 rpso:ribosomal protein bs18 (cl:escherichia coli ribosomal protein s15:eubacterial ribosomal protein s15 homology) (db:pir2.dat) F69700 F69700 Bacillus subtilis 1423 -11529182 219591 rpso ribosomal protein s15 (db:genpept-bct1) (de:b.subtilis ribc, rpso and pnpa genes.) (le:1195) (re:1464) (di:direct) BSRIBRPS Z80835 g1592691 Bacillus subtilis 1423 -11529182 304139 rpso ribosomal protein s15 bs18 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:139912) (re:140181) (di:direct) BSUB0009 Z99112 g2634040 Bacillus subtilis 1423 -11529182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747540	1368	23524	807	269

Description

6500725325 yqex:rpsu ribosomal protein s21:30s ribosomal protein s21:bs-b (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsU rpsU Bacillus subtilis 1423 -11529183 7000694539 rpsu ribosomal protein s21 rpsu:ribosomal protein bs-b (cl:escherichia coli ribosomal protein s21) (db:pir2.dat) D69701 D69701 Bacillus subtilis 1423 -11529183 216058 yqex (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:99061) (re:99234) (di:direct) BACJH642 D84432 g1303814 Bacillus subtilis 1423 -11529183 302937 rpsu ribosomal protein s21 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqex) (le:20196) (re:20369) (di:complement) BSUB0014 Z99117 g2634987 Bacillus subtilis 1423 -11529183 7500954870 yqex (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for dnaj, yqet, yqeu, yqev, yqew, yqex, yqey,complete and partial cds.) (nt:similar to 30s ribosomal protein s21 (rpsu) of b.) (le:4592) (re:4765) (di:d... D83717 D83717 g1890063 Bacillus subtilis 1423 -11529183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747542	1369	23525	627	208

Description

6500725326 yqeo:rpst ribosomal protein s20:30s ribosomal protein s20:bs20 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsT rpsT Bacillus subtilis 1423 -11529184 7000694538 rpst ribosomal protein s20 rpst:ribosomal protein bs20 (cl:escherichia coli ribosomal protein s20) (db:pir2.dat) C69701 C69701 Bacillus subtilis 1423 -11529184 216044 yqeo (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:83533) (re:83799) (di:complement) BACJH642 D84432 g1303800 Bacillus subtilis 1423 -11529184 7500954868 rpst ribosomal protein s20 bs20 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqeo) (le:35631) (re:35897) (di:direct) BSUB0014 Z99117 g2635001 Bacillus subtilis 1423 -11529184

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747544	1370	23526	384	127

Description

5000688592 ribosomal protein l27:50s ribosomal protein l27:bl30:bl24 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmA rpmA Bacillus subtilis 1423 -11529185 216849 rpma (de:50s ribosomal protein l27 (bl30) (bl24)) (db:swissprot) RL27_BACSU P05657 BACILLUS SUBTILIS 1423 -11529185 7000686374 rpma ribosomal protein l27:ribosomal protein bl24 rpma (cl:escherichia coli ribosomal protein l27:eubacterial ribosomal protein l27 homology) (db:pir2.dat) C21895 C21895 Bacillus subtilis 1423 -11529185 7500890127 l27 ribosomal protein (sr:bacillus subtilis (clone pbag1, sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis ribosomal protein l27 gene, upstream of spo0blocus, complete cds.) (nt:polypeptide homologous to e. coli ribosomal protein) (le:136) (re:420)... BACSPO0B1 K02665 g143592 Bacillus subtilis 1423 -11529185 219657 homologous to e.coli ribosomal protein l27 (db:genpept-bct1) (de:bacillus subtilis gene upstream of spoob locus for homolog ofribosomal protein l27 of e. coli.) (le:136) (re:420) (di:direct) BSSPOOUP X02656 g40186 Bacillus subtilis 1423 -11529185 7502851587 rpma ribosomal protein l27 bl24 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:59011) (re:59295) (di:complement) BSUB0015 Z99118 g2635259 Bacillus subtilis 1423 -11529185 95049 rpma (de:50s ribosomal protein l27 (bl30) (bl24)) (db:swissprot) RL27_BACSU P05657 BACILLUS SUBTILIS 1423 -11529185 149000 rpma ribosomal protein l27:ribosomal protein bl24 rpma (cl:escherichia coli ribosomal protein l27:eubacterial ribosomal protein l27 homology) (db:pir) C21895 C21895 Bacillus subtilis 1423 -11529185 6500725327 ribosomal protein l27:50s ribosomal protein l27:bl30:bl24 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmA rpmA Bacillus subtilis 1423 -11529185

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747572	1371	23527	192	63

Description

5000688588 ribosomal protein l21:50s ribosomal protein l21:bl20 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplU rplU Bacillus subtilis 1423 -11529186 7500890050 rplu (de:50s ribosomal protein l21 (bl20)) (db:swissprot) RL21_BACSU P26908 BACILLUS SUBTILIS 1423 -11529186 7000686365 rplu ribosomal protein l21:ribosomal protein bl20:rplu (cl:escherichia coli ribosomal protein l21) (db:pir2.dat) S18439 S18439 Bacillus subtilis 1423 -11529186 219648 l20 (db:genpept-bct1) (de:b.subtilis spoivfa, spoivfb, l20, orfx and l24 genes.) (nt:homolog of e.coli ribosomal protein l21) (le:1959) (re:2267) (di:direct) BSSPOIVFO X59528 g40173 Bacillus subtilis 1423 -11529186 7502851588 rplu ribosomal protein l21 bl20 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:59649) (re:59957) (di:complement) BSUB0015 Z99118 g2635261 Bacillus subtilis 1423 -11529186 94955 rplu (de:50s ribosomal protein l21 (bl20)) (db:swissprot) RL21_BACSU P26908 BACILLUS SUBTILIS 1423 -11529186 148952 rplu ribosomal protein l21:ribosomal protein bl20:rplu (cl:escherichia coli ribosomal protein l21) (db:pir) S18439 S18439 Bacillus subtilis 1423 -11529186 6500725328 ribosomal protein l21:50s ribosomal protein l21:bl20 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplU rplU Bacillus subtilis 1423 -11529186

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747573	1372	23528	696	232

Description

GTC ORF with score 244 to: (or:Arabidopsis thaliana) (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana bac t12h20.) (nt:similar to schizosaccharomyces pombe isp4 protein) (le:11336:11441:11976:12205) (re:11366:11839:12130:12302) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747578	1373	23529	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747659	1374	23530	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747661	1375	23531	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747676	1376	23532	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747681	1377	23533	882	293

Description

6500725329 ribosomal protein l20:50s ribosomal protein l20 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplT rplT Bacillus subtilis 1423 -11529187 1500687261 rplt (de:50s ribosomal protein l20) (db:swissprot) RL20_BACSU P55873 BACILLUS SUBTILIS 1423 -11529187 7000686363 rplt ribosomal protein l20 rplt (cl:escherichia coli ribosomal protein l20) (db:pir2.dat) F69696 F69696 Bacillus subtilis 1423 -11529187 220285 rplt ribosomal protein l20 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:156202) (re:156561) (di:complement) BSUB0015 Z99118 g2635350 Bacillus subtilis 1423 -11529187 304158 rplt ribosomal protein l20 (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to rplt of bacillus stearothermphilus;) (le:13346) (re:13705) (di:direct) BSZ75208 Z75208 g1770009 Bacillus subtilis 1423 -11529187

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747689	1378	23534	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747691	1379	23535	819	272

Description

6500725330 ribosomal protein l35:50s ribosomal protein l35 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmI rpmI Bacillus subtilis 1423 -11529188 7000694529 rpmi ribosomal protein l35 rpmi (cl:escherichia coli ribosomal protein l35) (db:pir2.dat) C69698 C69698 Bacillus subtilis 1423 -11529188 220284 rpmi ribosomal protein l35 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:156593) (re:156793) (di:complement) BSUB0015 Z99118 g2635351 Bacillus subtilis 1423 -11529188 304157 rpmi ribosomal protein l35 (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to rpmi of bacillus stearothermophilus;) (le:13114) (re:13314) (di:direct) BSZ75208 Z75208 g1770008 Bacillus subtilis 1423 -11529188

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747695	1380	23536	495	164

Description

GTC ORF with score 143 to: (fn:actin patch assembly and localization) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe wiskott-aldrich syndrome protein homolog(wsp1+) gene, complete cds, and btf3/beta-nac gene, partialsequence.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747698	1381	23537	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747703	1382	23538	882	293

Description

6500725331 ribosomal protein s4:30s ribosomal protein s4:bs4 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsD rpsD Bacillus subtilis 1423 -11529189 7000689310 rpsd ribosomal protein s4:ribosomal protein bs4 rpsd (cl:escherichia coli ribosomal protein s4) (db:pir2.dat) A37146 A37146 Bacillus subtilis 1423 -11529189 7500954796 rpsd ribosomal protein s4 (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:142790) (re:143392) (di:complement) AF008220 AF008220 g2293319 Bacillus subtilis 1423 -11529189 216647 rpsd ribosomal protein s4 (sr:b.subtilis (strain 168, isolate br151) dna) (db:genpept-bct1) (de:b.subtilis ribosomal protein s4 gene, complete cds and tyrosyl trnasynthetase (tyrs) gene, 3' end.) (le:756) (re:1358) (di:direct) BACRPSD M59358 g143467 Bacillus subtilis 1423 -11529189 4000710140 rpsd ribosomal protein s4 bs4 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:37035) (re:37637) (di:direct) BSUB0016 Z99119 g2635450 Bacillus subtilis 1423 -11529189 148363 rpsd ribosomal protein s4:ribosomal protein bs4 rpsd (cl:escherichia coli ribosomal protein s4) (db:pir) A37146 A37146 Bacillus subtilis 1423 -11529189

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747711	1383	23539	351	116

Description

GTC ORF with score 96 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f20o9 (essaiiproject).) (nt:contains est gb:r29877) (le:51619:52266:53037) (re:51815:52440:53198) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747721	1384	23540	588	195

Description

5000688596 ribosomal protein l31:50s ribosomal protein l31 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmE rpmE Bacillus subtilis 1423 -11529190 6000685112 rpme (de:50s ribosomal protein l31) (db:swissprot) RL31_BACSU Q03223 BACILLUS SUBTILIS 1423 -11529190 129153 rpme ribosomal protein l31 (cl:escherichia coli ribosomal protein l31) (db:pir1.dat) S55431 S55431 Bacillus subtilis 1423 -11529190 216591 rpme ribosomal protein l31 (sr:bacillus subtilis (transposon tn917 insertional library) dna) (db:genpept-bct1) (de:bacillus subtilis orfr, 3' end; orfq; transcriptional terminator(rho) gene; ribosomal protein l31; thymidine kinase (tdk) gene,complete cds.) (le:3045) (re:3245) (d... BACRHOTDKX M97678 g143435 Bacillus subtilis 1423 -11529190 6500725332 rpme ribosomal protein l31 (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (le:18497) (re:18697) (di:direct) BSDNA320D Z49782 g853770 Bacillus subtilis 1423 -11529190 219147 rpme ribosomal protein l31 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:205046) (re:205246) (di:complement) BSUB0019 Z99122 g2636232 Bacillus subtilis 1423 -11529190 304119 rpme ribosomal protein l31 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:3736) (re:3936) (di:complement) BSUB0020 Z99123 g2636244 Bacillus subtilis 1423 -11529190 95144 rpme (de:50s ribosomal protein l31) (db:swissprot) RL31_BACSU Q03223 BACILLUS SUBTILIS 1423 -11529190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747805	1385	23541	402	133

Description

GTC ORF with score 520 to: (db:genpept-pln1) (ec:4.2.99.10) (de:emericella nidulans o-acetyl-l-homoserine sulfhydrylase (cysd)gene, complete cds.) (nt:homocysteine synthase) (le:364:470:583:729:1137) (re:413:524:666:1088:1705) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747811	1386	23542	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747815	1387	23543	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747847	1388	23544	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747849	1389	23545	858	285

Description

5000688579 ribosomal protein l9:50s ribosomal protein l9:bl17 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplI rplI Bacillus subtilis 1423 -11529191 95493 rpli (de:50s ribosomal protein l9 (bl17)) (db:swissprot) RL9_BACSU P37437 BACILLUS SUBTILIS 1423 -11529191 7000686409 rpli ribosomal protein l9 rpli (cl:escherichia coli ribosomal protein l9) (db:pir2.dat) S65975 S65975 Bacillus subtilis 1423 -11529191 7500890361 rpli ribosomal protein l9 (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:11193) (re:11642) (di:complement) BAC180K D26185 g467335 Bacillus subtilis 1423 -11529191 214935 rpli ribosomal protein l9 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:163125) (re:163574) (di:complement) BSUB0021 Z99124 g2636597 Bacillus subtilis 1423 -11529191 206276 rpli ribosomal protein l9 rpli (cl:escherichia coli ribosomal protein l9) (db:pir) S65975 S65975 Bacillus subtilis 1423 -11529191 6500725333 ribosomal protein l9:50s ribosomal protein l9:bl17 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rplI rplI Bacillus subtilis 1423 -11529191

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747856	1390	23546	273	91

Description

6500725334 ribosomal protein s18:30s ribosomal protein s18:bs21 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsR rpsR Bacillus subtilis 1423 -11529192 7000689314 rpsr ribosomal protein s18 rpsr:ribosomal protein bs21 (cl:escherichia coli ribosomal protein s18) (db:pir2.dat) S66013 S66013 Bacillus subtilis 1423 -11529192 7500954851 rpsr ribosomal protein s18 (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:46599) (re:46844) (di:complement) BAC180K D26185 g467373 Bacillus subtilis 1423 -11529192 214973 rpsr ribosomal protein s18 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:198531) (re:198776) (di:complement) BSUB0021 Z99124 g2636636 Bacillus subtilis 1423 -11529192 206277 rpsr ribosomal protein s18 rpsr:ribosomal protein bs21 (cl:escherichia coli ribosomal protein s18) (db:pir) S66013 S66013 Bacillus subtilis 1423 -11529192

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747993	1391	23547	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501747999	1392	23548	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748003	1393	23549	468	155

Description

GTC ORF with score 315 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c28h8.) (nt:similar to yeast antiviral protein ski2 and) (le:26085:26897:27388:28779) (re:26850:27339:28734:29002) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748004	1394	23550	618	206

Description

GTC ORF with score 193 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c28h8.) (nt:similar to yeast antiviral protein ski2 and) (le:26085:26897:27388:28779) (re:26850:27339:28734:29002) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748022	1395	23551	345	114

Description

5000688604 ribosomal protein s6:30s ribosomal protein s6:bs9 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsF rpsF Bacillus subtilis 1423 -11529193 97358 rpsf (de:30s ribosomal protein s6 (bs9)) (db:swissprot) RS6_BACSU P21468 BACILLUS SUBTILIS 1423 -11529193 7000686513 rpsf ribosomal protein s6 bs9 rpsf:ribosomal protein bs9 (cl:escherichia coli ribosomal protein s6) (db:pir2.dat) S66015 S66015 Bacillus subtilis 1423 -11529193 7500891082 rpsf ribosomal protein s6 (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:47441) (re:47728) (di:complement) BAC180K D26185 g467375 Bacillus subtilis 1423 -11529193 214975 rpsf ribosomal protein s6 bs9 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:199373) (re:199660) (di:complement) BSUB0021 Z99124 g2636638 Bacillus subtilis 1423 -11529193 206278 rpsf ribosomal protein s6 bs9 rpsf:ribosomal protein bs9 (cl:escherichia coli ribosomal protein s6) (db:pir) S66015 S66015 Bacillus subtilis 1423 -11529193 6500725335 ribosomal protein s6:30s ribosomal protein s6:bs9 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpsF rpsF Bacillus subtilis 1423 -11529193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748031	1396	23552	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748045	1397	23553	1188	396

Description

5000688598 ribosomal protein l34:50s ribosomal protein l34 (gtcfc:10.4) (keggfc:14.2) (bsorffc:4.3.2) (db:gtc-bacillus subtilis) rpmH rpmH Bacillus subtilis 1423 -11529194 219457 rpmh (de:50s ribosomal protein l34) (db:swissprot) RL34_BACSU P05647 BACILLUS SUBTILIS 1423 -11529194 129192 rpmh ribosomal protein l34 (cl:escherichia coli ribosomal protein l34) (db:pir1.dat) R6BS34 I40435 Bacillus subtilis 1423 -11529194 214990 rpmh ribosomal protein l34 (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:63251) (re:63385) (di:complement) BAC180K D26185 g467390 Bacillus subtilis 1423 -11529194 219450 (db:genpept-bct1) (de:bacillus subtilis oric region.) (nt:pot. orf 44 (aa 1-44)) (le:425) (re:559) (di:complement) BSORIC X02369 g40013 Bacillus subtilis 1423 -11529194 7500890219 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:homologous to e.coli rpmh) (le:15) (re:149) (di:direct) BSORIGS X62539 g40021 Bacillus subtilis 1423 -11529194 6500725336 rpmh ribosomal protein l34 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:215183) (re:215317) (di:complement) BSUB0021 Z99124 g2636653 Bacillus subtilis 1423 -11529194 95192 rpmh (de:50s ribosomal protein l34) (db:swissprot) RL34_BACSU P05647 BACILLUS SUBTILIS 1423 -11529194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748054	1398	23554	1170	390

Description

6500725337 trna methyltransferase (gtcfc:10.6) (ec:2.1.1.31) (keggfc:14.1) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) trmD trmD Bacillus subtilis 1423 -11529195 7502851589 trmd (ec:2.1.1.31) (de:methyltransferase) (trna (gm37) methyltransferase)) (db:swissprot) TRMD_BACSU O31741 BACILLUS SUBTILIS 1423 -11529195 7000694832 trmd trna methyltransferase trmd (cl:trna (guanine-n1) methyltransferase) (db:pir2.dat) F69725 F69725 Bacillus subtilis 1423 -11529195 7500965383 trmd trna methyltransferase (db:genpept-bct1) (ec:2.1.1.31) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:76150) (re:76881) (di:direct) BSUB0009 Z99112 g2633975 Bacillus subtilis 1423 -11529195

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748059	1399	23555	402	133

Description

6500725338 ylxn:ymxf:trub trna pseudouridine 55 synthase (gtcfc:10.6) (keggfc:14.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) truB truB Bacillus subtilis 1423 -11529196 7500893520 trub (ec:4.2.1.70) (de:hydrolyase)) (db:swissprot) TRUB_BACSU P32732 BACILLUS SUBTILIS 1423 -11529196 7000694833 trub trna pseudouridine 5s synthase trub:p35 homolog (cl:escherichia coli protein p35) (db:pir2.dat) G69726 G69726 Bacillus subtilis 1423 -11529196 7500893522 trub trna pseudouridine 55 synthase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylxn, ymxf) (le:137857) (re:138786) (di:direct) BSUB0009 Z99112 g2634038 Bacillus subtilis 1423 -11529196

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748064	1400	23556	327	108

Description

6500725339 trna isopentenylpyrophosphate transferase (gtcfc:10.6) (ec:2.5.1.8) (keggfc:14.1) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) miaA miaA Bacillus subtilis 1423 -11529197 7000694831 miaa trna isopentenylpyrophosphate transferase miaa (cl:delta(2)-isopentenylpyrophosphate transferase) (db:pir2.dat) G69657 G69657 Bacillus subtilis 1423 -11529197 7500965382 miaa trna isopentenylpyrophosphate transferase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:84430) (re:85374) (di:direct) BSUB0010 Z99113 g2634117 Bacillus subtilis 1423 -11529197

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748066	1401	23557	1161	387

Description

6500725340 yqfk:glys glycyl-trna synthetase:beta subunit:glycyl-trna synthetase beta chain:glycine--trna ligase beta chain:glyrs (gtcfc:10.6) (ec:6.1.1.14) (keggfc:14.1) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) glyS glyS Bacillus subtilis 1423 -11529198 100047 glys (ec:6.1.1.14) (de:beta chain) (glyrs)) (db:swissprot) SYGB_BACSU P54381 BACILLUS SUBTILIS 1423 -11529198 7000686716 glys glycine--trna ligase:beta chain glys:glycyl-trna synthetase beta chain (cl:glycine--trna ligase beta chain) (ec:6.1.1.14) (db:pir2.dat) B69636 B69636 Bacillus subtilis 1423 -11529198 216073 yqfk (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:111835) (re:113874) (di:direct) BACJH642 D84432 g1303829 Bacillus subtilis 1423 -11529198 6000685246 glys glycyl-trna synthetase beta subunit (db:genpept-bct1) (ec:6.1.1.14) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqfk) (le:209746) (re:211785) (di:complement) BSUB0013 Z99116 g2634958 Bacillus subtilis 1423 -11529198 7500892410 glys glycyl-trna synthetase beta subunit (db:genpept-bct1) (ec:6.1.1.14) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqfk) (le:5556) (re:7595) (di:complement) BSUB0014 Z99117 g2634972 Bacillus subtilis 1423 -11529198 5000689453 (de:(glys) (pn:glycyl-trna synthetase beta chain:glycine--trna ligase beta chain:glyrs) (gtcfc:13.07) (ec:6.1.1.14) (sygb_bacsu) (keggfc:5.3:10.1:10.2) (db:gtc-bacillus subtilis)) glyS glyS Bacillus subtilis 1423 10041901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748074	1402	23558	396	131

Description

6500725341 yqfj:glyq glycyl-trna synthetase:alpha subunit:glycyl-trna synthetase alpha chain:glycine--trna ligase alpha chain:glyrs (gtcfc:10.6) (ec:6.1.1.14) (keggfc:14.1) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) glyQ glyQ Bacillus subtilis 1423 -11529199 100044 glyq (ec:6.1.1.14) (de:alpha chain) (glyrs)) (db:swissprot) SYGA_BACSU P54380 BACILLUS SUBTILIS 1423 -11529199 7000686714 glyq glycine--trna ligase:alpha chain glyq:glycyl-trna synthetase alpha chain (cl:glycine--trna ligase alpha chain) (ec:6.1.1.14) (db:pir2.dat) A69636 A69636 Bacillus subtilis 1423 -11529199 216072 yqfj (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:110955) (re:111842) (di:direct) BACJH642 D84432 g1303828 Bacillus subtilis 1423 -11529199 6000685244 glyq glycyl-trna synthetase alpha subunit (db:genpept-bct1) (ec:6.1.1.14) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqfj) (le:211778) (re:212665) (di:complement) BSUB0013 Z99116 g2634959 Bacillus subtilis 1423 -11529199 7500892403 glyq glycyl-trna synthetase alpha subunit (db:genpept-bct1) (ec:6.1.1.14) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqfj) (le:7588) (re:8475) (di:complement) BSUB0014 Z99117 g2634973 Bacillus subtilis 1423 -11529199 5000689452 (de:(glyq) (pn:glycyl-trna synthetase alpha chain:glycine--trna ligase alpha chain:glyrs) (gtcfc:13.07) (ec:6.1.1.14) (syga_bacsu) (keggfc:5.3:10.1:10.2) (db:gtc-bacillus subtilis)) glyQ glyQ Bacillus subtilis 1423 10041898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748077	1403	23559	270	89

Description

6500725342 trna-guanine transglycosylase (gtcfc:10.6) (ec:2.4.2.29) (keggfc:14.1) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) tgt tgt Bacillus subtilis 1423 -11529200 7500893006 tgt (ec:2.4.2.29) (de:transglycosylase) (guanine insertion enzyme)) (db:swissprot) TGT_BACSU O32053 BACILLUS SUBTILIS 1423 -11529200 7000694834 tgt queuine trna-ribosyltransferase (cl:queuine trna-ribosyltransferase) (ec:2.4.2.29) (db:pir2.dat) B69722 B69722 Bacillus subtilis 1423 -11529200 7500893008 tgt trna-guanine transglycosylase (fn:queuosine biosynthesis) (db:genpept-bct1) (ec:2.4.2.29) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:36858) (re:38003) (di:complement) BSUB0015 Z99118 g2635236 Bacillus subtilis 1423 -11529200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748078	1404	23560	354	117

Description

6500725343 s-adenosylmethionine trna ribosyltransferase (gtcfc:10.6) (ec:5.-.-.-) (keggfc:14.1) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) queA queA Bacillus subtilis 1423 -11529201 7502851590 quea (ec:5.-.-.-) (de:(queuosine biosynthesis protein quea)) (db:swissprot) QUEA_BACSU O32054 BACILLUS SUBTILIS 1423 -11529201 7000694570 quea s-adenosylmethionine:trna ribosyltransferase-isomerase::queuosine biosynthesis-related protein quea (cl:s-adenosylmethionine:trna ribosyltransferase-isomerase) (ec:5.-.-.-) (db:pir2.dat) A69688 A69688 Bacillus subtilis 1423 -11529201 7500965170 quea s-adenosylmethionine trna ribosyltransferase (fn:queuosine biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:38030) (re:39058) (di:complement) BSUB0015 Z99118 g2635237 Bacillus subtilis 1423 -11529201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748092	1405	23561	189	62

Description

6500725344 histidyl-trna synthetase (gtcfc:10.6) (keggfc:14.2) (bsorffc:4.3.1) (db:gtc-bacillus subtilis) hisZ hisZ Bacillus subtilis 1423 -11529202 7000693100 hisz histidine--trna ligase:hisz:histidyl-trna synthetase (ec:6.1.1.21) (db:pir2.dat) H69641 H69641 Bacillus subtilis 1423 -11529202 5500701770 hisz histidyl-trna synthetase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:187695) (re:188870) (di:complement) BSUB0018 Z99121 g2636006 Bacillus subtilis 1423 -11529202 7500964052 hiss histidyl-trna synthetase (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:38963) (re:40138) (di:direct) AF017113 AF017113 g2618864 Bacillus subtilis 1423 -11529202

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748197	1406	23562	567	188

Description

6500725345 fusa:fus elongation factor g:ef-g:vegetative protein 19:veg19 (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) fus fus Bacillus subtilis 1423 -11529203 7000692956 fus translation elongation factor ef-g fus (cl:translation elongation factor g:translation elongation factor tu homology) (db:pir2.dat) B69628 B69628 Bacillus subtilis 1423 -11529203 222752 fus elongation factor g (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:130683) (re:132761) (di:direct) BSUB0001 Z99104 g2632379 Bacillus subtilis 1423 -11529203 7500955431 fus elongation factor g (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for rna polymerase beta subunit, ribosomalproteins l12 and s7, elongation factors g and tu and ribosomalproteins s10 and l3, partial and complete cds.) (le:3771) (re:... D64127 D64127 g1644223 Bacillus subtilis 1423 -11529203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748198	1407	23563	291	96

Description

5000688641 elongation factor tu:ef-tu (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) tufA tufA Bacillus subtilis 1423 -11529204 69892 tufa (de:elongation factor tu (ef-tu) (p-40)) (db:swissprot) EFTU_BACSU P33166 BACILLUS SUBTILIS 1423 -11529204 7000685144 tufa translation elongation factor ef-tu tufa (cl:translation elongation factor tu:translation elongation factor tu homology) (db:pir2.dat) A60663 A60663 Bacillus subtilis 1423 -11529204 7500880954 tufa elongation factor tu (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:132881) (re:134071) (di:direct) BSUB0001 Z99104 g2632380 Bacillus subtilis 1423 -11529204 222753 tufa elongation factor tu (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for rna polymerase beta subunit, ribosomalproteins l12 and s7, elongation factors g and tu and ribosomalproteins s10 and l3, partial and complete cds.) (le:5969) (re:... D64127 D64127 g1644224 Bacillus subtilis 1423 -11529204 154157 tufa translation elongation factor ef-tu tufa (cl:translation elongation factor tu:translation elongation factor tu homology) (db:pir) A60663 A60663 Bacillus subtilis 1423 -11529204 6500725346 elongation factor tu:ef-tu (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) tufA tufA Bacillus subtilis 1423 -11529204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748215	1408	23564	675	224

Description

6500725347 methionine aminopeptidase:map:peptidase m (gtcfc:10.7) (ec:3.4.11.18) (keggfc:14.1) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) map map Bacillus subtilis 1423 -11529205 59381 map (ec:3.4.11.18) (de:methionine aminopeptidase, (map) (peptidase m)) (db:swissprot) AMPM_BACSU P19994 BACILLUS SUBTILIS 1423 -11529205 7000684574 map methionyl aminopeptidase:map (cl:escherichia coli methionyl aminopeptidase) (ec:3.4.11.18) (db:pir2.dat) JS0493 JS0493 Bacillus subtilis 1423 -11529205 7500876846 map methionine aminopeptidase (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044986 Bacillus subtilis 1423 -11529205 216698 map methionine aminopeptidase (db:genpept-bct1) (ec:3.4.11.18) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:146525) (re:147271) (di:direct) BSUB0001 Z99104 g2632405 Bacillus subtilis 1423 -11529205 216629 methionine amino peptidase (sr:bacillus subtilis (strain:207-21) dna) (db:genpept-bct2) (de:bacillus subtilis genes for ribosomal proteins, secy, adenylatekinase and methionine amino peptidase, complete cds.) (le:2705) (re:3451) (di:direct) BACSECY D00619 g216341 Bacillus subtilis 1423 -11529205 140292 map methionyl aminopeptidase:map (cl:escherichia coli methionyl aminopeptidase) (ec:3.4.11.18) (db:pir) JS0493 JS0493 Bacillus subtilis 1423 -11529205 5000688635 (de:(map) (pn:methionine aminopeptidase:map:peptidase m:methionine aminopeptidase :map) (gtcfc:10.07) (ec:3.4.11.18) (ampm_bacsu) (keggfc:11.1) (bsorffc:4.3.3) (db:gtc-bacillus subtilis)) map map Bacillus subtilis 1423 10002118

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748234	1409	23565	231	76

Description

6500725348 initiation factor if-i:translation initiation factor if-1 (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) infA infA Bacillus subtilis 1423 -11529206 7000694108 infa translation initiation factor if-1 (cl:translation initiation factor if-1) (db:pir2.dat) F69644 F69644 Bacillus subtilis 1423 -11529206 215148 infa initiation factor 1 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis initiation factor 1, ribosomal proteins b, s13, s11, l17and rna polymerase alpha core protein genes, complete cds.) (le:235) (re:453) (di:direct) BACALPHA M26414 g142459 Bacillus subtilis 1423 -11529206 216630 infa initiation factor if-1 (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044987 Bacillus subtilis 1423 -11529206 7500955443 infa initiation factor if-i (fn:protein synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:147583) (re:147801) (di:direct) BSUB0001 Z99104 g2632406 Bacillus subtilis 1423 -11529206

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748235	1410	23566	276	91

Description

5000688642 ycsb:sipu type i signal peptidase:signal peptidase i u:spase i:leader peptidase i (gtcfc:11.1:10.7) (ec:3.4.21.89) (keggfc:14.1) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) sipU sipU Bacillus subtilis 1423 -11529207 110898 sipu (ec:3.4.21.89) (de:signal peptidase i u, (spase i) (leader peptidase i)) (db:swissprot) LEPU_BACSU P42959 BACILLUS SUBTILIS 1423 -11529207 7000685730 sipu signal peptidase i sipu (cl:signal peptidase i sips) (db:pir2.dat) I39890 I39890 Bacillus subtilis 1423 -11529207 7500884930 another sips of b. subtilis (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:4532) (re:5095) (di:direct) BAC39R D38161 g790941 Bacillus subtilis 1423 -11529207 215094 sipu type i signal peptidase (db:genpept-bct1) (ec:3.4.21.89) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ycsb) (le:50842) (re:51405) (di:direct) BSUB0003 Z99106 g2632702 Bacillus subtilis 1423 -11529207 222664 sipu signal peptidase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:133240) (re:133803) (di:direct) D50453 D50453 g1805470 Bacillus subtilis 1423 -11529207 170546 sipu signal peptidase i sipu (db:pir) I39890 I39890 Bacillus subtilis 1423 -11529207 6500725349 ycsb type i signal peptidase:signal peptidase i u:spase i:leader peptidase i (gtcfc:11.1:10.7) (ec:3.4.21.89) (keggfc:14.1) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) sipU sipU Bacillus subtilis 1423 -11529207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748237	1411	23567	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748246	1412	23568	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748256	1413	23569	795	264

Description

6500725350 yhjf:sipv type i signal peptidase (gtcfc:11.1:10.7) (ec:3.4.21.89) (keggfc:14.1) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) sipV sipV Bacillus subtilis 1423 -11529208 7000694584 sipv signal peptidase i sipv (cl:signal peptidase i sips) (db:pir2.dat) A69708 A69708 Bacillus subtilis 1423 -11529208 4000714590 sipv type i signal peptidase (db:genpept-bct1) (ec:3.4.21.89) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yhjf) (le:122148) (re:122654) (di:direct) BSUB0006 Z99109 g2633385 Bacillus subtilis 1423 -11529208 7500965184 yhjf hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to signal peptidase i, like sipc from) (le:4443) (re:4949) (di:direct) BSY14081 Y14081 g2226178 Bacillus subtilis 1423 -11529208 7502851591 yhjf hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to signal peptidase i, like sipc from) (le:4443) (re:4949) (di:direct) BSY14081 Y14081 g2226178 Bacillus subtilis 1423 -11529208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748260	1414	23570	192	63

Description

6500725351 type i signal peptidase (gtcfc:11.1:10.7) (ec:3.4.21.89) (keggfc:14.1) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) sipT sipT Bacillus subtilis 1423 -11529209 7502851592 sipt (ec:3.4.21.89) (de:signal peptidase i t, (spase i) (leader peptidase i)) (db:swissprot) LEPT_BACSU P71013 BACILLUS SUBTILIS 1423 -11529209 7000694583 sipt signal peptidase i sipt (cl:signal peptidase i sips) (db:pir2.dat) G69707 G69707 Bacillus subtilis 1423 -11529209 7500965183 sipt signal peptidase i t (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to b. amyloliquifaciens signal peptidase i,) (le:16411) (re:16992) (di:direct) AF012285 AF012285 g3282126 Bacillus subtilis 1423 -11529209 220019 sipt sipt (sr:bacillus subtilis strain=168) (db:genpept-bct1) (de:bacillus subtilis fructose specific enzyme ii (frua) gene, partialcds, type i signal peptidase (sipt) gene, complete cds.) (nt:type i signal peptidase) (le:217) (re:798) (di:direct) BSU45883 U45883 g1518930 Bacillus subtilis 1423 -11529209 7500965182 sipt type i signal peptidase (db:genpept-bct1) (ec:3.4.21.89) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:115923) (re:116504) (di:direct) BSUB0008 Z99111 g2633812 Bacillus subtilis 1423 -11529209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748261	1415	23571	867	288

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748274	1416	23572	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748275	1417	23573	336	111

Description

6500725352 lspa:lsp lipoprotein signal peptidase:prolipoprotein signal peptidase:signal peptidase ii:spase ii (gtcfc:11.2) (ec:3.4.23.36) (keggfc:14.1) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) lsp lsp Bacillus subtilis 1423 -11529210 119889 lspa:lsp (ec:3.4.23.36) (de:peptidase) (signal peptidase ii) (spase ii)) (db:swissprot) LSPA_BACSU Q45479 BACILLUS SUBTILIS 1423 -11529210 7000685766 lsp lipoprotein signal peptidase::signal peptidase ii lsp (cl:lipoprotein signal peptidase) (ec:3.4.23.36) (db:pir2.dat) G69653 G69653 Bacillus subtilis 1423 -11529210 220035 lsp spase ii (db:genpept-bct1) (de:bacillus subtilis signal peptidase ii (lsp) gene, complete cds,isoleucyl-trna synthetase (iles) and pyrr genes, partial cds.) (nt:signal peptidase ii) (le:1192) (re:1656) (di:direct) BSU48870 U48870 g1373156 Bacillus subtilis 1423 -11529210 7500885169 lsp signal peptidase ii (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: lspa) (le:17727) (re:18191) (di:direct) BSUB0009 Z99112 g2633918 Bacillus subtilis 1423 -11529210

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748277	1418	23574	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748285	1419	23575	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748427	1420	23576	705	234

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748436	1421	23577	783	260

Description

6500725353 srb:ftsy signal recognition particle:docking protein:cell division protein ftsy homolog (gtcfc:11.3:12.8) (keggfc:14.2) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) ftsY ftsY Bacillus subtilis 1423 -11529211 7500965185 ftsy signal recognition particle docking protein (fn:involved in secretion of extracellular proteins) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: srb) (le:71119) (re:72108) (di:direct) BSUB0009 Z99112 g2633967 Bacillus subtilis 1423 -11529211 7000694585 ftsy signal recognition particle ftsy (db:pir) H69627 H69627 Bacillus subtilis 1423 -11529211

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748443	1422	23578	831	276

Description

6500725354 dna processing smf protein homolog (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) smf smf Bacillus subtilis 1423 -11529212 7500963953 smf (de:smf protein) (db:swissprot) SMF_BACSU P39813 BACILLUS SUBTILIS 1423 -11529212 7000692941 smf dna processing smf protein homolog smf (db:pir2.dat) H69708 H69708 Bacillus subtilis 1423 -11529212 5500687817 smf dna processing smf protein homolog (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:83559) (re:84452) (di:direct) BSUB0009 Z99112 g2633983 Bacillus subtilis 1423 -11529212 7502851593 smf smf protein (db:genpept-bct1) (de:bacillus subtilis ylqg to codv gene region.) (le:2727) (re:3620) (di:direct) BSYLQGCOD AJ000975 g2462969 Bacillus subtilis 1423 -11529212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748445	1423	23579	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748456	1424	23580	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748457	1425	23581	528	175

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748465	1426	23582	219	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748488	1427	23583	1449	483

Description

GTC ORF with score 231 to: (fn:synthesis of type 3 pneumococcal capsule) (db:genpept-bct1) (de:s.pneumoniae dexb, cap3a, cap3b and cap3c genes and orfs.) (nt:expression and characterization of this gene has) (le:7111) (re:8364) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748503	1428	23584	1284	428

Description

6500725355 elongation factor ts (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) tsf tsf Bacillus subtilis 1423 -11529213 7000692957 tsf translation elongation factor ef-ts tsf (cl:translation elongation factor ef-ts) (db:pir2.dat) B69727 B69727 Bacillus subtilis 1423 -11529213 7500955435 tsf elongation factor ts (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:119747) (re:120628) (di:direct) BSUB0009 Z99112 g2634022 Bacillus subtilis 1423 -11529213

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748510	1429	23585	876	292

Description

6500725356 initiation factor if-2:translation initiation factor if-2 (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) infB infB Bacillus subtilis 1423 -11529214 7500955428 infb initiation factor if-2 (fn:protein synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:134980) (re:137130) (di:direct) BSUB0009 Z99112 g2634035 Bacillus subtilis 1423 -11529214 7000694109 infb initiation factor if-2 infb (cl:translation initiation factor if-2:translation elongation factor tu homology) (db:pir) G69644 G69644 Bacillus subtilis 1423 -11529214

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748644	1430	23586	528	175

Description

6500725357 ymxe:ylxo:rbfa ribosome-binding factor a:p15b protein (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) rbfA rbfA Bacillus subtilis 1423 -11529215 7500889411 rbfa (de:ribosome-binding factor a (p15b protein)) (db:swissprot) RBFA_BACSU P32731 BACILLUS SUBTILIS 1423 -11529215 7000686278 rbfa ribosome-binding factor a rbfa (cl:escherichia coli protein p15b) (db:pir2.dat) G36905 G36905 Bacillus subtilis 1423 -11529215 5000688639 orf6 (db:genpept-bct1) (de:b.subtilis infb-nusa operon.) (le:5131) (re:5484) (di:direct) BSORF1T7A Z18631 g580902 Bacillus subtilis 1423 -11529215 219446 rbfa ribosome-binding factor a (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymxe, ylxo) (le:137422) (re:137775) (di:direct) BSUB0009 Z99112 g2634037 Bacillus subtilis 1423 -11529215 93164 rbfa (de:ribosome-binding factor a (p15b protein)) (db:swissprot) RBFA_BACSU P32731 BACILLUS SUBTILIS 1423 -11529215 157254 rbfa ribosome-binding factor a rbfa (cl:escherichia coli protein p15b) (db:pir) G36905 G36905 Bacillus subtilis 1423 -11529215

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748656	1431	23587	396	131

Description

GTC ORF with score 130 to: (fn:high copy suppressor of cgs1-10 putative) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe rs6/17a ribosomal protein homolog (rph1)gene, complete cds.) (le:54:222) (re:71:581) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748657	1432	23588	246	81

Description

GTC ORF with score 194 to: (fn:high copy suppressor of cgs1-10 putative) (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe rs6/l7a ribosomal protein homolog (rph1)gene, complete cds.) (le:54:222) (re:71:581) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748667	1433	23589	345	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748671	1434	23590	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748676	1435	23591	1122	374

Description

6500725358 peptide synthetase (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) ppsE ppsE Bacillus subtilis 1423 -11529216 7000694361 ppse peptide synthetase ppse (cl:peptide synthetase ppse:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) E69681 E69681 Bacillus subtilis 1423 -11529216 7500955887 ppse peptide synthetase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:178253) (re:182092) (di:complement) BSUB0010 Z99113 g2634213 Bacillus subtilis 1423 -11529216

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748687	1436	23592	924	307

Description

6500725359 peptide synthetase (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) ppsD ppsD Bacillus subtilis 1423 -11529217 7000694360 ppsd peptide synthetase ppsd (cl:surfactin synthetase:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) D69681 D69681 Bacillus subtilis 1423 -11529217 219526 pps4 peptide synthetase orf4 (db:genpept-bct1) (de:b.subtilis genes for peptide synthetase and penicillin bindingprotein.) (le:25122) (re:35933) (di:direct) BSPEPSYN Z34883 g1805669 Bacillus subtilis 1423 -11529217 7500955888 ppsd peptide synthetase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:182100) (re:192911) (di:complement) BSUB0010 Z99113 g2634214 Bacillus subtilis 1423 -11529217

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748692	1437	23593	456	152

Description

6500725360 cypbs:ppib peptidyl-prolyl isomerase:peptidyl-prolyl cis-trans isomerase b:ppiase b:rotamase b (gtcfc:10.7) (ec:5.2.1.8) (keggfc:14.1) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) ppiB ppiB Bacillus subtilis 1423 -11529218 215498 ppib (ec:5.2.1.8) (de:(rotamase b)) (db:swissprot) CYPB_BACSU P35137 BACILLUS SUBTILIS 1423 -11529218 7000684964 ppib peptidylprolyl isomerase:ppib (cl:peptidylprolyl isomerase) (ec:5.2.1.8) (db:pir2.dat) (mp:210 (degrees)) S45537 S45537 Bacillus subtilis 1423 -11529218 7500879875 ppib peptidyl-prolyl isomerase (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:3819) (re:4250) (di:direct) BACDIA L09228 g410119 Bacillus subtilis 1423 -11529218 5000688636 cypbs cis-trans isomerase (db:genpept-bct1) (de:b.subtilis cypbs gene for peptidyl-prolyl-cis-trans isomerase.) (le:1432) (re:1863) (di:direct) BSCYPB X73898 g580848 Bacillus subtilis 1423 -11529218 219121 ppib peptidyl-prolyl isomerase (db:genpept-bct1) (ec:5.2.1.8) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: cypbs) (le:39333) (re:39764) (di:complement) BSUB0013 Z99116 g2634771 Bacillus subtilis 1423 -11529218 67555 ppib (ec:5.2.1.8) (de:(rotamase b)) (db:swissprot) CYPB_BACSU P35137 BACILLUS SUBTILIS 1423 -11529218 142084 ppib peptidylprolyl isomerase:ppib (cl:peptidylprolyl isomerase) (ec:5.2.1.8) (db:pir) (mp:210 (degrees)) S45537 S45537 Bacillus subtilis 1423 -11529218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748701	1438	23594	540	179

Description

5000689339 yqhu:yqgf:efp elongation factor p:ef-p (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) efp efp Bacillus subtilis 1423 -11529219 69865 efp (de:elongation factor p (ef-p)) (db:swissprot) EFP_BACSU P49778 BACILLUS SUBTILIS 1423 -11529219 7000685141 efp translation elongation factor ef-p efp (cl:translation elongation factor ef-p) (db:pir2.dat) A69620 A69620 Bacillus subtilis 1423 -11529219 216146 yqhu (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:180933) (re:181490) (di:direct) BACJH642 D84432 g1303902 Bacillus subtilis 1423 -11529219 7500880939 efp elongation factor p (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqhu, yqgf) (le:142131) (re:142688) (di:complement) BSUB0013 Z99116 g2634879 Bacillus subtilis 1423 -11529219 6500725361 yqhu:yqgf elongation factor p:ef-p (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) efp efp Bacillus subtilis 1423 -11529219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748706	1439	23595	429	143

Description

5000689328 yqhe:sipw type i signal peptidase:hypothetical 20.7 kd protein in comgg-sinr intergenic region (gtcfc:11.1) (ec:3.4.21.89) (keggfc:14.2) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) sipW sipW Bacillus subtilis 1423 -11529220 115928 sipw (ec:3.4.21.89) (de:signal peptidase i w, (spase i) (leader peptidase i)) (db:swissprot) LEPW_BACSU P54506 BACILLUS SUBTILIS 1423 -11529220 7000688421 sipw signal peptidase i sipw (db:pir2.dat) B69708 B69708 Bacillus subtilis 1423 -11529220 216128 yqhe (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:165103) (re:165675) (di:direct) BACJH642 D84432 g1303884 Bacillus subtilis 1423 -11529220 7500884931 sipw type i signal peptidase (db:genpept-bct1) (ec:3.4.21.89) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqhe) (le:157946) (re:158518) (di:complement) BSUB0013 Z99116 g2634897 Bacillus subtilis 1423 -11529220 6500725362 yqhe type i signal peptidase:hypothetical 20.7 kd protein in comgg-sinr intergenic region (gtcfc:11.1) (ec:3.4.21.89) (keggfc:14.2) (bsorffc:4.3.3:6.4.1) (db:gtc-bacillus subtilis) sipW sipW Bacillus subtilis 1423 -11529220

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748708	1440	23596	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748711	1441	23597	339	112

Description

6500725363 initiation factor if-3:translation initiation factor if-3 (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) infC infC Bacillus subtilis 1423 -11529221 7000694110 infc translation initiation factor if-3 infc (cl:translation initiation factor if-3) (db:pir2.dat) H69644 H69644 Bacillus subtilis 1423 -11529221 220283 infc initiation factor if-3 (fn:protein synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:156806) (re:157327) (di:complement) BSUB0015 Z99118 g2635352 Bacillus subtilis 1423 -11529221 304156 infc translation initiation factor if3 (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to infc of bacillus stearothermophilus;) (le:12580) (re:13101) (di:direct) BSZ75208 Z75208 g1770007 Bacillus subtilis 1423 -11529221

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748722	1442	23598	240	79

Description

6500725364 peptide chain release factor 2 (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) prfB prfB Bacillus subtilis 1423 -11529222 7502851594 prfb (de:peptide chain release factor 2 (rf-2)) (db:swissprot) RF2_BACSU P28367 BACILLUS SUBTILIS 1423 -11529222 7000694358 prfb translation releasing factor rf-2:peptide chain release factor 2:prfb (cl:translation releasing factor) (db:pir1.dat) JN0146 H69681 Bacillus subtilis 1423 -11529222 5500687272 prfb peptide chain release factor 2 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:29109:30139) (re:30137:30210) (di:complementjoin) BSUB0019 Z99122 g2636055 Bacillus subtilis 1423 -11529222 5500687273 prfb release factor 2 (db:genpept-bct2) (de:bacillus subtilis release factor 2 (prfb) gene, complete cds.) (nt:orf3) (le:75:148) (re:146:1176) (di:directjoin) AF013188 AF013188 g2331287 Bacillus subtilis 1423 -11529222 7500953635 prfb putative peptide chain release factor rf-2 (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:83:156) (re:154:1184) (di:directjoin) AF017113 AF017113 g2618874 Bacillus subtilis 1423 -11529222 7502851595 prfb release factor 2 (db:genpept) (de:bacillus subtilis release factor 2 (prfb) gene, complete cds.) (nt:orf3; naturally occurring frame-shift) (le:75:148) (re:146:1176) (di:directjoin) AF013188 AF013188 g2331287 Bacillus subtilis 1423 -11529222

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748723	1443	23599	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748726	1444	23600	951	316

Description

5000688637 peptide chain release factor 1:rf-1 (gtcfc:10.7) (keggfc:14.2) (bsorffc:4.3.3) (db:gtc-bacillus subtilis) prfA prfA Bacillus subtilis 1423 -11529223 304125 prfa (de:peptide chain release factor 1 (rf-1)) (db:swissprot) RF1_BACSU P45872 BACILLUS SUBTILIS 1423 -11529223 154401 prfa:rf-1 translation releasing factor rf-1:peptide chain release factor 1 (cl:translation releasing factor) (db:pir1.dat) S55437 S55437 Bacillus subtilis 1423 -11529223 6500725365 prfa peptide chain release factor 1 (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:gtg start codon) (le:23623) (re:24693) (di:direct) BSDNA320D Z49782 g853776 Bacillus subtilis 1423 -11529223 219153 prfa peptide chain release factor 1 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:199050) (re:200120) (di:complement) BSUB0019 Z99122 g2636226 Bacillus subtilis 1423 -11529223 94085 prfa (de:peptide chain release factor 1 (rf-1)) (db:swissprot) RF1_BACSU P45872 BACILLUS SUBTILIS 1423 -11529223

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748731	1445	23601	537	178

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748732	1446	23602	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748737	1447	23603	204	67

Description

6500725366 dnah:dnaj:dnak:dnaa hypothetical protein:chromosomal replication initiator protein dnaa (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaA dnaA Bacillus subtilis 1423 -11529224 219451 dnaa:dnah (de:chromosomal replication initiator protein dnaa) (db:swissprot) DNAA_BACSU P05648 BACILLUS SUBTILIS 1423 -11529224 131305 dnaa replication initiation protein dnaa (cl:replication initiation protein dnaa) (db:pir1.dat) (mp:0) IQBSOC A22930 Bacillus subtilis 1423 -11529224 214991 dnaa initiation protein of replicaton (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:64012) (re:65352) (di:direct) BAC180K D26185 g467391 Bacillus subtilis 1423 -11529224 5000688644 (db:genpept-bct1) (de:bacillus subtilis oric region.) (nt:pot. orf 446 (aa 1-446)) (le:1186) (re:2526) (di:direct) BSORIC X02369 g40014 Bacillus subtilis 1423 -11529224 7500880389 dnaa (fn:initiation of chromosome replication (dna) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: dnah, dnaj, dnak) (le:410) (re:1750) (di:direct) BSUB0001 Z99104 g2632268 Bacillus subtilis 1423 -11529224 68823 dnaa:dnah (de:chromosomal replication initiator protein dnaa) (db:swissprot) DNAA_BACSU P05648 BACILLUS SUBTILIS 1423 -11529224

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748743	1448	23604	267	88

Description

5000688650 yaas:holb dna polymerase iii:delta subunit:hypothetical 37.6 kd protein in xpac-abrb intergenic region (gtcfc:10.8) (ec:2.7.7.7) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) holB holB Bacillus subtilis 1423 -11529225 109512 holb (ec:2.7.7.7) (de:dna polymerase iii, delta' subunit,) (db:swissprot) HOLB_BACSU P37540 BACILLUS SUBTILIS 1423 -11529225 7000687120 holb dna polymerase iii delta subunit holb:dnah homolog holb (db:pir2.dat) S66061 S66061 Bacillus subtilis 1423 -11529225 7500883459 similar to b. subtilis dnah (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:104265) (re:105254) (di:direct) BAC180K D26185 g467421 Bacillus subtilis 1423 -11529225 215021 holb dna polymerase iii delta subunit (db:genpept-bct1) (ec:2.7.7.7) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yaas) (le:40663) (re:41652) (di:direct) BSUB0001 Z99104 g2632298 Bacillus subtilis 1423 -11529225 206168 holb dna polymerase iii delta subunit holb:dnah homolog holb (db:pir) S66061 S66061 Bacillus subtilis 1423 -11529225 6500725367 yaas dna polymerase iii:delta subunit:hypothetical 37.6 kd protein in xpac-abrb intergenic region (gtcfc:10.8) (ec:2.7.7.7) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) holB holB Bacillus subtilis 1423 -11529225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748751	1449	23605	261	86

Description

GTC ORF with score 202 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c56c10.) (nt:similar to human transcription factor btf3 and to) (le:13681:13789:13967) (re:13739:13917:14075) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748889	1450	23606	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748902	1451	23607	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748918	1452	23608	486	162

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748923	1453	23609	600	199

Description

5000688679 yacj:rada:sms dna repair protein homolog:dna repair protein rada homolog:dna repair protein sms homolog (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) sms sms Bacillus subtilis 1423 -11529226 109607 rada:sms (de:dna repair protein rada homolog (dna repair protein sms homolog)) (db:swissprot) RADA_BACSU P37572 BACILLUS SUBTILIS 1423 -11529226 7000686264 sms dna repair protein homolog sms (cl:dna repair protein sms) (db:pir2.dat) S66116 S66116 Bacillus subtilis 1423 -11529226 7500889336 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:169695) (re:171071) (di:direct) BAC180K D26185 g467475 Bacillus subtilis 1423 -11529226 215075 sms dna repair protein homolog (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yacj) (le:106093) (re:107469) (di:direct) BSUB0001 Z99104 g2632354 Bacillus subtilis 1423 -11529226 206253 sms dna repair protein homolog sms (db:pir) S66116 S66116 Bacillus subtilis 1423 -11529226 6500725368 yacj:rada dna repair protein homolog:dna repair protein rada homolog:dna repair protein sms homolog (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) sms sms Bacillus subtilis 1423 -11529226

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748950	1454	23610	573	190

Description

6500725369 dna topoisomerase iii (gtcfc:10.8) (ec:5.99.1.2) (keggfc:14.1) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) topB topB Bacillus subtilis 1423 -11529227 7000692946 topb dna topoisomerase iii topb (db:pir2.dat) H69724 H69724 Bacillus subtilis 1423 -11529227 302681 topb probable dna topoisomerase iii (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (ec:5.99.1.2) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:9617) (re:11800) (di:direct) AB001488 AB001488 g1881236 Bacillus subtilis 1423 -11529227 7500963957 topb dna topoisomerase iii (db:genpept-bct1) (ec:5.99.1.2) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:73361) (re:75544) (di:direct) BSUB0003 Z99106 g2632726 Bacillus subtilis 1423 -11529227

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748981	1455	23611	273	90

Description

6500725370 ylqa:smc chromosome segregation smc protein homolg:hypothetical 135.4 kd protein in rnc-srb intergenic region:orf4 (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) smc smc Bacillus subtilis 1423 -11529228 7000692374 smc chromosome segregation smc protein:minichromosome stabilizing protein smc (cl:conserved hypothetical p115 protein) (db:pir2.dat) G69708 G69708 Bacillus subtilis 1423 -11529228 7500963536 smc chromosome segregation smc protein homolg (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylqa) (le:67539) (re:71099) (di:direct) BSUB0009 Z99112 g2633966 Bacillus subtilis 1423 -11529228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501748985	1456	23612	654	217

Description

GTC ORF with score 311 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c17g10.) (nt:similar to alcohol dehydrogenase/ribitol) (le:35008:35306:35576) (re:35261:35529:35789) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749150	1457	23613	654	218

Description

5000688643 integrase/recombinase:probable integrase/recombinase codv (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) codV codV Bacillus subtilis 1423 -11529229 65300 codv (de:probable integrase/recombinase codv) (db:swissprot) CODV_BACSU P39776 BACILLUS SUBTILIS 1423 -11529229 7000684861 codv integrase/recombinase codv (cl:probable site-specific integrase/recombinase xerc) (db:pir2.dat) G69601 G69601 Bacillus subtilis 1423 -11529229 7500879047 codv codv (db:genpept-bct1) (de:bacillus subtilis jh642 dipeptide permease operon regulators, codv,codw, codx, and cody genes, complete cds.) (le:293) (re:1207) (di:direct) BSU13634 U13634 g535348 Bacillus subtilis 1423 -11529229 219815 codv integrase/recombinase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:88166) (re:89080) (di:direct) BSUB0009 Z99112 g2633986 Bacillus subtilis 1423 -11529229 1500685157 codv integrase/recombinase codv (db:pir) G69601 G69601 Bacillus subtilis 1423 -11529229 6500725371 integrase/recombinase:probable integrase/recombinase codv (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) codV codV Bacillus subtilis 1423 -11529229

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749154	1458	23614	522	173

Description

6500725372 dna gyrase-like protein:subunit b (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) grlB grlB Bacillus subtilis 1423 -11529230 7000692929 grlb dna gyrase-like protein subunit b grlb (cl:dna topoisomerase (atp-hydrolyzing) chain b) (db:pir2.dat) C69637 C69637 Bacillus subtilis 1423 -11529230 7500963946 grlb grlb (fn:gyrase like protein beta subunit) (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:15237) (re:17120) (di:direct) BC170DEGR Z73234 g1405461 Bacillus subtilis 1423 -11529230 217892 grlb dna gyrase-like protein subunit b (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:151616) (re:153499) (di:direct) BSUB0010 Z99113 g2634192 Bacillus subtilis 1423 -11529230

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749157	1459	23615	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749158	1460	23616	972	324

Description

6500725373 dna gyrase-like protein:subunit a (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) grlA grlA Bacillus subtilis 1423 -11529231 7502851596 parc:grla (ec:5.99.1.-) (de:topoisomerase iv subunit a,) (db:swissprot) PARC_BACSU Q45066 BACILLUS SUBTILIS 1423 -11529231 7000692928 grla dna gyrase-like protein subunit a grla (cl:dna topoisomerase (atp-hydrolyzing) chain a:phage t4 dna topoisomerase (atp-hydrolyzing) medium chain homology) (db:pir2.dat) B69637 B69637 Bacillus subtilis 1423 -11529231 7500963945 grla grla (fn:gyrase like protein alpha subunit) (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:17124) (re:19544) (di:direct) BC170DEGR Z73234 g1405462 Bacillus subtilis 1423 -11529231 217893 grla dna gyrase-like protein subunit a (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:153503) (re:155923) (di:direct) BSUB0010 Z99113 g2634193 Bacillus subtilis 1423 -11529231

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749181	1461	23617	318	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749182	1462	23618	402	133

Description

5000688649 replication termination protein:replication terminator protein (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) rtp rtp Bacillus subtilis 1423 -11529232 216657 rtp (de:replication termination protein (replication terminator protein)) (db:swissprot) RTP_BACSU P14382 BACILLUS SUBTILIS 1423 -11529232 7000686530 rtp replication terminator protein rtp:clockwise replication fork arrest protein:13k (db:pir2.dat) A32807 A32807 Bacillus subtilis 1423 -11529232 7500891206 (sr:b.subtilis (strain w23) dna) (db:genpept-bct1) (de:b.subtilis rtp gene, complete cds and proc gene (put.), 5' end.) (nt:replication terminator protein (rtp; terc)) (le:1642) (re:2010) (di:direct) BACRTP M24523 g143479 Bacillus subtilis 1423 -11529232 219692 (db:genpept-bct1) (de:bacillus subtilis dna for replication terminus terc.) (nt:orf 2 (aa 1-122)) (le:836) (re:1204) (di:direct) BSTERC X06168 g40206 Bacillus subtilis 1423 -11529232 6500725374 rtp replication terminator protein (fn:clockwise-fork arrest at terc) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:16970) (re:17338) (di:complement) BSUB0011 Z99114 g2634243 Bacillus subtilis 1423 -11529232 7500891207 rtp replication terminator protein (db:genpept-bct2) (de:bacillus vallismortis replication terminator protein (rtp) gene,complete cds.) (nt:rtp) (le:76) (re:444) (di:direct) AF045054 AF045054 g3282813 Bacillus vallismortis 72361 -11529232 97622 rtp (de:replication termination protein (replication terminator protein)) (db:swissprot) RTP_BACSU P14382 BACILLUS SUBTILIS 1423 -11529232 170497 rtp replication terminator protein rtp:clockwise replication fork arrest protein:13k (db:pir) A32807 A32807 Bacillus subtilis 1423 -11529232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749195	1463	23619	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749205	1464	23620	927	309

Description

5000688646 hypothetical protein:dna replication protein dnad (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaD dnaD Bacillus subtilis 1423 -11529233 68862 dnad (de:dna replication protein dnad) (db:swissprot) DNAD_BACSU P39787 BACILLUS SUBTILIS 1423 -11529233 7000685074 dnad chromosome replication initiation protein dnad (db:pir2.dat) I40524 I40524 Bacillus subtilis 1423 -11529233 7500880413 dnad (fn:dna synthesis; initiation of chromosome) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, ... BACYPIA L47709 g1146248 Bacillus subtilis 1423 -11529233 217170 dnad dnad protein (fn:dna replication initiation) (db:genpept-bct1) (de:bacillus subtilis 168 asparaginyl-trna synthetase (asns) andendonuclease iii (joob) genes, partial cds and dnad protein (dnad)and (jooc) genes, complete cds.) (le:329) (re:1027) (di:direct) BSU11289 U11289 g533098 Bacillus subtilis 1423 -11529233 219791 dnad (fn:initiation of chromosome replication (dna) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:149135) (re:149833) (di:complement) BSUB0012 Z99115 g2634653 Bacillus subtilis 1423 -11529233 169974 dnad chromosome replication initiation protein dnad (db:pir) I40524 I40524 Bacillus subtilis 1423 -11529233 6500725375 hypothetical protein:dna replication protein dnad (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaD dnaD Bacillus subtilis 1423 -11529233

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749217	1465	23621	555	185

Description

5000689074 atp-dependent helicase:probable atp-dependent helicase ding homolog (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dinG dinG Bacillus subtilis 1423 -11529234 68663 ding (de:probable atp-dependent helicase ding homolog) (db:swissprot) DING_BACSU P54394 BACILLUS SUBTILIS 1423 -11529234 7000685052 ding atp-dependent dna helicase ding (db:pir2.dat) G69615 G69615 Bacillus subtilis 1423 -11529234 217165 ding (fn:dna-damage inducible protein) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds... BACYPIA L47709 g1146243 Bacillus subtilis 1423 -11529234 7500880324 ding atp-dependent helicase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:153373) (re:156168) (di:complement) BSUB0012 Z99115 g2634658 Bacillus subtilis 1423 -11529234 6500725376 atp-dependent helicase:probable atp-dependent helicase ding homolog (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dinG dinG Bacillus subtilis 1423 -11529234

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749232	1466	23622	222	73

Description

6500725377 atp-dependent dna helicase:atp-dependent dna helicase recq (gtcfc:10.8) (ec:3.6.1.-) (keggfc:14.1) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) recQ recQ Bacillus subtilis 1423 -11529235 93825 recq (ec:3.6.1.-) (de:atp-dependent dna helicase recq,) (db:swissprot) RECQ_BACSU P50729 BACILLUS SUBTILIS 1423 -11529235 7000686290 recq atp-dependent dna helicase homolog:atp-dependent dna helicase recq (cl:dead/h box helicase homology) (db:pir2.dat) A69691 A69691 Bacillus subtilis 1423 -11529235 6000685079 recq atp-dependent dna helicase (db:genpept-bct1) (ec:3.6.1.-) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:210616) (re:212106) (di:complement) BSUB0012 Z99115 g2634720 Bacillus subtilis 1423 -11529235 7500889583 recq atp-dependent dna helicase (db:genpept-bct1) (ec:3.6.1.-) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:10896) (re:12386) (di:complement) BSUB0013 Z99116 g2634737 Bacillus subtilis 1423 -11529235 216706 recs dna or rna helicase:dna-dependent atpase (fn:dna repair and homologous recombination) (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexly... BACSERA L47648 g1146200 Bacillus subtilis 1423 -11529235 5000688533 recs dna or rna helicase:dna-dependent atpase (fn:dna repair and homologous recombination) (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic e... BACSERA L47648 g1146200 Bacillus subtilis 1423 -11529235

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749234	1467	23623	222	73

Description

6500725378 ykqm:ripx integrase/recombinase:probable integrase/recombinase ripx (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) ripX ripX Bacillus subtilis 1423 -11529236 94400 ripx (de:probable integrase/recombinase ripx) (db:swissprot) RIPX_BACSU P46352 BACILLUS SUBTILIS 1423 -11529236 7000686333 ripx integrase/recombinase ripx (cl:probable site-specific integrase/recombinase xerc) (db:pir2.dat) A69693 A69693 Bacillus subtilis 1423 -11529236 216238 yqkm (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:270169) (re:271059) (di:direct) BACJH642 D84432 g1303994 Bacillus subtilis 1423 -11529236 7500889796 ripx integrase/recombinase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ykqm) (le:52560) (re:53450) (di:complement) BSUB0013 Z99116 g2634786 Bacillus subtilis 1423 -11529236 5000688648 (de:(ripx) (pn:probable integrase) (gtcfc:10.08) (ec:) (ripx_bacsu) (keggfc:11.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis)) ripX ripX Bacillus subtilis 1423 10036380

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749244	1468	23624	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749367	1469	23625	336	111

Description

6500725379 dnae:dnag dna primase (gtcfc:10.8) (ec:2.7.7.-) (keggfc:14.1) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaG dnaG Bacillus subtilis 1423 -11529237 216076 dnag:dnae (ec:2.7.7.-) (de:dna primase,) (db:swissprot) PRIM_BACSU P05096 BACILLUS SUBTILIS 1423 -11529237 7000686174 dnag dna primase:dnag (cl:dna primase) (ec:2.7.7.-) (db:pir2.dat) A22282 A22282 Bacillus subtilis 1423 -11529237 7500888460 (sr:b.subtilis dna, clone pcps1) (db:genpept-bct1) (de:b.subtilis dnae gene encoding dna primase, complete cds.) (nt:dna primase) (le:21) (re:1832) (di:direct) BACDNAE M10040 g142865 Bacillus subtilis 1423 -11529237 215551 dnae (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:116265) (re:118076) (di:direct) BACJH642 D84432 g1303832 Bacillus subtilis 1423 -11529237 5000688492 (db:genpept-bct1) (de:bacillus subtilis sigma 43 operon with p23-dnae-rpod genes (dnaefor dna primase, rpod for rna polymerase).) (nt:dnae (aa 1-603)) (le:1479) (re:3290) (di:direct) BSSIG43 X03897 g40142 Bacillus subtilis 1423 -11529237 219623 dnag dna primase (fn:initiation of okazaki fragments (dna) (db:genpept-bct1) (ec:2.7.7.-) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: dnae) (le:205544) (re:207355) (di:complement) BSUB0013 Z99116 g2634954 Bacillus subtilis 1423 -11529237 6000685025 dnag dna primase (fn:initiation of okazaki fragments (dna) (db:genpept-bct1) (ec:2.7.7.-) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: dnae) (le:1354) (re:3165) (di:complement) BSUB0014 Z99117 g2634968 Bacillus subtilis 1423 -11529237 91028 dnag:dnae (ec:2.7.7.-) (de:dna primase,) (db:swissprot) PRIM_BACSU P05096 BACILLUS SUBTILIS 1423 -11529237 170446 dnag dna primase dnag (db:pir) A22282 A22282 Bacillus subtilis 1423 -11529237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749377	1470	23626	546	181

Description

6500725380 holliday junction dna helicase (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) ruvB ruvB Bacillus subtilis 1423 -11529238 7000693106 ruvb holliday junction dna helicase ruvb (cl:ruvb protein) (db:pir2.dat) F69702 F69702 Bacillus subtilis 1423 -11529238 7500964054 ruvb holliday junction dna helicase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:39281) (re:40045) (di:complement) BSUB0015 Z99118 g2635238 Bacillus subtilis 1423 -11529238

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749380	1471	23627	1029	342

Description

6500725381 holliday junction dna helicase (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) ruvA ruvA Bacillus subtilis 1423 -11529239 7500891218 ruva (de:probable holliday junction dna helicase ruva) (db:swissprot) RUVA_BACSU O05392 BACILLUS SUBTILIS 1423 -11529239 7000693105 ruva holliday junction dna helicase ruva (cl:holliday junction dna helicase ruva) (db:pir2.dat) E69702 E69702 Bacillus subtilis 1423 -11529239 7500891220 ruva holliday junction dna helicase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:40296) (re:40901) (di:complement) BSUB0015 Z99118 g2635239 Bacillus subtilis 1423 -11529239

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749385	1472	23628	930	310

Description

6500725382 ytxa:dnay:dnai helicase loader:primosomal protein dnai (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaI dnaI Bacillus subtilis 1423 -11529240 220272 dnai (de:primosomal protein dnai) (db:swissprot) DNAI_BACSU P06567 BACILLUS SUBTILIS 1423 -11529240 131308 dnai primosome component helicase loader dnai:dnaa protein homolog:44k:hypothetical protein y dnab 3 region (cl:44k dnaa protein homolog) (db:pir1.dat) IQBS44 B24720 Bacillus subtilis 1423 -11529240 219159 dnai dnai (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:215003) (re:215938) (di:direct) AF008220 AF008220 g2293281 Bacillus subtilis 1423 -11529240 4000707041 (db:genpept-bct1) (de:bacillus subtilis dnab gene for initiation of chromosomalreplication.) (nt:orf 311 (aa 1-311)) (le:1843) (re:2778) (di:direct) BSDNAB X04963 g39881 Bacillus subtilis 1423 -11529240 304145 dnai helicase loader (fn:dna synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ytxa, dnay) (le:167129) (re:168064) (di:complement) BSUB0015 Z99118 g2635363 Bacillus subtilis 1423 -11529240 5000688647 dnai replication protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:dna synthesis; putative primosome component) (le:1843) (re:2778) (di:direct) BSZ75208 Z75208 g1769996 Bacillus subtilis 1423 -11529240 68863 dnai (de:primosomal protein dnai) (db:swissprot) DNAI_BACSU P06567 BACILLUS SUBTILIS 1423 -11529240

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749398	1473	23629	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749400	1474	23630	429	143

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749409	1475	23631	393	131

Description

5000688645 membrane attachment protein:replication initiation and membrane attachment protein (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaB dnaB Bacillus subtilis 1423 -11529241 68851 dnab (de:replication initiation and membrane attachment protein) (db:swissprot) DNAB_BACSU P07908 BACILLUS SUBTILIS 1423 -11529241 7000685069 dnab chromosome replication initiation / membrane attachment protein dnab:dnab protein (db:pir2.dat) B26580 B26580 Bacillus subtilis 1423 -11529241 4000707040 dnab dnab (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:213557) (re:214975) (di:direct) AF008220 AF008220 g2293280 Bacillus subtilis 1423 -11529241 215549 dnab replication initiation protein (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:b.subtilis dnab gene, encoding the replication initiation andmembrane attachment protein, complete cds, clone pdnab12.) (nt:the part of the protein encoded by 634-693 binds... BACDNAB M15183 g142863 Bacillus subtilis 1423 -11529241 220271 dnab membrane attachment protein (fn:initiation of chromosome replication (dna) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:168092) (re:169510) (di:complement) BSUB0015 Z99118 g2635364 Bacillus subtilis 1423 -11529241 304144 dnab replication initiation protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:the part of the protein encoded by 634-693 binds to) (le:397) (re:1815) (di:direct) BSZ75208 Z75208 g1769995 Bacillus subtilis 1423 -11529241 170491 dnab chromosome replication initiation / membrane attachment protein dnab:dnab protein (db:pir) B26580 B26580 Bacillus subtilis 1423 -11529241 6500725383 membrane attachment protein:replication initiation and membrane attachment protein (gtcfc:10.8) (keggfc:14.2) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaB dnaB Bacillus subtilis 1423 -11529241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749413	1476	23632	546	181

Description

6500725384 replicative dna helicase (gtcfc:10.8) (ec:3.6.1.-) (keggfc:14.1) (bsorffc:4.1.1) (db:gtc-bacillus subtilis) dnaC dnaC Bacillus subtilis 1423 -11529242 68860 dnac (ec:3.6.1.-) (de:replicative dna helicase,) (db:swissprot) DNAC_BACSU P37469 BACILLUS SUBTILIS 1423 -11529242 7000685073 dnac replicative dna helicase dnac (cl:phage p22 gene 12 protein) (db:pir2.dat) S65970 S65970 Bacillus subtilis 1423 -11529242 7500880412 dnac replicative dna helicase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:5467) (re:6831) (di:complement) BAC180K D26185 g467330 Bacillus subtilis 1423 -11529242 214930 dnac replicative dna helicase (fn:dna synthesis) (db:genpept-bct1) (ec:3.6.1.-) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:157399) (re:158763) (di:complement) BSUB0021 Z99124 g2636591 Bacillus subtilis 1423 -11529242 206273 dnac replicative dna helicase dnac (db:pir) S65970 S65970 Bacillus subtilis 1423 -11529242 5000688527 (de:(dnac) (pn:replicative dna helicase) (gtcfc:9.06) (ec:3.6.1.-) (dnac_bacsu) (keggfc:9.7) (bsorffc:4.1.1) (db:gtc-bacillus subtilis)) dnaC dnaC Bacillus subtilis 1423 10011445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749419	1477	23633	1140	379

Description

5000688938 integral membrane protein:sigma-k factor processing regulatory protein bofa:bypass-of-forespore protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) bofA bofA Bacillus subtilis 1423 -11529243 304137 bofa (de:protein)) (db:swissprot) BOFA_BACSU P24282 BACILLUS SUBTILIS 1423 -11529243 7000684727 bofa pro-sigma k processing regulatory protein bofa:bypass-of-forespore a:pro-sigma-k processing machinery inhibitor bofa:sigma-k activation protein (db:pir2.dat) B41869 B41869 Bacillus subtilis 1423 -11529243 7500877879 bofa activation of sigma-k during sporulation (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:93372) (re:93635) (di:direct) BAC180K D26185 g467413 Bacillus subtilis 1423 -11529243 219570 (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (nt:orf87) (le:3219) (re:3482) (di:direct) BSRECM X17014 g40075 Bacillus subtilis 1423 -11529243 6500725385 bofa integral membrane protein (fn:inhibitor of the pro-sigma-k processing) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:29770) (re:30033) (di:direct) BSUB0001 Z99104 g2632290 Bacillus subtilis 1423 -11529243 7502851597 (db:genpept) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (nt:orf87) (le:3219) (re:3482) (di:direct) BSRECM X17014 g40075 Bacillus subtilis 1423 -11529243 61917 bofa (de:protein)) (db:swissprot) BOFA_BACSU P24282 BACILLUS SUBTILIS 1423 -11529243 170447 bofa pro-sigma k processing regulatory protein bofa:bypass-of-forespore a:pro-sigma-k processing machinery inhibitor bofa:sigma-k activation protein (db:pir) B41869 B41869 Bacillus subtilis 1423 -11529243 215013 (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (nt:orf87) (le:3219) (re:3482) (di:direct) BSRECM X17014 g40075 Bacillus subtilis 1423 -11529243

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749427	1478	23634	765	254

Description

6500725386 atp-binding membrane protein:tunicamycin resistance protein (gtcfc:11.1:13.3) (keggfc:14.2) (bsorffc:5.1.1:7.4.1) (db:gtc-bacillus subtilis) tmrB tmrB Bacillus subtilis 1423 -11529244 7000694835 tmrb tunicamycin resistance protein (cl:tunicamycin resistance protein) (db:pir1.dat) YTBST E69724 Bacillus subtilis 1423 -11529244 222580 tmrb atp-binding membrane protein (fn:tunicamycin resistance) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:144078) (re:144671) (di:complement) BSUB0002 Z99105 g2632600 Bacillus subtilis 1423 -11529244 7500955417 tmrb tunicamycin resistance protein (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:18381) (re:18974) (di:complement) D50453 D50453 g1805386 Bacillus subtilis 1423 -11529244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749595	1479	23635	336	111

Description

5000688680 lipoprotein:lipoprotein lpla precursor (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lplA lplA Bacillus subtilis 1423 -11529245 82403 lpla (de:lipoprotein lpla precursor) (db:swissprot) LPLA_BACSU P37966 BACILLUS SUBTILIS 1423 -11529245 7000685762 lpla lipoprotein lpla:lysis protein lpla (cl:bacillus subtilis lipoprotein lpla) (db:pir2.dat) I39876 I39876 Bacillus subtilis 1423 -11529245 7500885126 lpla lipoprotein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:178337) (re:179845) (di:direct) BSUB0004 Z99107 g2633023 Bacillus subtilis 1423 -11529245 216293 lpla lysis protein (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct2) (de:bacillus subtilis lysis protein (lpla) gene, complete cds.) (le:482) (re:1990) (di:direct) BACLPLA L03376 g431272 Bacillus subtilis 1423 -11529245 170324 lpla lipoprotein lpla:lysis protein lpla (db:pir) I39876 I39876 Bacillus subtilis 1423 -11529245 6500725387 lipoprotein:lipoprotein lpla precursor (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lplA lplA Bacillus subtilis 1423 -11529245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749596	1480	23636	201	67

Description

6500725388 transmembrane lipoprotein:lplb protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lplB lplB Bacillus subtilis 1423 -11529246 7000694811 lplb transmembrane lipoprotein lplb (db:pir2.dat) A69653 A69653 Bacillus subtilis 1423 -11529246 7500965365 lplb transmembrane lipoprotein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:179900) (re:180856) (di:direct) BSUB0004 Z99107 g2633024 Bacillus subtilis 1423 -11529246

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749615	1481	23637	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749622	1482	23638	747	249

Description

5000688682 transmembrane lipoprotein:lplc protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lplC lplC Bacillus subtilis 1423 -11529247 82407 lplc (de:lplc protein) (db:swissprot) LPLC_BACSU P39129 BACILLUS SUBTILIS 1423 -11529247 7000685763 lplc transmembrane lipoprotein lplc (db:pir2.dat) B69653 B69653 Bacillus subtilis 1423 -11529247 216295 lplc transmembrane protein (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis (clone p149.3) transmembrane protein (lplc) gene,complete cds.) (nt:putative) (le:11) (re:898) (di:direct) BACLPLC L19164 g450566 Bacillus subtilis 1423 -11529247 7500885129 lplc transmembrane lipoprotein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:180870) (re:181757) (di:direct) BSUB0004 Z99107 g2633025 Bacillus subtilis 1423 -11529247 6500725389 transmembrane lipoprotein:lplc protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lplC lplC Bacillus subtilis 1423 -11529247

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749623	1483	23639	330	109

Description

6500725390 hydrolytic enzyme:lpld protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lplD lplD Bacillus subtilis 1423 -11529248 7502851598 lpld (de:lpld protein) (db:swissprot) LPLD_BACSU P39130 BACILLUS SUBTILIS 1423 -11529248 7000693116 lpld hydrolytic enzyme lpld (db:pir2.dat) C69653 C69653 Bacillus subtilis 1423 -11529248 7500964061 lpld hydrolytic enzyme (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:181766) (re:183106) (di:direct) BSUB0004 Z99107 g2633026 Bacillus subtilis 1423 -11529248

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749629	1484	23640	699	232

Description

GTC ORF with score 613 to: (fn:transfers mannose from gdp-mannose to dolichol) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe dolichol monophosphate mannose synthase(dpm1+) mrna, complete cds.) (le:47) (re:757) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749635	1485	23641	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749636	1486	23642	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749637	1487	23643	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749651	1488	23644	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749663	1489	23645	1356	451

Description

6500725391 ykvc:eag small membrane protein:hypothetical 16.4 kd protein in spo0e 3region (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) eag eag Bacillus subtilis 1423 -11529249 7500880783 eag (de:hypothetical 16.4 kd protein in spo0e 3'region) (db:swissprot) EAG_BACSU P06630 BACILLUS SUBTILIS 1423 -11529249 7000685131 eag small membrane protein eag (db:pir2.dat) S03747 S03747 Bacillus subtilis 1423 -11529249 5000688632 (db:genpept-bct1) (de:bacillus subtilis spooe gene for sporulation regulatory protein andunidentified reading frame (3' to spooe gene).) (nt:unidentified reading frame (aa 1-143)) (le:530) (re:961) (di:direct) BSSPOOE Y00526 g40183 Bacillus subtilis 1423 -11529249 219655 eag small membrane protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ykvc; small membrane protein) (le:35703) (re:36134) (di:direct) BSUB0008 Z99111 g2633736 Bacillus subtilis 1423 -11529249 69625 eag (de:hypothetical 16.4 kd protein in spo0e 3'region) (db:swissprot) EAG_BACSU P06630 BACILLUS SUBTILIS 1423 -11529249 170557 eag small membrane protein eag (db:pir) S03747 S03747 Bacillus subtilis 1423 -11529249

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749674	1490	23646	357	118

Description

6500725392 pal:slp small peptidoglycan-associated lipoprotein:related lipoprotein precursor (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) slp slp Bacillus subtilis 1423 -11529250 98615 slp:pal (de:pal-related lipoprotein precursor) (db:swissprot) SLP_BACSU P39910 BACILLUS SUBTILIS 1423 -11529250 7000686606 slp small peptidoglycan-associated lipoprotein slp precursor:pal-related lipoprotein:peptidoglycan-associated lipoprotein homolog (db:pir2.dat) B54546 B54546 Bacillus subtilis 1423 -11529250 220085 slp pal-related lipoprotein (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to pal-related lipoprotein encoded by) (le:38430) (re:38804) (di:complement) AF012285 AF012285 g3282146 Bacillus subtilis 1423 -11529250 7500891695 slp pal-related lipoprotein (sr:b.subtilis (strain 168) brb1 (saca321 metb5) cell line dna, clone) (db:genpept-bct1) (de:b.subtilis pyruvate dehydrogenase complex genes, complete cds;pal-related lipoprotein (slp) gene, complete cds, lysinedecarboxylase (cad) gene, partial cds.) (... BACPYDHY M57435 g143381 Bacillus subtilis 1423 -11529250 216550 slp small peptidoglycan-associated lipoprotein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: pal) (le:137942) (re:138316) (di:complement) BSUB0008 Z99111 g2633833 Bacillus subtilis 1423 -11529250 170548 slp small peptidoglycan-associated lipoprotein slp precursor:pal-related lipoprotein:peptidoglycan-associated lipoprotein homolog (db:pir) B54546 B54546 Bacillus subtilis 1423 -11529250 5000688684 (de:(slp) (pn:-related lipoprotein precursor:pal-related lipoprotein precursor) (gn:pal) (gtcfc:11.01) (ec:) (slp_bacsu) (keggfc:11.2) (bsorffc:5.1.0) (db:gtc-bacillus subtilis)) slp slp Bacillus subtilis 1423 10040491

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749681	1491	23647	324	107

Description

6500725393 integral membrane protein:cytochrome c-type biogenesis protein ccda (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) ccdA ccdA Bacillus subtilis 1423 -11529251 219727 ccda (de:cytochrome c-type biogenesis protein ccda) (db:swissprot) CCDA_BACSU P45706 BACILLUS SUBTILIS 1423 -11529251 7000684765 ccda cytochrome c late step biosynthesis protein ccda (db:pir2.dat) D69597 D69597 Bacillus subtilis 1423 -11529251 217880 ccda ccda (fn:cytochrome c-type biogenesis protein) (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:4910) (re:5617) (di:direct) BC170DEGR Z73234 g1405449 Bacillus subtilis 1423 -11529251 308412 ccda (db:genpept-bct1) (de:b.subtilis orf120, orf160, tkt and ccda genes.) (nt:required for cytochrome c synthesis) (le:1696) (re:2403) (di:direct) BSTKTCCDA X87845 g870925 Bacillus subtilis 1423 -11529251 7502851599 ccda integral membrane protein (fn:required for a late step of cytochrome c) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:141289) (re:141996) (di:direct) BSUB0010 Z99113 g2634177 Bacillus subtilis 1423 -11529251 63407 ccda (de:cytochrome c-type biogenesis protein ccda) (db:swissprot) CCDA_BACSU P45706 BACILLUS SUBTILIS 1423 -11529251 169897 ccda cytochrome c late step biosynthesis protein ccda (db:pir) D69597 D69597 Bacillus subtilis 1423 -11529251

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749683	1492	23648	666	221

Description

6500725394 comd:come3:comec putative integral membrane protein:come operon protein 3 (gtcfc:11.1:13.12) (keggfc:14.2) (bsorffc:5.1.1:6.6.1) (db:gtc-bacillus subtilis) comEC comEC Bacillus subtilis 1423 -11529252 216042 comec (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:79741) (re:82071) (di:direct) BACJH642 D84432 g1303798 Bacillus subtilis 1423 -11529252 7500964891 comec putative integral membrane protein (fn:specifically required for dna uptake but not) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: comd) (le:37359) (re:39689) (di:complement) BSUB0014 Z99117 g2635003 Bacillus subtilis 1423 -11529252 7000694158 comec late competence operon required for dna binding and uptake comec (db:pir) E69602 E69602 Bacillus subtilis 1423 -11529252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749827	1493	23649	375	124

Description

GTC ORF with score 173 to: (sr:human) (db:genpept-pri2) (de:homo sapiens dna sequence from pac 422h11 on chromosome6p21.1-22.2. contains the gene coding for two isoforms of a knownserine kinase. contains ests, stss and a gss, complete sequence.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749830	1494	23650	408	136

Description

6500725395 comd:come1:comea integral membrane protein:come operon protein 1 (gtcfc:11.1:13.12) (keggfc:14.2) (bsorffc:5.1.1:6.6.1) (db:gtc-bacillus subtilis) comEA comEA Bacillus subtilis 1423 -11529253 64868 comea:come1 (de:come operon protein 1) (db:swissprot) CME1_BACSU P39694 BACILLUS SUBTILIS 1423 -11529253 7000684844 comea late competence operon required for dna binding and uptake comea (db:pir2.dat) S39863 S39863 Bacillus subtilis 1423 -11529253 7500878901 comea (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:78484) (re:79101) (di:direct) BACJH642 D84432 g1303796 Bacillus subtilis 1423 -11529253 215368 comea integral membrane protein (fn:required for dna binding and uptake) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: comd) (le:40329) (re:40946) (di:complement) BSUB0014 Z99117 g2635005 Bacillus subtilis 1423 -11529253 216040 (sr:bacillus subtilis dna) (db:genpept-bct2) (de:bacillus subtilis come operon encoding orf1, orf2, orf3 andreverse-orf genes, complete cds.) (le:1346) (re:1963) (di:direct) BACCOME L15202 g289260 Bacillus subtilis 1423 -11529253 169924 comea late competence operon required for dna binding and uptake comea (db:pir) S39863 S39863 Bacillus subtilis 1423 -11529253 5000689910 (de:(comea) (pn:come operon protein 1:come operon protein 1) (gn:come1) (gtcfc:13.12) (ec:) (cme1_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comEA comEA Bacillus subtilis 1423 10007529

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749832	1495	23651	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749837	1496	23652	480	159

Description

6500725396 yrdo:czcd cation-efflux system membrane protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) czcD czcD Bacillus subtilis 1423 -11529254 7000692331 czcd cation-efflux system membrane protein czcd (cl:zinc transporter znt-2) (db:pir2.dat) C69612 C69612 Bacillus subtilis 1423 -11529254 1500692685 yrdo cation transport protein yrdo (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934656 Bacillus subtilis 1423 -11529254 7500963499 czcd cation-efflux system membrane protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrdo) (le:123711) (re:124646) (di:complement) BSUB0014 Z99117 g2635110 Bacillus subtilis 1423 -11529254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749844	1497	23653	204	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749849	1498	23654	648	215

Description

6500725397 protein-export membrane protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) secF secF Bacillus subtilis 1423 -11529255 7000694459 secf protein-export membrane protein secf (db:pir2.dat) H69704 H69704 Bacillus subtilis 1423 -11529255 7500965109 secf protein-export membrane protein (fn:protein secretional) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:31035) (re:32750) (di:complement) BSUB0015 Z99118 g2635229 Bacillus subtilis 1423 -11529255

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749850	1499	23655	354	117

Description

6500725398 ysee:araq integral membrane protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) araQ araQ Bacillus subtilis 1423 -11529256 7000694144 araq l-arabinose transport integral membrane protein araq (cl:maltose transport protein malg) (db:pir2.dat) C69588 C69588 Bacillus subtilis 1423 -11529256 220297 araq integral membrane protein (fn:l-arabinose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ysee) (le:143823) (re:144668) (di:complement) BSUB0015 Z99118 g2635338 Bacillus subtilis 1423 -11529256 304170 ysee hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to lacg of agrobacterium radiobacter;) (le:25239) (re:26084) (di:direct) BSZ75208 Z75208 g1770021 Bacillus subtilis 1423 -11529256

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749864	1500	23656	885	295

Description

6500725399 ysed:arap integral membrane protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) araP araP Bacillus subtilis 1423 -11529257 7000694143 arap l-arabinose transport integral membrane protein arap (cl:inner membrane protein ugpa) (db:pir2.dat) B69588 B69588 Bacillus subtilis 1423 -11529257 220296 arap integral membrane protein (fn:l-arabinose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ysed) (le:144669) (re:145610) (di:complement) BSUB0015 Z99118 g2635339 Bacillus subtilis 1423 -11529257 304169 ysed hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to lacf of agrobacterium radiobacter;) (le:24297) (re:25238) (di:direct) BSZ75208 Z75208 g1770020 Bacillus subtilis 1423 -11529257

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749880	1501	23657	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749882	1502	23658	477	158

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749891	1503	23659	402	133

Description

5000689461 putative membrane protein:csba protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) csbA csbA Bacillus subtilis 1423 -11529258 66601 csba (de:csba protein) (db:swissprot) CSBA_BACSU P37953 BACILLUS SUBTILIS 1423 -11529258 7500879441 csba (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis csba and uvr/dina genes, complete cds.) (nt:putative membrane protein; putative) (le:380) (re:610) (di:direct) BACCSBA M80473 g142780 Bacillus subtilis 1423 -11529258 215433 dina dnase inhibitor (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dnase inhibitor (dina76) gene, complete cds andpromoter region.) (le:64) (re:294) (di:direct) BACDINA76 M64048 g142842 Bacillus subtilis 1423 -11529258 215526 csba putative membrane protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:17086) (re:17316) (di:complement) BSUB0019 Z99122 g2636044 Bacillus subtilis 1423 -11529258 5500684521 csba csba (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:12977) (re:13207) (di:direct) AF017113 AF017113 g2618840 Bacillus subtilis 1423 -11529258 170337 csba probable membrane protein csba (db:pir) I39816 I39816 Bacillus subtilis 1423 -11529258 7000684910 csba probable membrane protein csba (db:pir) I39816 F69607 Bacillus subtilis 1423 -11529258 6500725400 putative membrane protein:csba protein (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) csbA csbA Bacillus subtilis 1423 -11529258

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749894	1504	23660	357	118

Description

6500725401 lppx:lyta membrane bound lipoprotein:membrane-bound protein lyta precursor (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lytA lytA Bacillus subtilis 1423 -11529259 82773 lyta:lppx (de:membrane-bound protein lyta precursor) (db:swissprot) LYTA_BACSU Q02112 BACILLUS SUBTILIS 1423 -11529259 7000685777 lyta major autolysin lytc secretion protein lyta precursor (cl:bacillus subtilis major autolysin secretion protein lyta) (db:pir2.dat) B47679 B47679 Bacillus subtilis 1423 -11529259 7500885219 lppx lipoprotein (sr:bacillus subtilis (strain:168s) dna) (db:genpept-bct1) (de:bacillus subtilis modifier protein of major autolysin (cwba) geneand assumed lipoprotein (lppx) gene, complete cds.) (le:955) (re:1263) (di:direct) BACCWBA D10388 g216256 Bacillus subtilis 1423 -11529259 215451 lyta membrane bound protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtillis membrane bound protein (lyta and lytr); amidaseenhancer (lytb); and amidase (lytc) genes, complete cds's.) (le:1196) (re:1504) (di:direct) BACLYTABCD M87645 g143157 Bacillus subtilis 1423 -11529259 216301 lyta membrane bound lipoprotein (fn:involved in the secretion of major autolysin) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: lppx) (le:64759) (re:65067) (di:complement) BSUB0019 Z99122 g2636090 Bacillus subtilis 1423 -11529259 170327 lyta major autolysin lytc secretion protein lyta precursor (db:pir) B47679 B47679 Bacillus subtilis 1423 -11529259 5000688695 (de:(lyta) (pn:membrane-bound protein lyta precursor) (gn:lppx) (gtcfc:11.02) (ec:) (lyta_bacsu) (keggfc:11.2) (bsorffc:5.2.0) (db:gtc-bacillus subtilis)) lytA lytA Bacillus subtilis 1423 10024993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749895	1505	23661	549	182

Description

5000688697 membrane-bound protein:membrane-bound protein lytr (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lytR lytR Bacillus subtilis 1423 -11529260 82779 lytr (de:membrane-bound protein lytr) (db:swissprot) LYTR_BACSU Q02115 BACILLUS SUBTILIS 1423 -11529260 7000685780 lytr lyt divergon expression attenuator lytr (cl:bacillus subtilis probable transcription regulator yvhj) (db:pir2.dat) A47679 A47679 Bacillus subtilis 1423 -11529260 7500885224 lytr membrane bound protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtillis membrane bound protein (lyta and lytr); amidaseenhancer (lytb); and amidase (lytc) genes, complete cds's.) (le:92) (re:1012) (di:complement) BACLYTABCD M87645 g143156 Bacillus subtilis 1423 -11529260 216300 lytr membrane-bound protein (fn:attenuator role for lytabc and lytr expression) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:65251) (re:66171) (di:direct) BSUB0019 Z99122 g2636091 Bacillus subtilis 1423 -11529260 170326 lytr lyt divergon expression attenuator lytr (db:pir) A47679 A47679 Bacillus subtilis 1423 -11529260 6500725402 membrane-bound protein:membrane-bound protein lytr (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) lytR lytR Bacillus subtilis 1423 -11529260

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749906	1506	23662	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501749913	1507	23663	678	225

Description

5000688694 membrane-bound protein:minor teichoic acids biosynthesis protein ggab (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) ggaB ggaB Bacillus subtilis 1423 -11529261 73570 ggab (de:minor teichoic acids biosynthesis protein ggab) (db:swissprot) GGAB_BACSU P46918 BACILLUS SUBTILIS 1423 -11529261 7000685384 ggab galactosamine-containing minor teichoic acid biosynthesis ggab (db:pir2.dat) E69631 E69631 Bacillus subtilis 1423 -11529261 219822 ggab (fn:involved in the secondary teichoic acid) (db:genpept-bct1) (de:bacillus subtilis minor teichoic acid synthesis genes ggaa andggab, complete cds.) (le:1643) (re:4345) (di:direct) BSU13979 U13979 g915199 Bacillus subtilis 1423 -11529261 7500882313 ggab membrane-bound protein (fn:biosynthesis of galactosamine-containing minor) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:69179) (re:71881) (di:complement) BSUB0019 Z99122 g2636094 Bacillus subtilis 1423 -11529261 6500725403 membrane-bound protein:minor teichoic acids biosynthesis protein ggab (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) ggaB ggaB Bacillus subtilis 1423 -11529261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750064	1508	23664	378	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750065	1509	23665	585	195

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750071	1510	23666	414	137

Description

5000688693 membrane-bound protein:minor teichoic acids biosynthesis protein ggaa (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) ggaA ggaA Bacillus subtilis 1423 -11529262 73569 ggaa (de:minor teichoic acids biosynthesis protein ggaa) (db:swissprot) GGAA_BACSU P46917 BACILLUS SUBTILIS 1423 -11529262 7000685383 ggaa galactosamine-containing minor teichoic acid biosynthesis ggaa (db:pir2.dat) D69631 D69631 Bacillus subtilis 1423 -11529262 219821 ggaa (fn:involved in the secondary teichoic acid) (db:genpept-bct1) (de:bacillus subtilis minor teichoic acid synthesis genes ggaa andggab, complete cds.) (le:179) (re:1519) (di:direct) BSU13979 U13979 g915198 Bacillus subtilis 1423 -11529262 7500882312 ggaa membrane-bound protein (fn:biosynthesis of galactosamine-containing minor) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:72005) (re:73345) (di:complement) BSUB0019 Z99122 g2636095 Bacillus subtilis 1423 -11529262 6500725404 membrane-bound protein:minor teichoic acids biosynthesis protein ggaa (gtcfc:11.1) (keggfc:14.2) (bsorffc:5.1.1) (db:gtc-bacillus subtilis) ggaA ggaA Bacillus subtilis 1423 -11529262

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750079	1511	23667	690	229

Description

6500725405 n-acetylmuramoyl-l-alanine amidase:germination-specific n-acetylmuramoyl-l-alanine amidase:cell wall hydrolase:autolysin (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) cwlD cwlD Bacillus subtilis 1423 -11529263 219116 cwld (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) CWLD_BACSU P50864 BACILLUS SUBTILIS 1423 -11529263 7000684948 cwld n-acetylmuramoyl-l-alanine amidase germination cwld (db:pir2.dat) G69610 G69610 Bacillus subtilis 1423 -11529263 5000688719 clwd (db:genpept-bct1) (de:b.subtilis cwld, rec223 and gerd genes.) (le:567) (re:1280) (di:direct) BSCWLD X74737 g1177251 Bacillus subtilis 1423 -11529263 222742 cwld n-acetylmuramoyl-l-alanine amidase (fn:cell wall hydrolase) (db:genpept-bct1) (ec:3.5.1.28) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:156611) (re:157324) (di:direct) BSUB0001 Z99104 g2632420 Bacillus subtilis 1423 -11529263 7500879597 cwld putative cell wall hydrolase cwld (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:6172) (re:6885) (di:direct) D64126 D64126 g1644212 Bacillus subtilis 1423 -11529263 7502851600 clwd (db:genpept) (de:b.subtilis cwld, rec223 and gerd genes.) (le:567) (re:1280) (di:direct) BSCWLD X74737 g1177251 Bacillus subtilis 1423 -11529263 66879 cwld (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) CWLD_BACSU P50864 BACILLUS SUBTILIS 1423 -11529263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750091	1512	23668	1059	352

Description

6500725406 n-acetylmuramoyl-l-alanine amidase:n-acetylmuramoyl-l-alanine amidase xyla precursor:cell wall hydrolase:autolysin (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) xlyA xlyA Bacillus subtilis 1423 -11529264 219508 xlya (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) XLYA_BACSU P39800 BACILLUS SUBTILIS 1423 -11529264 7000687047 xlya n-acetylmuramoyl-l-alanine amidase xlya:pbsx prophage-mediated lysis protein xlya (cl:bacillus n-acetylmuramoyl-l-alanine amidase) (db:pir2.dat) I39938 I39938 Bacillus subtilis 1423 -11529264 7500894475 xlya n-acetylmuramoyl-l-alanine amidase (sr:bacillus subtilis (strain 168) (library: lambda embl3) dna) (db:genpept-bct1) (de:bacillus subtilis 168 endogenous defective prophage pbsx encodingn-acetylmuramoyl-l-alanine amidase (xlya) gene and xepa, xhla, andxhlb genes, complete cds.) (le:1504... BACPBSX L25924 g496176 Bacillus subtilis 1423 -11529264 216445 xlya n-acetylmuramoyl-l-alanine amidase (fn:pbsx encoded cell autolysin) (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to cwla of the skin element) (le:26421) (re:27314) (di:direct) BSPBSXSE Z70177 g1225965 Bacillus subtilis 1423 -11529264 5000688723 xyla n-acetylmuramoyl-l-alanine amidase (db:genpept-bct1) (de:b.subtilis defective prophage pbsx xhla, xhlb, and xyla genes.) (le:1576) (re:2469) (di:direct) BSPBSXXHL Z36941 g535797 Bacillus subtilis 1423 -11529264 219512 xlya n-acetylmuramoyl-l-alanine amidase (fn:major role in defective prophage pbsx-mediated) (db:genpept-bct1) (ec:3.5.1.28) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:152370) (re:153263) (di:direct) BSUB0007 Z99110 g2633635 Bacillus subtilis 1423 -11529264 108134 xlya (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) XLYA_BACSU P39800 BACILLUS SUBTILIS 1423 -11529264 170363 xlya n-acetylmuramoyl-l-alanine amidase xlya:pbsx prophage-mediated lysis protein xlya (cl:bacillus n-acetylmuramoyl-l-alanine amidase) (db:pir) I39938 I39938 Bacillus subtilis 1423 -11529264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750104	1513	23669	699	233

Description

6500725407 phospho-n-acetylmuramoyl-pentapeptide transferase:phospho-n-acetylmuramoyl-pentapeptide-transferase (gtcfc:11.4) (ec:2.7.8.13) (keggfc:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) mraY mraY Bacillus subtilis 1423 -11529265 7500885856 mray (ec:2.7.8.13) (de:(udp-murnac-pentapeptide phosphotransferase)) (db:swissprot) MRAY_BACSU Q03521 BACILLUS SUBTILIS 1423 -11529265 7000685867 mray phospho-n-acetylmuramoyl-pentapeptide-transferase:mray (cl:phospho-n-acetylmuramoyl-pentapeptide-transferase) (ec:2.7.8.13) (db:pir2.dat) (mp:133 (degrees)) C47691 C47691 Bacillus subtilis 1423 -11529265 5000688721 mray (fn:peptidoglycan precursor synthesis) (db:genpept-bct1) (ec:2.7.8.13) (de:b.subtilis genes spovd, mure, mray, murd.) (le:1930) (re:2904) (di:direct) BSSPOG Z15056 g40163 Bacillus subtilis 1423 -11529265 219640 mray phospho-n-acetylmuramoyl-pentapeptide (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:2.7.8.13) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:192536) (re:193510) (di:direct) BSUB0008 Z99111 g2633890 Bacillus subtilis 1423 -11529265 84201 mray (ec:2.7.8.13) (de:(udp-murnac-pentapeptide phosphotransferase)) (db:swissprot) MRAY_BACSU Q03521 BACILLUS SUBTILIS 1423 -11529265 170438 mray phospho-n-acetylmuramoyl-pentapeptide-transferase:mray (ec:2.7.8.13) (db:pir) (mp:133 (degrees)) C47691 C47691 Bacillus subtilis 1423 -11529265

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750108	1514	23670	474	157

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750131	1515	23671	327	108

Description

6500725408 udp-n-acetylglucosamine-n-acetylmuramyl-:pentapaptidepyrophosphoryl-undecaprenol n-acetylglucosamine transferase:murg protein:upd-n-acetylglucosamine--n-acetylmuramyl-:pentapeptidepyrophosphoryl-undecaprenol n-acetylglucosamine transferase (gtcfc:11.4) (ec:2.7.8.13) (keggfc:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) murG murG Bacillus subtilis 1423 -11529266 154442 murg phospho-n-acetylmuramoyl-pentapeptide-transferase::murg protein:upd-n-acetylglucosamine--n-acetylmuramyl- pentapeptide pyrophosphoryl-undecaprenol n-acetylgl... (cl:murg protein) (ec:2.7.8.13) (db:pir2.dat) JC1275 S25763 Bacillus subtilis 1423 -11529266 7500955463 murg n-acetylglucosaminyl transferase (db:genpept-bct1) (ec:2.7.8.13) (de:bacillus subtilis murg & partial spove genes.) (nt:phospho-n-acetylmuramoyl-pentapeptide- transferase) (le:198) (re:1289) (di:direct) BSMURG X64259 g39995 Bacillus subtilis 1423 -11529266 219399 murg udp-n-acetylglucosamine-n-acetylmuramyl- (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (ec:2.7.8.13) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:196150) (re:197241) (di:direct) BSUB0008 Z99111 g2633893 Bacillus subtilis 1423 -11529266 7000689423 murg udp-n-acetylglucosamine-n-acetylmuramyl- pentapeptide pyrophos murg (cl:murg protein) (db:pir) G69662 G69662 Bacillus subtilis 1423 -11529266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750147	1516	23672	498	165

Description

6500725409 n-acetylmuramoyl-l-alanine amidase:sporulation-specific n-acetylmuramoyl-l-alanine amidase:cell wall hydrolase:autolysin (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) cwlC cwlC Bacillus subtilis 1423 -11529267 7500964992 cwlc n-acetylmuramoyl-l-alanine amidase (fn:sporulation-specific mother cell wall) (db:genpept-bct1) (ec:3.5.1.28) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:90853) (re:91620) (di:complement) BSUB0010 Z99113 g2634125 Bacillus subtilis 1423 -11529267 7000694279 cwlc n-acetylmuramoyl-l-alanine amidase sporulation mother cell wa cwlc (db:pir) F69610 F69610 Bacillus subtilis 1423 -11529267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750158	1517	23673	903	300

Description

6500725410 hypothetical protein:probable n-acetylmuramoyl-l-alanine amidase precursor:cell wall hydrolase:autolysin (gtcfc:11.4:14.1) (ec:3.5.1.28) (keggfc:7.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqeE yqeE Bacillus subtilis 1423 -11529268 115853 yqee (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) YQEE_BACSU P54450 BACILLUS SUBTILIS 1423 -11529268 7000688348 yqee n-acetylmuramoyl-l-alanine amidase homolog yqee (cl:bacillus n-acetylmuramoyl-l-alanine amidase) (db:pir2.dat) A69951 A69951 Bacillus subtilis 1423 -11529268 216029 yqee (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:69959) (re:70711) (di:direct) BACJH642 D84432 g1303785 Bacillus subtilis 1423 -11529268 7500952395 yqee (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to n-acetylmuramoyl-l-alanine amidase) (le:48719) (re:49471) (di:complement) BSUB0014 Z99117 g2635016 Bacillus subtilis 1423 -11529268 5000688724 (de:(yqee) (pn:probable n-acetylmuramoyl-l-alanine amidase precursor:cell wall hydrolase:autolysin) (gtcfc:11.04) (ec:3.5.1.28) (yqee_bacsu) (keggfc:7.3) (db:gtc-bacillus subtilis)) yqeE yqeE Bacillus subtilis 1423 10057579

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750171	1518	23674	690	229

Description

6500725411 n-acetylmuramoyl-l-alanine amidase:n-acetylmuramoyl-l-alanine amidase cwla precursor:cell wall hydrolase:autolysin (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) cwlA cwlA Bacillus subtilis 1423 -11529269 216799 cwla (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) CWLA_BACSU P24808 BACILLUS SUBTILIS 1423 -11529269 170361 cwla n-acetylmuramoyl-l-alanine amidase:30k cwla precursor:cell wall hydrolase:minor autolysin cwla (cl:bacillus n-acetylmuramoyl-l-alanine amidase) (ec:3.5.1.28) (db:pir2.dat) C44816 S26671 Bacillus subtilis 1423 -11529269 7500879595 cwla n-acetylmuramoyl-l-alanine amidase (sr:bacillus subtilis (strain 168) dna, clone lambda pe3) (db:genpept-bct1) (ec:3.5.1.28) (de:bacillus subtilis n-acetylmuramoyl-l-alanine amidase (cwla) gene,complete cds.) (le:1013) (re:1831) (di:direct) BACCWLAA M59232 g142802 Bacillus subtilis 1423 -11529269 215456 cwla (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:54219) (re:55037) (di:direct) BACJH642 D84432 g1303768 Bacillus subtilis 1423 -11529269 216012 cwla cell wall lytic enzyme autolysin (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:35974) (re:36792) (di:direct) BACSKIN D32216 g1217875 Bacillus subtilis 1423 -11529269 5000688717 cwla hydrolase (db:genpept-bct1) (de:bacillus subtilis cwla gene for cell wall hydrolase.) (le:114) (re:932) (di:direct) BSCWLAGE X51424 g39874 Bacillus subtilis 1423 -11529269 219114 cwla n-acetylmuramoyl-l-alanine amidase (fn:cell wall hydrolase (minor autolysin)) (db:genpept-bct1) (ec:3.5.1.28) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:64393) (re:65211) (di:complement) BSUB0014 Z99117 g2635035 Bacillus subtilis 1423 -11529269 66876 cwla (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) CWLA_BACSU P24808 BACILLUS SUBTILIS 1423 -11529269 7000684946 cwla n-acetylmuramoyl-l-alanine amidase:30k cwla precursor:cell wall hydrolase:minor autolysin cwla (cl:bacillus n-acetylmuramoyl-l-alanine amidase) (ec:3.5.1.28) (db:pir) C44816 C44816 Bacillus subtilis 1423 -11529269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750178	1519	23675	567	188

Description

6500725412 hypothetical protein:similar to n-acetylmuramoyl-l-alanine amidase (gtcfc:11.4:14.1) (ec:3.5.1.28) (keggfc:7.3) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yrvJ yrvJ Bacillus subtilis 1423 -11529270 7000694284 yrvj n-acetylmuramoyl-l-alanine amidase homolog yrvj (db:pir2.dat) B69981 B69981 Bacillus subtilis 1423 -11529270 7500964995 yrvj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to n-acetylmuramoyl-l-alanine amidase) (le:22629) (re:24185) (di:direct) BSUB0015 Z99118 g2635222 Bacillus subtilis 1423 -11529270

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750305	1520	23676	1029	342

Description

6500725413 cwlb:lytc n-acetylmuramoyl-l-alanine amidase:major autolysin:cwbp49:n-acetylmuramoyl-l-alanine amidase precursor:cell wall hydrolase:autolysin (gtcfc:11.4) (ec:3.5.1.28) (keggfc:7.3) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) lytC lytC Bacillus subtilis 1423 -11529271 66877 lytc:cwlb (ec:3.5.1.28) (de:(cell wall hydrolase) (autolysin)) (db:swissprot) CWLB_BACSU Q02114 BACILLUS SUBTILIS 1423 -11529271 7000684947 lytc n-acetylmuramoyl-l-alanine amidase:50k lytc precursor:major autolysin lytc:major vegetative autolytic amidase:v-amidase (ec:3.5.1.28) (db:pir2.dat) B41322 B41322 Bacillus subtilis 1423 -11529271 7500879596 cwlb n-acetylmuramoyl-l-alanine amidase (sr:bacillus subtilis (strain 168s) dna) (db:genpept-bct1) (ec:3.5.1.28) (de:bacillus subtilis n-acetylmuramoyl-l-alanine amidase (cwlb) gene,complete cds.) (le:742) (re:2232) (di:direct) BACCWLB M81324 g142806 Bacillus subtilis 1423 -11529271 216303 lytc amidase (fn:cell wall binding protein) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtillis membrane bound protein (lyta and lytr); amidaseenhancer (lytb); and amidase (lytc) genes, complete cds's.) (le:3684) (re:5174) (di:direct) BACLYTABCD M87645 g143159 Bacillus subtilis 1423 -11529271 215459 lytc n-acetylmuramoyl-l-alanine amidase major (db:genpept-bct1) (ec:3.5.1.28) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: cwlb) (le:61089) (re:62579) (di:complement) BSUB0019 Z99122 g2636088 Bacillus subtilis 1423 -11529271 170362 lytc n-acetylmuramoyl-l-alanine amidase:50k lytc precursor:major autolysin lytc:major vegetative autolytic amidase:v-amidase (ec:3.5.1.28) (db:pir) B41322 B41322 Bacillus subtilis 1423 -11529271 215453 lytc amidase (fn:cell wall binding protein) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtillis membrane bound protein (lyta and lytr); amidaseenhancer (lytb); and amidase (lytc) genes, complete cds's.) (le:3684) (re:5174) (di:direct) BACLYTABCD M87645 g143159 Bacillus subtilis 1423 -11529271 5000688720 (de:(lytc) (pn:n-acetylmuramoyl-l-alanine amidase precursor:n-acetylmuramoyl-l-alanine amidase cwlb precursor :cell wall hydrolase:autolysin) (gn:cwlb) (gtcfc:11.04) (ec:3.5.1.28) (cwlb_bacsu) (keggfc:7.3) (bsorffc:5.2.0) (db:g) lytC lytC Bacillus subtilis 1423 10009495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750317	1521	23677	987	329

Description

5000689553 ycsm:yzsa:pbpc penicillin-binding protein 3:pbp 3 (gtcfc:11.4:13.3) (keggfc:14.2) (bsorffc:5.2.1:7.4.1) (db:gtc-bacillus subtilis) pbpC pbpC Bacillus subtilis 1423 -11529272 110909 pbpc (de:penicillin-binding protein 3 (pbp 3)) (db:swissprot) PBPC_BACSU P42971 BACILLUS SUBTILIS 1423 -11529272 7000686093 pbpc penicillin-binding protein 3 pbpc (db:pir2.dat) I39902 I39902 Bacillus subtilis 1423 -11529272 7500887705 penicillin-binding protein 2 (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:14425) (re:16431) (di:direct) BAC39R D38161 g790944 Bacillus subtilis 1423 -11529272 215106 pbpc penicillin-binding protein 3 (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ycsm, yzsa) (le:60737) (re:62743) (di:direct) BSUB0003 Z99106 g2632714 Bacillus subtilis 1423 -11529272 222675 pbpc penicillin-binding protein iii pbp3 (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:143132) (re:145138) (di:direct) D50453 D50453 g1805481 Bacillus subtilis 1423 -11529272 170421 pbpc penicillin-binding protein 3 pbpc (db:pir) I39902 I39902 Bacillus subtilis 1423 -11529272 6500725414 ycsm:yzsa penicillin-binding protein 3:pbp 3 (gtcfc:11.4:13.3) (keggfc:14.2) (bsorffc:5.2.1:7.4.1) (db:gtc-bacillus subtilis) pbpC pbpC Bacillus subtilis 1423 -11529272

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750318	1522	23678	297	98

Description

6500725415 pona:pbpf penicillin-binding protein 1a:pbp-1a (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbpF pbpF Bacillus subtilis 1423 -11529273 88750 pbpf:pona (de:penicillin-binding protein 1a (pbp-1a)) (db:swissprot) PBPF_BACSU P38050 BACILLUS SUBTILIS 1423 -11529273 7000686097 pbpf:pona penicillin-binding protein 1a germination pbpf:pona homolog (db:pir2.dat) A40614 A40614 Bacillus subtilis 1423 -11529273 7500887709 pbpf penicillin-binding protein 1a (fn:involved in germination (peptidoglycan) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: pona) (le:83824) (re:85968) (di:direct) BSUB0006 Z99109 g2633347 Bacillus subtilis 1423 -11529273 4000707242 pbpf penicillin-binding protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p38050; pbpf_bacsu.) (le:3683) (re:5827) (di:direct) BSY14083 Y14083 g2226229 Bacillus subtilis 1423 -11529273 170428 pbpf:pona penicillin-binding protein 1a germination pbpf:pona homolog (db:pir) A40614 A40614 Bacillus subtilis 1423 -11529273 5000688707 (de:(pbpf) (pn:penicillin-binding protein 1a:pbp-1a) (gn:pona) (gtcfc:11.02) (ec:) (pbpf_bacsu) (keggfc:11.2) (bsorffc:5.2.0) (db:gtc-bacillus subtilis)) pbpF pbpF Bacillus subtilis 1423 10030877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750331	1523	23679	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750343	1524	23680	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750354	1525	23681	447	148

Description

6500725416 yism:wpra cell wall-associated protein precursor:cwbp23:cwbp52:cell wall-associated protease precursor:contains:cell wall-associated polypeptides cwbp23 and cwbp52 (gtcfc:11.4:10.11) (ec:3.4.21.-) (keggfc:14.1) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) wprA wprA Bacillus subtilis 1423 -11529274 7502851601 wpra (ec:3.4.21.-) (de:wall-associated polypeptides cwbp23 and cwbp52)) (db:swissprot) WPRA_BACSU P54423 BACILLUS SUBTILIS 1423 -11529274 7000692336 wpra cell wall-associated protein precursor wpra (cl:subtilisin homology) (db:pir2.dat) F69730 F69730 Bacillus subtilis 1423 -11529274 3000694796 wpra cell wall-associated protein precursor cwbp23 (db:genpept-bct1) (ec:3.4.21.-) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yism) (le:153761) (re:156445) (di:direct) BSUB0006 Z99109 g2633413 Bacillus subtilis 1423 -11529274 7500963503 wpra (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:cell-wall associated protease; differences with the) (le:10987) (re:13671) (di:direct) BSY09476 Y09476 g2145378 Bacillus subtilis 1423 -11529274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750361	1526	23682	207	68

Description

6500725417 yjpb:xlyb n-acetylmuramoyl-l-alanine amidase (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) xlyB xlyB Bacillus subtilis 1423 -11529275 7000694278 xlyb n-acetylmuramoyl-l-alanine amidase pbsx prophage-mediated lys orf xlyb (cl:bacillus n-acetylmuramoyl-l-alanine amidase) (db:pir2.dat) B69734 B69734 Bacillus subtilis 1423 -11529275 6000689467 xlyb n-acetylmuramoyl-l-alanine amidase (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (le:2... AF034138 AF034138 g2645866 Bacillus subtilis 1423 -11529275 7500954314 xlyb n-acetylmuramoyl-l-alanine amidase (fn:involved in defective prophage pbsx-mediated) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: yjpb) (le:122618) (re:123571) (di:direct) BSUB0007 Z99110 g2633600 Bacillus subtilis 1423 -11529275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750362	1527	23683	786	261

Description

5000688699 cell-shape determining protein:mrebh protein (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) mreBH mreBH Bacillus subtilis 1423 -11529276 84213 mrebh (de:mrebh protein) (db:swissprot) MREH_BACSU P39763 BACILLUS SUBTILIS 1423 -11529276 7000685869 mrebh cell-shape determining protein mrebh (cl:rod shape-determining protein envb) (db:pir2.dat) C69660 C69660 Bacillus subtilis 1423 -11529276 7500885869 mrebh unknown (fn:rod shape determining protein (by similarity to) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to mrebh encoded by genbank accession) (le:21677) (re:22684) (di:complement) AF012285 AF012285 g3282132 Bacillus subtilis 1423 -11529276 215162 mrebh (sr:bacillus subtilis (sub_species:marburg, strain:168) (db:genpept-bct1) (de:bacillus subtilis genes for amps, mrebh, orf1, kinc, orf3, orf4 andorf5.) (le:1218) (re:2225) (di:complement) BACAMOKOOO D37799 g520840 Bacillus subtilis 1423 -11529276 220071 mrebh cell-shape determining protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:121189) (re:122196) (di:complement) BSUB0008 Z99111 g2633818 Bacillus subtilis 1423 -11529276 6500725418 cell-shape determining protein:mrebh protein (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) mreBH mreBH Bacillus subtilis 1423 -11529276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750380	1528	23684	1194	398

Description

5000688704 penicillin-binding protein 2b:pbp-2b (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbpB pbpB Bacillus subtilis 1423 -11529277 88745 pbpb (de:penicillin-binding protein 2b (pbp-2b)) (db:swissprot) PBPB_BACSU Q07868 BACILLUS SUBTILIS 1423 -11529277 7000686092 pbpb penicillin-binding protein 2b cell-division septum pbpb (db:pir2.dat) C53292 C53292 Bacillus subtilis 1423 -11529277 7500887702 pbpb penicillin-binding protein 2b (fn:formation of the cell-division septum (late) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:186559) (re:188709) (di:direct) BSUB0008 Z99111 g2633887 Bacillus subtilis 1423 -11529277 216440 pbpb high molecular weight penicillin binding (fn:cell wall enzyme required for cell division;) (db:genpept-bct1) (de:b.subtilis ylla, yllb, yllc, ftsl, pbpb and spovd genes.) (nt:required for cell division) (le:3580) (re:5730) (di:direct) BSYLLSPO Z68230 g1122762 Bacillus subtilis 1423 -11529277 220248 pbpb penicillin-binding protein (fn:cell wall enzyme required for cell division) (sr:bacillus subtilis (strain 168trpc2) dna) (db:genpept-bct2) (de:bacillus subtilis penicillin-binding protein (pbpb and spovd)genes, complete and partial cds respectively.) (nt:second putative start co... BACPBPSPOV L09703 g304165 Bacillus subtilis 1423 -11529277 170422 pbpb penicillin-binding protein 2b cell-division septum pbpb (db:pir) C53292 C53292 Bacillus subtilis 1423 -11529277 6500725419 penicillin-binding protein 2b:pbp-2b (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbpB pbpB Bacillus subtilis 1423 -11529277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750522	1529	23685	513	170

Description

5000688988 penicillin-binding protein:stage v sporulation protein d:sporulation specific penicillin-binding protein (gtcfc:11.4:13.3) (keggfc:14.2) (bsorffc:5.2.1:7.4.1) (db:gtc-bacillus subtilis) spoVD spoVD Bacillus subtilis 1423 -11529278 7500891951 spovd (de:binding protein)) (db:swissprot) SP5D_BACSU Q03524 BACILLUS SUBTILIS 1423 -11529278 7000686647 spovd penicillin-binding protein spore cortex spovd:stage v sporulation protein d (db:pir2.dat) (mp:133 (degrees)) S49570 S49570 Bacillus subtilis 1423 -11529278 219670 spovd spovd (fn:sporulation specific penicillin-binding) (db:genpept-bct1) (de:b.subtilis pbp2b, spovd, and mure genes.) (le:240) (re:2177) (di:direct) BSSPOVD Z25865 g580936 Bacillus subtilis 1423 -11529278 6500725420 spovd penicillin-binding protein (fn:required for spore morphogenesis (spore cortex)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:188826) (re:190763) (di:direct) BSUB0008 Z99111 g2633888 Bacillus subtilis 1423 -11529278 99157 spovd (de:binding protein)) (db:swissprot) SP5D_BACSU Q03524 BACILLUS SUBTILIS 1423 -11529278 206285 spovd penicillin-binding protein spore cortex spovd:stage v sporulation protein d (db:pir) (mp:133 (degrees)) S49570 S49570 Bacillus subtilis 1423 -11529278

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750524	1530	23686	375	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750525	1531	23687	723	240

Description

GTC ORF with score 385 to: (fn:activates transcription of fus1 in the absence) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae serine/threonine kinase (ste20) gene anddominant truncation allele, complete coding ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750552	1532	23688	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750558	1533	23689	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750566	1534	23690	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750569	1535	23691	252	83

Description

6500725421 penicillin-binding protein (gtcfc:11.4:13.3) (keggfc:14.2) (bsorffc:5.2.1:7.4.1) (db:gtc-bacillus subtilis) pbpX pbpX Bacillus subtilis 1423 -11529279 7000694357 pbpx penicillin-binding protein pbpx (db:pir2.dat) C69673 C69673 Bacillus subtilis 1423 -11529279 7500965047 pbpx penicillin-binding protein (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:166806) (re:167981) (di:direct) BSUB0009 Z99112 g2634067 Bacillus subtilis 1423 -11529279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750572	1536	23692	510	169

Description

5000688703 penicillin-binding protein:putative penicillin binding protein precursor (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbp pbp Bacillus subtilis 1423 -11529280 7500887710 pbp (de:putative penicillin binding protein precursor) (db:swissprot) PBP_BACSU P39844 BACILLUS SUBTILIS 1423 -11529280 7000686098 pbp penicillin binding protein pbp (cl:d-alanyl-d-alanine carboxypeptidase) (db:pir2.dat) I40455 I40455 Bacillus subtilis 1423 -11529280 219522 pbp putative penicillin binding protein (db:genpept-bct1) (de:b.subtilis genes for peptide synthetase and penicillin bindingprotein.) (le:163) (re:1638) (di:direct) BSPEPSYN Z34883 g509467 Bacillus subtilis 1423 -11529280 6500725422 pbp penicillin-binding protein (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:216395) (re:217870) (di:complement) BSUB0010 Z99113 g2634218 Bacillus subtilis 1423 -11529280 88753 pbp (de:putative penicillin binding protein precursor) (db:swissprot) PBP_BACSU P39844 BACILLUS SUBTILIS 1423 -11529280 170419 pbp penicillin binding protein pbp (db:pir) I40455 I40455 Bacillus subtilis 1423 -11529280

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750573	1537	23693	666	221

Description

5000688708 penicillin-binding proteins 1a and 1b:penicillin-binding proteins 1a/1b:pbp1 (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) ponA ponA Bacillus subtilis 1423 -11529281 88740 pona (de:penicillin-binding proteins 1a/1b (pbp1)) (db:swissprot) PBPA_BACSU P39793 BACILLUS SUBTILIS 1423 -11529281 7000686091 pona penicillin-binding protein 1a/1b pona (db:pir2.dat) I40529 I40529 Bacillus subtilis 1423 -11529281 7500887700 pona penicillin-binding protein 1 (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:39.1% of identity to the s... BACPONAYPP L47838 g1146169 Bacillus subtilis 1423 -11529281 216488 pona penicillin-binding proteins 1a and 1b (db:genpept-bct1) (de:bacillus subtilis 168 penicillin-binding proteins 1a and 1b (pona)gene, complete cds, orfx gene, partial cds, orf1 and orfy genes,complete cds.) (nt:the product expressed from the translation of the) (le:1325) (re:4069) (di:direct) BSU11883 U11883 g520541 Bacillus subtilis 1423 -11529281 219804 pona penicillin-binding proteins 1a and 1b (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:145146) (re:147890) (di:direct) BSUB0012 Z99115 g2634650 Bacillus subtilis 1423 -11529281 170429 pona penicillin-binding protein 1a/1b pona (db:pir) I40529 I40529 Bacillus subtilis 1423 -11529281 6500725423 penicillin-binding proteins 1a and 1b:penicillin-binding proteins 1a/1b:pbp1 (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) ponA ponA Bacillus subtilis 1423 -11529281

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750584	1538	23694	1170	390

Description

5000689305 yqgf:pbpa penicillin-binding protein 2a:hypothetical 80.1 kd protein in soda-comga intergenic region (gtcfc:11.4:13.3) (keggfc:14.2) (bsorffc:5.2.1:7.4.1) (db:gtc-bacillus subtilis) pbpA pbpA Bacillus subtilis 1423 -11529282 115900 yqgf (de:hypothetical 80.1 kd protein in soda-comga intergenic region) (db:swissprot) YQGF_BACSU P54488 BACILLUS SUBTILIS 1423 -11529282 7000688396 pbpa penicillin-binding protein 2a spore outgrowth pbpa (cl:penicillin-binding protein 2b) (db:pir2.dat) E69672 E69672 Bacillus subtilis 1423 -11529282 216097 yqgf (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:135684) (re:137834) (di:direct) BACJH642 D84432 g1303853 Bacillus subtilis 1423 -11529282 7500952443 pbpa penicillin-binding protein 2a (fn:involved in the synthesis of peptidoglycan) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqgf) (le:185787) (re:187937) (di:complement) BSUB0013 Z99116 g2634933 Bacillus subtilis 1423 -11529282 6500725424 yqgf penicillin-binding protein 2a:hypothetical 80.1 kd protein in soda-comga intergenic region (gtcfc:11.4:13.3) (keggfc:14.2) (bsorffc:5.2.1:7.4.1) (db:gtc-bacillus subtilis) pbpA pbpA Bacillus subtilis 1423 -11529282

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750595	1539	23695	1128	376

Description

6500725425 chitosanase:chitosanase precursor (gtcfc:11.4) (ec:3.2.1.132) (keggfc:14.1) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) csn csn Bacillus subtilis 1423 -11529283 5500684991 csn (ec:3.2.1.132) (de:chitosanase precursor,) (db:swissprot) CHIS_BACSU O07921 BACILLUS SUBTILIS 1423 -11529283 7000684812 csn chitosanase csn (db:pir2.dat) C69608 C69608 Bacillus subtilis 1423 -11529283 1500692665 csn chitosanase precursor (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:19495) (re:20328) (di:direct) BS233DEG X92868 g2108281 Bacillus subtilis 1423 -11529283 1500692666 csn chitosanase precursor (db:genpept-bct1) (de:bacillus subtilis alcohol dehydrogenase (adhb) gene, partial cds,hypothetical spore coat protein (yraf), hypothetical spore coatprotein (yrag), yrah (yrah), yrai (yrai), yraj (yraj), yrak (yrak),yral (yral), chitosanase precursor ... BSU93875 U93875 g1934630 Bacillus subtilis 1423 -11529283 7500878660 csn chitosanase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:147803) (re:148636) (di:complement) BSUB0014 Z99117 g2635134 Bacillus subtilis 1423 -11529283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750598	1540	23696	546	181

Description

6500725426 rodb:mred cell-shape determining protein:rod shape-determining protein mred (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) mreD mreD Bacillus subtilis 1423 -11529284 84210 mred:rodb (de:rod shape-determining protein mred) (db:swissprot) MRED_BACSU Q01467 BACILLUS SUBTILIS 1423 -11529284 7000685868 mred cell shape determinant mred (db:pir2.dat) E45239 E45239 Bacillus subtilis 1423 -11529284 7500885866 mred mred protein (fn:required for cell shape determination) (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orfa, orfb, mreb, mrec, mred, minc, and mindgenes, complete coding regions.) (nt:location of rodb1 mutation) (l... BACDIVREG M96343 g142857 Bacillus subtilis 1423 -11529284 215544 mred (fn:cell shape determining) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis (mreb) gene complete cds, (mrec) gene completecds, (mred) gene complete cds, (minc) gene complete cds, (mind)gene complete cds.) (nt:putative) ... BACMREMIN M95582 g143214 Bacillus subtilis 1423 -11529284 216358 mred cell-shape determining protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: rodb) (le:63449) (re:63967) (di:complement) BSUB0015 Z99118 g2635266 Bacillus subtilis 1423 -11529284 169902 mred cell shape determinant mred (db:pir) E45239 E45239 Bacillus subtilis 1423 -11529284 5000688701 (de:(mred) (pn:rod shape-determining protein mred) (gn:rodb) (gtcfc:11.02) (ec:) (mred_bacsu) (keggfc:11.2) (bsorffc:5.2.0) (db:gtc-bacillus subtilis)) mreD mreD Bacillus subtilis 1423 10026411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750599	1541	23697	498	165

Description

GTC ORF with score 120 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750606	1542	23698	738	245

Description

GTC ORF with score 103 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750716	1543	23699	330	109

Description

6500725427 cell-shape determining protein:rod shape-determining protein mrec (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) mreC mreC Bacillus subtilis 1423 -11529285 7000692350 mrec cell-shape determining protein mrec (db:pir2.dat) E69660 E69660 Bacillus subtilis 1423 -11529285 215543 mrec mrec protein (fn:required for cell shape determination) (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orfa, orfb, mreb, mrec, mred, minc, and mindgenes, complete coding regions.) (le:2593) (re:3465) (di:direct) BACDIVREG M96343 g142856 Bacillus subtilis 1423 -11529285 7500963514 mrec cell-shape determining protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:63964) (re:64836) (di:complement) BSUB0015 Z99118 g2635267 Bacillus subtilis 1423 -11529285

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750718	1544	23700	510	169

Description

6500725428 divivb:mreb cell-shape determining protein:rod shape-determining protein mreb (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) mreB mreB Bacillus subtilis 1423 -11529286 7000692349 envb::mreb rod shape-determining protein envb:cell shape determinant mreb (cl:rod shape-determining protein envb) (db:pir2.dat) D69660 D69660 Bacillus subtilis 1423 -11529286 215542 mreb mreb protein (fn:required for cell shape determination) (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orfa, orfb, mreb, mrec, mred, minc, and mindgenes, complete coding regions.) (le:1549) (re:2562) (di:direct) BACDIVREG M96343 g142855 Bacillus subtilis 1423 -11529286 7500963513 mreb cell-shape determining protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: divivb) (le:64867) (re:65880) (di:complement) BSUB0015 Z99118 g2635268 Bacillus subtilis 1423 -11529286

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750720	1545	23701	738	245

Description

5000688705 penicillin-binding protein 4:penicillin-binding protein 4 precursor:pbp 4 (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbpD pbpD Bacillus subtilis 1423 -11529287 88748 pbpd (de:penicillin-binding protein 4 precursor (pbp 4)) (db:swissprot) PBPD_BACSU P40750 BACILLUS SUBTILIS 1423 -11529287 7000686095 pbpd penicillin-binding protein 4 pbpd (db:pir2.dat) A55220 A55220 Bacillus subtilis 1423 -11529287 7500887707 pbpd penicillin-binding protein 4 (db:genpept-bct1) (de:bacillus subtilis orf1, partial cds, penicillin-binding protein 4(pbpd) gene, complete cds, and orf2, complete cds.) (le:865) (re:2739) (di:direct) BSU11882 U11882 g520536 Bacillus subtilis 1423 -11529287 219800 pbpd penicillin-binding protein 4 (fn:peptidoglycan biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:35990) (re:37864) (di:direct) BSUB0017 Z99120 g2635645 Bacillus subtilis 1423 -11529287 1500685373 pbpd penicillin-binding protein 4 (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuga to yugd.) (le:5423) (re:7297) (di:direct) BSZ93933 Z93933 g1934784 Bacillus subtilis 1423 -11529287 170423 pbpd penicillin-binding protein 4 pbpd (db:pir) A55220 A55220 Bacillus subtilis 1423 -11529287 6500725429 penicillin-binding protein 4:penicillin-binding protein 4 precursor:pbp 4 (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbpD pbpD Bacillus subtilis 1423 -11529287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750721	1546	23702	666	222

Description

5000688706 penicillin-binding protein 4 (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbpE pbpE Bacillus subtilis 1423 -11529288 88749 pbpe (de:penicillin-binding protein 4* (pbp 4*) (pbp 4a)) (db:swissprot) PBPE_BACSU P32959 BACILLUS SUBTILIS 1423 -11529288 7000686096 pbpe spore cortex penicillin-binding protein 4* pbpe (db:pir2.dat) A36908 A36908 Bacillus subtilis 1423 -11529288 7500887708 pbpe penicillin-binding protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis penicillin-binding protein 4 (pbpe) gene, andamino acid racemase gene, complete cds's.) (le:246) (re:1601) (di:direct) BACPBPE L10629 g143290 Bacillus subtilis 1423 -11529288 216433 pbpe penicillin-binding protein 4* (fn:spore cortex formation (peptidoglycan) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:133628) (re:134983) (di:complement) BSUB0018 Z99121 g2635957 Bacillus subtilis 1423 -11529288 170424 pbpe spore cortex penicillin-binding protein 4* pbpe (db:pir) A36908 A36908 Bacillus subtilis 1423 -11529288 6500725430 penicillin-binding protein 4 (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) pbpE pbpE Bacillus subtilis 1423 -11529288

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750724	1547	23703	267	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750727	1548	23704	198	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750731	1549	23705	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750732	1550	23706	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750734	1551	23707	468	155

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750745	1552	23708	672	223

Description

6500725431 yvhd:tuad udp-glucose 6-dehydrogenase (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tuaD tuaD Bacillus subtilis 1423 -11529289 7000692269 tuad biosynthesis of teichuronic acid udp-glucose 6-dehydrogenase tuad (cl:gdpmannose dehydrogenase) (db:pir2.dat) F69727 F69727 Bacillus subtilis 1423 -11529289 7000692270 tuad udp-glucose dehydrogenase (db:genpept-bct1) (de:bacillus subtilis 168 teichuronic acid operon, tuaabcdefgh genes,complete sequence.) (le:3599) (re:4984) (di:direct) AF015609 AF015609 g2454559 Bacillus subtilis 1423 -11529289 7500963450 tuad udp-glucose 6-dehydrogenase (fn:biosynthesis of teichuronic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvhd) (le:56109) (re:57494) (di:complement) BSUB0019 Z99122 g2636084 Bacillus subtilis 1423 -11529289

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750754	1553	23709	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750757	1554	23710	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750764	1555	23711	219	72

Description

6500725432 cwba:lytb modifier protein of major autolysin lytc:cwbp76:amidase enhancer precursor:modifier protein of major autolysin (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) lytB lytB Bacillus subtilis 1423 -11529290 82774 lytb:cwba (de:amidase enhancer precursor (modifier protein of major autolysin)) (db:swissprot) LYTB_BACSU Q02113 BACILLUS SUBTILIS 1423 -11529290 7000685778 lytb n-acetylmuramoyl-l-alanine amidase modifier precursor lytb:major autolysin lytc modifier lytb:probable cell wall-binding protein a (db:pir2.dat) A41322 A41322 Bacillus subtilis 1423 -11529290 216302 lytb amidase enhancer (fn:cell wall binding protein) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtillis membrane bound protein (lyta and lytr); amidaseenhancer (lytb); and amidase (lytc) genes, complete cds's.) (le:1528) (re:3645) (di:direct) BACLYTABCD M87645 g143158 Bacillus subtilis 1423 -11529290 215452 lytb modifier protein of major autolysin lytc (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: cwba) (le:62618) (re:64735) (di:complement) BSUB0019 Z99122 g2636089 Bacillus subtilis 1423 -11529290 170364 lytb n-acetylmuramoyl-l-alanine amidase modifier precursor lytb:major autolysin lytc modifier lytb:probable cell wall-binding protein a (db:pir) A41322 A41322 Bacillus subtilis 1423 -11529290 5000688696 (de:(lytb) (pn:amidase enhancer precursor:modifier protein of major autolysin) (gn:cwba) (gtcfc:11.02) (ec:) (lytb_bacsu) (keggfc:11.2) (bsorffc:5.2.0) (db:gtc-bacillus subtilis)) lytB lytB Bacillus subtilis 1423 10024994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750768	1556	23712	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750769	1557	23713	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750778	1558	23714	573	191

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750779	1559	23715	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750784	1560	23716	360	119

Description

GTC ORF with score 155 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid f43g9, complete sequence.) (nt:predicted using genefinder; cdna est yk236h6.3) (le:10234:10491:10638:10965) (re:10443:10588:10867:11110) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750785	1561	23717	288	95

Description

5000688715 atp-binding protein:teichoic acid translocation atp-binding protein tagh (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagH tagH Bacillus subtilis 1423 -11529291 100422 tagh (de:teichoic acid translocation atp-binding protein tagh) (db:swissprot) TAGH_BACSU P42954 BACILLUS SUBTILIS 1423 -11529291 7000686750 tagh teichoic acid translocation atp-binding protein tagh (cl:atp-binding cassette homology) (db:pir2.dat) S69203 S69203 Bacillus subtilis 1423 -11529291 7500892737 tagh atp-binding protein (fn:teichoic acid translocation) (db:genpept-bct1) (de:bacillus subtilis 168 highly hydrophobic integral membrane protein(tagg) gene and atp-binding protein (tagh) gene, complete cds.) (le:1134) (re:2717) (di:direct) BSU13832 U13832 g755153 Bacillus subtilis 1423 -11529291 219820 tagh atp-binding protein (fn:teichoic acid translocation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:75534) (re:77117) (di:complement) BSUB0019 Z99122 g2636096 Bacillus subtilis 1423 -11529291 206156 tagh teichoic acid translocation atp-binding protein tagh (db:pir) S69203 S69203 Bacillus subtilis 1423 -11529291 6500725433 atp-binding protein:teichoic acid translocation atp-binding protein tagh (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagH tagH Bacillus subtilis 1423 -11529291

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750802	1562	23718	600	199

Description

5000688714 permease:teichoic acid translocation permease protein tagg (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagG tagG Bacillus subtilis 1423 -11529292 100421 tagg (de:teichoic acid translocation permease protein tagg) (db:swissprot) TAGG_BACSU P42953 BACILLUS SUBTILIS 1423 -11529292 7000686749 tagg teichoic acid permease tagg:integral membrane protein tagg (db:pir2.dat) S69202 S69202 Bacillus subtilis 1423 -11529292 7500892736 tagg highly hydrophobic integral membrane protein (fn:teichoic acid translocation) (db:genpept-bct1) (de:bacillus subtilis 168 highly hydrophobic integral membrane protein(tagg) gene and atp-binding protein (tagh) gene, complete cds.) (le:287) (re:1114) (di:direct) BSU13832 U13832 g755152 Bacillus subtilis 1423 -11529292 219819 tagg permease (fn:teichoic acid translocation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:77137) (re:77964) (di:complement) BSUB0019 Z99122 g2636097 Bacillus subtilis 1423 -11529292 206263 tagg teichoic acid permease tagg:integral membrane protein tagg (db:pir) S69202 S69202 Bacillus subtilis 1423 -11529292 6500725434 permease:teichoic acid translocation permease protein tagg (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagG tagG Bacillus subtilis 1423 -11529292

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750939	1563	23719	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750954	1564	23720	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750962	1565	23721	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750966	1566	23722	594	197

Description

5000688713 rodc:tag3:tagf cdp-glycerol polyglycerol phosphate glycero-phosphotransferase:teichoic acid biosynthesis protein f (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagF tagF Bacillus subtilis 1423 -11529293 219600 tagf:rodc:tag3 (de:teichoic acid biosynthesis protein f) (db:swissprot) TAGF_BACSU P13485 BACILLUS SUBTILIS 1423 -11529293 7000686748 rodc:tag-3:tagf probable cdpglycerol glycerophosphotransferase::cdp-glycerol:polyglycerol phosphate glycero-phosphotransferase tagf:rodc protein:teichoic-acid synthase (ec:2.7.8.12) (db:pir2.dat) (mp:310 degrees) S06049 S06049 Bacillus subtilis 1423 -11529293 7500892735 (db:genpept-bct1) (de:bacillus subtilis rodc operon.) (nt:rodc (tag3) polypeptide (aa 1-746)) (le:2178) (re:4418) (di:direct) BSRODC X15200 g40100 Bacillus subtilis 1423 -11529293 170517 tagf cdp-glycerol:polyglycerol phosphate (fn:teichoic acid biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: rodc) (le:78129) (re:80369) (di:complement) BSUB0019 Z99122 g2636098 Bacillus subtilis 1423 -11529293 100420 tagf:rodc:tag3 (de:teichoic acid biosynthesis protein f) (db:swissprot) TAGF_BACSU P13485 BACILLUS SUBTILIS 1423 -11529293 6500725435 rodc:tag3 cdp-glycerol polyglycerol phosphate glycero-phosphotransferase:teichoic acid biosynthesis protein f (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagF tagF Bacillus subtilis 1423 -11529293

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750972	1567	23723	546	181

Description

6500725436 glycerol-3-phosphate cytidylyltransferase:gct:cdp-glycerol pyrophosphorylase:teichoic acid biosynthesis protein d (gtcfc:11.4) (ec:2.7.7.39) (keggfc:14.1) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagD tagD Bacillus subtilis 1423 -11529294 100417 tagd (ec:2.7.7.39) (de:d)) (db:swissprot) TAGD_BACSU P27623 BACILLUS SUBTILIS 1423 -11529294 7000686746 tagd glycerol-3-phosphate cytidylyltransferase:tagd (ec:2.7.7.39) (db:pir2.dat) A49757 A49757 Bacillus subtilis 1423 -11529294 7500892733 tagd (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis taga, tagb, tagc and tagd genes, complete cds.) (nt:putative) (le:11) (re:400) (di:complement) BACTAGABCD M57497 g143723 Bacillus subtilis 1423 -11529294 216945 tagd glycerol-3-phosphate cytidylyltransferase (fn:teichoic acid biosynthesis) (db:genpept-bct1) (ec:2.7.7.39) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:82551) (re:82940) (di:complement) BSUB0019 Z99122 g2636100 Bacillus subtilis 1423 -11529294 170021 tagd glycerol-3-phosphate cytidylyltransferase:tagd (ec:2.7.7.39) (db:pir) A49757 A49757 Bacillus subtilis 1423 -11529294 5000688712 (de:(tagd) (pn:glycerol-3-phosphate cytidylyltransferase:gct:cdp-glycerol pyrophosphorylase:teichoic acid biosynthesis protein d:probable glycerol-3-phosphate cytidylyltransferase :cdp- glycerol pyrophosphorylase:techoic acid biosynthes) tagD tagD Bacillus subtilis 1423 10042269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750976	1568	23724	618	206

Description

5000688709 hypothetical protein:teichoic acid biosynthesis protein a (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagA tagA Bacillus subtilis 1423 -11529295 100413 taga (de:teichoic acid biosynthesis protein a) (db:swissprot) TAGA_BACSU P27620 BACILLUS SUBTILIS 1423 -11529295 7000686743 taga polyglycerol phosphate techoic acid biosynthesis protein taga (db:pir2.dat) B49757 B49757 Bacillus subtilis 1423 -11529295 7500892730 taga (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis taga, tagb, tagc and tagd genes, complete cds.) (nt:putative) (le:800) (re:1570) (di:direct) BACTAGABCD M57497 g143724 Bacillus subtilis 1423 -11529295 216946 taga (fn:polyglycerol phosphate assembly and export) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:83340) (re:84110) (di:direct) BSUB0019 Z99122 g2636101 Bacillus subtilis 1423 -11529295 170625 taga polyglycerol phosphate techoic acid biosynthesis protein taga (db:pir) B49757 B49757 Bacillus subtilis 1423 -11529295 6500725437 hypothetical protein:teichoic acid biosynthesis protein a (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagA tagA Bacillus subtilis 1423 -11529295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750988	1569	23725	942	313

Description

5000688710 hypothetical protein:teichoic acid biosynthesis protein b precursor (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagB tagB Bacillus subtilis 1423 -11529296 100414 tagb (de:teichoic acid biosynthesis protein b precursor) (db:swissprot) TAGB_BACSU P27621 BACILLUS SUBTILIS 1423 -11529296 7000686744 tagb polyglycerol phosphate techoic acid biosynthesis protein tagb (db:pir2.dat) C49757 C49757 Bacillus subtilis 1423 -11529296 7500892731 tagb (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis taga, tagb, tagc and tagd genes, complete cds.) (nt:putative) (le:1603) (re:2748) (di:direct) BACTAGABCD M57497 g143725 Bacillus subtilis 1423 -11529296 216947 tagb (fn:polyglycerol phosphate assembly and export) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:84143) (re:85288) (di:direct) BSUB0019 Z99122 g2636102 Bacillus subtilis 1423 -11529296 170626 tagb polyglycerol phosphate techoic acid biosynthesis protein tagb (db:pir) C49757 C49757 Bacillus subtilis 1423 -11529296 6500725438 hypothetical protein:teichoic acid biosynthesis protein b precursor (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagB tagB Bacillus subtilis 1423 -11529296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750993	1570	23726	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750998	1571	23727	594	197

Description

6500725439 dinc:tagc hypothetical protein:teichoic acid biosynthesis protein c (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) tagC tagC Bacillus subtilis 1423 -11529297 100416 tagc:dinc (de:teichoic acid biosynthesis protein c) (db:swissprot) TAGC_BACSU P27622 BACILLUS SUBTILIS 1423 -11529297 7000686745 tagc polyglycerol phosphate techoic acid biosynthesis protein tagc:hypothetical protein dna damage-inducible c18 promoter 3 region (db:pir2.dat) D49757 D49757 Bacillus subtilis 1423 -11529297 7500892732 tagc (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis taga, tagb, tagc and tagd genes, complete cds.) (nt:putative) (le:2868) (re:4196) (di:direct) BACTAGABCD M57497 g143727 Bacillus subtilis 1423 -11529297 216949 tagc (fn:polyglycerol phosphate assembly and export) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: dinc) (le:85408) (re:86736) (di:direct) BSUB0019 Z99122 g2636103 Bacillus subtilis 1423 -11529297 170623 tagc polyglycerol phosphate techoic acid biosynthesis protein tagc:hypothetical protein dna damage-inducible c18 promoter 3 region (db:pir) D49757 D49757 Bacillus subtilis 1423 -11529297 5000688711 (de:(tagc) (pn:teichoic acid biosynthesis protein c:techoic acid biosynthesis protein c) (gn:dinc) (gtcfc:11.02) (ec:) (tagc_bacsu) (keggfc:11.2) (bsorffc:5.2.0) (db:gtc-bacillus subtilis)) tagC tagC Bacillus subtilis 1423 10042268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501750999	1572	23728	438	145

Description

6500725440 cwlg:lytd n-acetylglucosaminidase:major autolysin:cwbp90:beta-n-acetylglucosaminidase precursor (gtcfc:11.4) (keggfc:14.1) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) lytD lytD Bacillus subtilis 1423 -11529298 82778 lytd:cwlg (ec:3.2.1.-) (de:beta-n-acetylglucosaminidase precursor,) (db:swissprot) LYTD_BACSU P39848 BACILLUS SUBTILIS 1423 -11529298 7000685779 lytd beta-n-acetylhexosaminidase:lytd precursor:major autolysin lytd:n-acetylglucosaminidase (ec:3.2.1.52) (db:pir2.dat) S60137 S60137 Bacillus subtilis 1423 -11529298 7500885223 cwlg beta-n-acetylglucosaminidase (fn:hydrolyze beta-1,4 glycan bond between the) (sr:bacillus subtilis (strain ac327) dna, clones peh4 and pwcev4) (db:genpept-bct1) (ec:3.2.1.30) (de:bacillus subtilis gene for beta-n-acetylglucosaminidase, completecds.) (le:1296) (re:3938) (di:direct) BACORFX D45048 g1129074 Bacillus subtilis 1423 -11529298 216423 lytd n-acetylglucosaminidase (fn:hydrolyses bond between the) (db:genpept-bct1) (ec:3.2.1.30) (de:bacillus subtilis n-acetylglucosaminidase (lytd) gene, completecds.) (le:1265) (re:3907) (di:direct) BSU02562 U02562 g476093 Bacillus subtilis 1423 -11529298 219760 lytd n-acetylglucosaminidase major autolysin (fn:hydrolyses bond between the) (db:genpept-bct1) (ec:3.2.1.30) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: cwlg) (le:86796) (re:89438) (di:complement) BSUB0019 Z99122 g2636104 Bacillus subtilis 1423 -11529298 169890 lytd beta-n-acetylhexosaminidase:lytd precursor:major autolysin lytd:n-acetylglucosaminidase (ec:3.2.1.52) (db:pir) S60137 S60137 Bacillus subtilis 1423 -11529298 5000688516 (de:(lytd) (pn:beta-n-acetylglucosaminidase precursor:n-acetylglucosaminidase precursor) (gn:cwlg) (gtcfc:7.02) (ec:3.2.1.-) (lytd_bacsu) (keggfc:4.3:7.1) (bsorffc:5.2.0) (db:gtc-bacillus subtilis)) lytD lytD Bacillus subtilis 1423 10024998

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751005	1573	23729	648	215

Description

6500725441 ipa-5r:dae:dlta d-alanyl-d-alanine carrier protein ligase:d-alanine-activating enzyme:dae:d-alanine-d-alanyl carrier protein ligase:dcl (gtcfc:11.4) (ec:6.3.2.-) (keggfc:14.1) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) dltA dltA Bacillus subtilis 1423 -11529299 7500880363 dlta:dae:ipa-5r (ec:6.3.2.-) (de:carrier protein ligase) (dcl)) (db:swissprot) DLTA_BACSU P39581 BACILLUS SUBTILIS 1423 -11529299 7000685061 dlta d-alanyl-d-alanine carrier protein ligase dlta:protein ipa-5r (cl:acetate--coa ligase homology) (db:pir2.dat) S39660 S39660 Bacillus subtilis 1423 -11529299 219242 ipa-5r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:3780) (re:5291) (di:complement) BSGENR X73124 g413929 Bacillus subtilis 1423 -11529299 7502851602 dlta d-alanyl-d-alanine carrier protein ligase dcl (fn:d-alanine esterification of lipoteichoic acid) (db:genpept-bct1) (ec:6.3.2.-) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-5r, dae) (le:152669) (re:154180) (di:direct) BSUB0020 Z99123 g2636385 Bacillus subtilis 1423 -11529299 68755 dlta:dae:ipa-5r (ec:6.3.2.-) (de:carrier protein ligase) (dcl)) (db:swissprot) DLTA_BACSU P39581 BACILLUS SUBTILIS 1423 -11529299 170101 dlta d-alanyl-d-alanine carrier protein ligase dlta (cl:acetate--coa ligase homology) (db:pir) S39660 S39660 Bacillus subtilis 1423 -11529299

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751010	1574	23730	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751023	1575	23731	1134	378

Description

6500725442 ipa-4r:dltb hypothetical protein:dltb protein (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) dltB dltB Bacillus subtilis 1423 -11529300 7500880364 dltb:ipa-4r (de:dltb protein) (db:swissprot) DLTB_BACSU P39580 BACILLUS SUBTILIS 1423 -11529300 7000685062 dltb dltb protein:protein ipa-4r (db:pir2.dat) S39659 S39659 Bacillus subtilis 1423 -11529300 5000688689 ipa-4r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:2596) (re:3783) (di:complement) BSGENR X73124 g413928 Bacillus subtilis 1423 -11529300 219241 dltb (fn:d-alanine esterification of lipoteichoic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-4r) (le:154177) (re:155364) (di:direct) BSUB0020 Z99123 g2636386 Bacillus subtilis 1423 -11529300 68757 dltb:ipa-4r (de:dltb protein) (db:swissprot) DLTB_BACSU P39580 BACILLUS SUBTILIS 1423 -11529300 170100 dltb d-alanine transfer from dcp to undecaprenol-phosphate dltb (db:pir) S39659 S39659 Bacillus subtilis 1423 -11529300

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751026	1576	23732	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751034	1577	23733	501	167

Description

6500725443 ipa-3r:dltc d-alanyl carrier protein:dcp (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) dltC dltC Bacillus subtilis 1423 -11529301 7500880365 dltc:ipa-3r (de:d-alanyl carrier protein (dcp)) (db:swissprot) DLTC_BACSU P39579 BACILLUS SUBTILIS 1423 -11529301 7000685063 dltc d-alanine carrier protein dltc:protein ipa-3r (cl:acyl carrier protein homology) (db:pir2.dat) S39658 S39658 Bacillus subtilis 1423 -11529301 5000688690 ipa-3r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:2343) (re:2579) (di:complement) BSGENR X73124 g413927 Bacillus subtilis 1423 -11529301 219240 dltc d-alanyl carrier protein dcp (fn:d-alanine esterification of lipoteichoic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-3r) (le:155381) (re:155617) (di:direct) BSUB0020 Z99123 g2636387 Bacillus subtilis 1423 -11529301 68759 dltc:ipa-3r (de:d-alanyl carrier protein (dcp)) (db:swissprot) DLTC_BACSU P39579 BACILLUS SUBTILIS 1423 -11529301 170099 dltc d-alanine carrier protein dltc (cl:acyl carrier protein homology) (db:pir) S39658 S39658 Bacillus subtilis 1423 -11529301

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751190	1578	23734	327	108

Description

GTC ORF with score 93 to: (or:Homo sapiens) (sr:human t-cell line hpb-all, cdna to mrna) (db:genpept-pri1) (de:human hla-b-associated transcript 3 (bat3) mrna, complete cds.) (nt:hla-b-associated transcript 3 (bat3)) (le:250) (re:3648) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751205	1579	23735	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751208	1580	23736	465	154

Description

6500725444 ipa-2r:dltd hypothetical protein:protein dltd precursor (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) dltD dltD Bacillus subtilis 1423 -11529302 7500880366 dltd:ipa-2r (de:protein dltd precursor) (db:swissprot) DLTD_BACSU P39578 BACILLUS SUBTILIS 1423 -11529302 7000685064 dltd undecaprenol-phosphate--poly glycerophosphate chain d-alanine transfer protein dltd:protein ipa-2r (db:pir2.dat) S39657 S39657 Bacillus subtilis 1423 -11529302 5000688691 ipa-2r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:1165) (re:2343) (di:complement) BSGENR X73124 g413926 Bacillus subtilis 1423 -11529302 219239 dltd (fn:d-alanine esterification of lipoteichoic acid) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-2r) (le:155617) (re:156795) (di:direct) BSUB0020 Z99123 g2636388 Bacillus subtilis 1423 -11529302 68761 dltd:ipa-2r (de:protein dltd precursor) (db:swissprot) DLTD_BACSU P39578 BACILLUS SUBTILIS 1423 -11529302 170098 dltd undecaprenol-phosphate--poly glycerophosphate chain d-alanine transfer protein dltd (db:pir) S39657 S39657 Bacillus subtilis 1423 -11529302

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751224	1581	23737	663	220

Description

6500725445 ipa-1r:dlte hypothetical protein:dlte protein (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) dltE dltE Bacillus subtilis 1423 -11529303 7500880367 dlte:ipa-1r (de:dlte protein) (db:swissprot) DLTE_BACSU P39577 BACILLUS SUBTILIS 1423 -11529303 7000685065 dlte lipoteichoic acid biosynthesis protein dlte (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) S39656 S39656 Bacillus subtilis 1423 -11529303 5000688692 ipa-1r (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:316) (re:1074) (di:complement) BSGENR X73124 g413925 Bacillus subtilis 1423 -11529303 219238 dlte (fn:involved in lipoteichoic acid biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-1r) (le:156886) (re:157644) (di:direct) BSUB0020 Z99123 g2636389 Bacillus subtilis 1423 -11529303 68763 dlte:ipa-1r (de:dlte protein) (db:swissprot) DLTE_BACSU P39577 BACILLUS SUBTILIS 1423 -11529303 170097 dlte lipoteichoic acid biosynthesis protein dlte (db:pir) S39656 S39656 Bacillus subtilis 1423 -11529303

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751226	1582	23738	294	97

Description

6500725446 n17g:wapa cell wall-associated protein precursor:cwbp200:105:62:wall-associated protein precursor (gtcfc:11.4) (keggfc:14.2) (bsorffc:5.2.1) (db:gtc-bacillus subtilis) wapA wapA Bacillus subtilis 1423 -11529304 107893 wapa:n17g (de:wall-associated protein precursor) (db:swissprot) WAPA_BACSU Q07833 BACILLUS SUBTILIS 1423 -11529304 7000687003 wapa cell wall-associated protein precursor wapa (cl:cell wall-associated protein wapa) (db:pir2.dat) S32920 S32920 Bacillus subtilis 1423 -11529304 7500894366 n17g::wapa wapa protein (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (le:18778) (re:25782) (di:direct) BACHUTWAPA D31856 g603782 Bacillus subtilis 1423 -11529304 215876 wapa wall-associated protein:258-kda precursor (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis wapa and orf genes for wall-associated proteinand hypothetical proteins.) (le:6881) (re:13885) (di:direct) BACHYPTP D29985 g849029 Bacillus subtilis 1423 -11529304 215891 wapa wall-associated protein (sr:bacillus subtilis (strain w168) (library: lambda gt11) dna) (db:genpept-bct1) (de:bacillus subtilis orf1, 3' end; wall-associated protein (wala)gene, complete cds; complete orf3.) (le:706) (re:7710) (di:direct) BACWAPAX L05634 g304179 Bacillus subtilis 1423 -11529304 217051 wapa cell wall-associated protein precursor cwbp200 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:23053) (re:30057) (di:complement) BSUB0021 Z99124 g2636469 Bacillus subtilis 1423 -11529304 170664 wapa cell wall-associated protein precursor wapa (db:pir) S32920 S32920 Bacillus subtilis 1423 -11529304 5000688716 (de:(wapa) (pn:wall-associated protein precursor) (gn:n17g) (gtcfc:11.02) (ec:) (wapa_bacsu) (keggfc:11.2) (bsorffc:5.2.0) (db:gtc-bacillus subtilis)) wapA wapA Bacillus subtilis 1423 10049630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751231	1583	23739	834	277

Description

GTC ORF with score 780 to: (fn:catalyzes the hydrolysis of glucosides) (db:genpept-pln1) (ec:3.2.1.21) (de:coccidioides immitis cytosolic beta-glucosidase (bgl1) gene,complete cds.) (nt:bgl1) (le:660:1500:1810) (re:1436:1751:3393) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751246	1584	23740	681	226

Description

5000688746 proton/glutamate symport protein:proton glutamate symport protein:glutamate-aspartate carrier protein (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) gltP gltP Bacillus subtilis 1423 -11529305 74128 gltp (de:protein)) (db:swissprot) GLTP_BACSU P39817 BACILLUS SUBTILIS 1423 -11529305 7000685428 gltp h+/glutamate symport protein gltp (db:pir2.dat) B57142 B57142 Bacillus subtilis 1423 -11529305 7500882561 gltp proton/glutamate symport protein (fn:glutamate uptake) (db:genpept-bct1) (de:bacillus subtilis proton/glutamate symport protein (gltp) gene,complete cds.) (le:499) (re:1743) (di:direct) BSU15147 U15147 g558840 Bacillus subtilis 1423 -11529305 219825 gltp proton/glutamate symport protein (fn:glutamate uptake) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:58857) (re:60101) (di:complement) BSUB0002 Z99105 g2632520 Bacillus subtilis 1423 -11529305 7500882562 gltp proton glutamate symport protein (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:56508) (re:57752) (di:complement) AB006424 AB006424 g3599656 Bacillus subtilis 1423 -11529305 170017 gltp h+/glutamate symport protein gltp (db:pir) B57142 B57142 Bacillus subtilis 1423 -11529305 6500725447 proton/glutamate symport protein:proton glutamate symport protein:glutamate-aspartate carrier protein (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) gltP gltP Bacillus subtilis 1423 -11529305

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751252	1585	23741	270	89

Description

6500725448 glycine betaine abc transporter:atp-binding protein:glycine betaine transport atp-binding protein opuaa (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuAA opuAA Bacillus subtilis 1423 -11529306 222564 opuaa glycine betaine abc transporter atp-binding (fn:glycine betaine transport (osmoprotection)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:125917) (re:127173) (di:direct) BSUB0002 Z99105 g2632584 Bacillus subtilis 1423 -11529306 7500955206 opuaa glycine betain/l-proline transport atpase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:220) (re:1476) (di:direct) D50453 D50453 g1805370 Bacillus subtilis 1423 -11529306 7000693061 opuaa glycine betaine abc transporter atp-binding protein opuaa (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir) D69669 D69669 Bacillus subtilis 1423 -11529306

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751265	1586	23742	1083	361

Description

5000688759 glycine betaine abc transporter:permease:glycine betaine transport system permease protein opuab (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuAB opuAB Bacillus subtilis 1423 -11529307 87853 opuab (de:glycine betaine transport system permease protein opuab) (db:swissprot) OPUB_BACSU P46921 BACILLUS SUBTILIS 1423 -11529307 7000686055 opuab glycine betaine abc transporter permease opuab (db:pir2.dat) I40536 I40536 Bacillus subtilis 1423 -11529307 7500887348 opuab glycine betaine abc transporter permease (fn:glycine betaine transport (osmoprotection)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:127175) (re:128023) (di:direct) BSUB0002 Z99105 g2632585 Bacillus subtilis 1423 -11529307 219830 opuab glycine betain/l-proline transmembrane protein (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:1478) (re:2326) (di:direct) D50453 D50453 g1805371 Bacillus subtilis 1423 -11529307 222565 opuab transmembrane protein (db:genpept-bct2) (de:bacillus subtilis atpase (opuaa), transmembrane protein (opuab) andglycine betaine-binding protein precursor (opuac) genes, completecds.) (le:1484) (re:2332) (di:direct) BSU17292 U17292 g984804 Bacillus subtilis 1423 -11529307 170647 opuab glycine betaine abc transporter permease opuab (db:pir) I40536 I40536 Bacillus subtilis 1423 -11529307 6500725449 glycine betaine abc transporter:permease:glycine betaine transport system permease protein opuab (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuAB opuAB Bacillus subtilis 1423 -11529307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751267	1587	23743	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751273	1588	23744	486	161

Description

5000688760 glycine betaine abc transporter:glycine betaine-binding protein:glycine betaine-binding protein precursor (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuAC opuAC Bacillus subtilis 1423 -11529308 87854 opuac (de:glycine betaine-binding protein precursor) (db:swissprot) OPUC_BACSU P46922 BACILLUS SUBTILIS 1423 -11529308 7000686056 opuac glycine betaine abc transporter glycine betaine-binding protein opuac precursor (db:pir2.dat) I40537 I40537 Bacillus subtilis 1423 -11529308 7500887349 opuac glycine betaine abc transporter glycine (fn:glycine betaine transport (osmoprotection)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:128023) (re:128904) (di:direct) BSUB0002 Z99105 g2632586 Bacillus subtilis 1423 -11529308 219831 opuac glycine betain-binding protein precursor (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:2326) (re:3207) (di:direct) D50453 D50453 g1805372 Bacillus subtilis 1423 -11529308 222566 opuac glycine betaine-binding protein precursor (db:genpept-bct2) (de:bacillus subtilis atpase (opuaa), transmembrane protein (opuab) andglycine betaine-binding protein precursor (opuac) genes, completecds.) (le:2332) (re:3213) (di:direct) BSU17292 U17292 g984805 Bacillus subtilis 1423 -11529308 170024 opuac glycine betaine abc transporter glycine betaine-binding protein opuac precursor (db:pir) I40537 I40537 Bacillus subtilis 1423 -11529308 6500725450 glycine betaine abc transporter:glycine betaine-binding protein:glycine betaine-binding protein precursor (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuAC opuAC Bacillus subtilis 1423 -11529308

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751406	1589	23745	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751407	1590	23746	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751408	1591	23747	639	212

Description

6500725451 nrg-21:gabp gamma-aminobutyrate:gaba permease:4-amino butyrate transport carrier:gama-aminobutyrate permease (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) gabP gabP Bacillus subtilis 1423 -11529309 72877 gabp (de:permease)) (db:swissprot) GABP_BACSU P46349 BACILLUS SUBTILIS 1423 -11529309 7000685343 gabp gamma-aminobutyrate permease gabp (cl:arginine permease) (db:pir2.dat) C69628 C69628 Bacillus subtilis 1423 -11529309 220054 gabp gabp (fn:gamma-aminobutyric acid permease) (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:4-aminobutyrate... BSU51115 U51115 g1708639 Bacillus subtilis 1423 -11529309 298012 gabp gamma-aminobutyrate gaba permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: nrg-21) (le:84172) (re:85581) (di:complement) BSUB0004 Z99107 g2632944 Bacillus subtilis 1423 -11529309

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751409	1592	23748	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751416	1593	23749	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751429	1594	23750	384	127

Description

6500725452 yerk:opue proline transporter (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuE opuE Bacillus subtilis 1423 -11529310 7000694450 opue sodium/proline symporter opue:proline transporter opue (cl:proline carrier protein) (db:pir2.dat) H69670 H69670 Bacillus subtilis 1423 -11529310 1500696453 opue opue (fn:osmoprotectant uptake) (db:genpept-bct1) (de:bacillus subtilis sapb (sapb), opue (opue), yeda (yeda) genes,complete cds, and yedb (yedb) gene, partial cds.) (nt:53 kda; complements e.coli strains with defects in) (le:968) (re:2446) (di:complement) AF011545 AF011545 g2465556 Bacillus subtilis 1423 -11529310 5500687242 opue osmoregulated proline transporter (db:genpept-bct1) (de:bacillus subtilis strain jh642 amidase-like protein, partial cds,osmoregulated proline transporter (opue) gene, complete cds andsapb (sapb) gene, partial cds.) (nt:opue) (le:982) (re:2460) (di:direct) BSU92466 U92466 g2114423 Bacillus subtilis 1423 -11529310 7500955292 opue proline transporter (fn:osmoprotection) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yerk) (le:125646) (re:127124) (di:complement) BSUB0004 Z99107 g2632980 Bacillus subtilis 1423 -11529310

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751441	1595	23751	300	99

Description

5000688728 oligopeptide abc transporter:atp-binding protein:oligopeptide transport atp-binding protein appd (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appD appD Bacillus subtilis 1423 -11529311 59882 appd (de:oligopeptide transport atp-binding protein appd) (db:swissprot) APPD_BACSU P42064 BACILLUS SUBTILIS 1423 -11529311 7000684595 appd oligopeptide transport atp-binding protein appd (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) I40543 I40543 Bacillus subtilis 1423 -11529311 7500877000 appd appd (db:genpept-bct1) (de:bacillus subtilis permease system app operon appd (appd), appf(appf), appa (appa), appb (appb), and appc (appc) genes, completecds.) (le:672) (re:1658) (di:direct) BSU20909 U20909 g677943 Bacillus subtilis 1423 -11529311 219864 appd oligopeptide abc transporter atp-binding (fn:oligopeptide transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:16554) (re:17540) (di:direct) BSUB0007 Z99110 g2633490 Bacillus subtilis 1423 -11529311 169867 appd oligopeptide abc transporter atp-binding protein appd (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir) I40543 I40543 Bacillus subtilis 1423 -11529311 6500725453 oligopeptide abc transporter:atp-binding protein:oligopeptide transport atp-binding protein appd (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appD appD Bacillus subtilis 1423 -11529311

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751444	1596	23752	945	315

Description

5000688729 oligopeptide abc transporter:atp-binding protein:oligopeptide transport atp-binding protein appf (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appF appF Bacillus subtilis 1423 -11529312 59883 appf (de:oligopeptide transport atp-binding protein appf) (db:swissprot) APPF_BACSU P42065 BACILLUS SUBTILIS 1423 -11529312 7000684596 appf oligopeptide transport atp-binding protein appf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) I40544 I40544 Bacillus subtilis 1423 -11529312 7500877001 appf appf (db:genpept-bct1) (de:bacillus subtilis permease system app operon appd (appd), appf(appf), appa (appa), appb (appb), and appc (appc) genes, completecds.) (le:1655) (re:2644) (di:direct) BSU20909 U20909 g677944 Bacillus subtilis 1423 -11529312 219865 appf oligopeptide abc transporter atp-binding (fn:oligopeptide transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:17537) (re:18526) (di:direct) BSUB0007 Z99110 g2633491 Bacillus subtilis 1423 -11529312 169868 appf oligopeptide abc transporter atp-binding protein appf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir) I40544 I40544 Bacillus subtilis 1423 -11529312 6500725454 oligopeptide abc transporter:atp-binding protein:oligopeptide transport atp-binding protein appf (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appF appF Bacillus subtilis 1423 -11529312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751448	1597	23753	405	135

Description

GTC ORF with score 140 to: (db:genpept-bct1) (ec:1.1.1.67) (de:pseudomonas fluorescens mannitol operon, mtle (mtle), mtlf (mtlf),mtlg (mtlg), mtlk (mtlk), mannitol dehydrogenase (mtld), xylulosekinase (mtly) and fructokinase (mtlz) genes, complete ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751454	1598	23754	573	190

Description

GTC ORF with score 151 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c16a3.) (nt:spbc16a3.06, probable adenosine deaminase; contains) (le:10730:10965:11022:11170) (re:10923:10979:11111:12037) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751469	1599	23755	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751497	1600	23756	795	264

Description

5000688725 oligopeptide abc transporter:oligopeptide-binding protein:oligopeptide-binding protein appa precursor (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appA appA Bacillus subtilis 1423 -11529313 59877 appa (de:oligopeptide-binding protein appa precursor) (db:swissprot) APPA_BACSU P42061 BACILLUS SUBTILIS 1423 -11529313 7000684592 appa oligopeptide abc transporter oligopeptide-binding protein appa (cl:dipeptide transport protein) (db:pir2.dat) I40545 I40545 Bacillus subtilis 1423 -11529313 7500876995 appa appa (db:genpept-bct1) (de:bacillus subtilis permease system app operon appd (appd), appf(appf), appa (appa), appb (appb), and appc (appc) genes, completecds.) (le:2732) (re:4363) (di:direct) BSU20909 U20909 g677945 Bacillus subtilis 1423 -11529313 219866 appa oligopeptide abc transporter (fn:oligopeptide transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:18614) (re:20245) (di:direct) BSUB0007 Z99110 g2633492 Bacillus subtilis 1423 -11529313 169864 appa oligopeptide abc transporter oligopeptide-binding protein appa (db:pir) I40545 I40545 Bacillus subtilis 1423 -11529313 6500725455 oligopeptide abc transporter:oligopeptide-binding protein:oligopeptide-binding protein appa precursor (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appA appA Bacillus subtilis 1423 -11529313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751508	1601	23757	468	155

Description

5000688726 oligopeptide abc transporter:permease:oligopeptide transport permease protein appb (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appB appB Bacillus subtilis 1423 -11529314 59878 appb (de:oligopeptide transport permease protein appb) (db:swissprot) APPB_BACSU P42062 BACILLUS SUBTILIS 1423 -11529314 7000684593 appb oligopeptide abc transporter permease appb (cl:oligopeptide permease protein oppb) (db:pir2.dat) I40546 I40546 Bacillus subtilis 1423 -11529314 7500876996 appb appb (db:genpept-bct1) (de:bacillus subtilis permease system app operon appd (appd), appf(appf), appa (appa), appb (appb), and appc (appc) genes, completecds.) (le:4439) (re:5392) (di:direct) BSU20909 U20909 g677946 Bacillus subtilis 1423 -11529314 219867 appb oligopeptide abc transporter permease (fn:oligopeptide transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:20321) (re:21274) (di:direct) BSUB0007 Z99110 g2633493 Bacillus subtilis 1423 -11529314 169865 appb oligopeptide abc transporter permease appb (db:pir) I40546 I40546 Bacillus subtilis 1423 -11529314 6500725456 oligopeptide abc transporter:permease:oligopeptide transport permease protein appb (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appB appB Bacillus subtilis 1423 -11529314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751516	1602	23758	246	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751631	1603	23759	603	201

Description

5000688727 oligopeptide abc transporter:permease:oligopeptide transport permease protein appc (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appC appC Bacillus subtilis 1423 -11529315 59880 appc (de:oligopeptide transport permease protein appc) (db:swissprot) APPC_BACSU P42063 BACILLUS SUBTILIS 1423 -11529315 7000684594 appc oligopeptide abc transporter permease appc (cl:oligopeptide permease protein oppb) (db:pir2.dat) I40547 I40547 Bacillus subtilis 1423 -11529315 7500876998 appc appc (db:genpept-bct1) (de:bacillus subtilis permease system app operon appd (appd), appf(appf), appa (appa), appb (appb), and appc (appc) genes, completecds.) (le:5409) (re:6320) (di:direct) BSU20909 U20909 g677947 Bacillus subtilis 1423 -11529315 219868 appc oligopeptide abc transporter permease (fn:oligopeptide transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:21291) (re:22202) (di:direct) BSUB0007 Z99110 g2633494 Bacillus subtilis 1423 -11529315 169866 appc oligopeptide abc transporter permease appc (db:pir) I40547 I40547 Bacillus subtilis 1423 -11529315 6500725457 oligopeptide abc transporter:permease:oligopeptide transport permease protein appc (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) appC appC Bacillus subtilis 1423 -11529315

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751632	1604	23760	261	86

Description

6500725458 spo0ka:oppa oligopeptide abc transporter:binding protein:oligopeptide-binding protein oppa precursor (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) oppA oppA Bacillus subtilis 1423 -11529316 7000694338 oppa:spo0ka oligopeptide abc transport system substrate-binding protein oppa precursor:oppa homolog:sporulation initiation protein spo0ka (cl:dipeptide transport protein) (db:pir2.dat) A38447 A38447 Bacillus subtilis 1423 -11529316 7500965030 spo0ka sporulation protein (sr:b.subtilis (strain jh642) dna, clones pdr20/21, pj12/3 and pj17) (db:genpept-bct1) (de:bacillus subtilis spo0k operon.) (le:477) (re:2114) (di:direct) BACSPO0K M57689 g143603 Bacillus subtilis 1423 -11529316 216857 oppa oligopeptide abc transporter binding protein (fn:required for initiation of sporulation,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: spo0ka) (le:24931) (re:26568) (di:direct) BSUB0007 Z99110 g2633497 Bacillus subtilis 1423 -11529316 170385 oppa:spo0ka oligopeptide abc transport system substrate-binding protein oppa precursor:oppa homolog:sporulation initiation protein spo0ka (db:pir) A38447 A38447 Bacillus subtilis 1423 -11529316

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751635	1605	23761	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751639	1606	23762	357	118

Description

6500725459 spo0kb:oppb oligopeptide abc transporter:permease:oligopeptide transport system permease protein oppb (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) oppB oppB Bacillus subtilis 1423 -11529317 7000694339 oppb:spo0kb oligopeptide transport system permease protein oppb:sporulation initiation protein spo0kb (cl:oligopeptide permease protein oppb) (db:pir2.dat) H69668 H69668 Bacillus subtilis 1423 -11529317 7500955183 oppb oligopeptide abc transporter permease (fn:required for initiation of sporulation,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: spo0kb) (le:26676) (re:27611) (di:direct) BSUB0007 Z99110 g2633498 Bacillus subtilis 1423 -11529317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751650	1607	23763	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751658	1608	23764	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751680	1609	23765	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751686	1610	23766	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751687	1611	23767	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751691	1612	23768	612	203

Description

6500725460 spo0kc:oppc oligopeptide abc transporter:permease:oligopeptide transport system permease protein oppc (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) oppC oppC Bacillus subtilis 1423 -11529318 219436 oppc:spo0kc (de:oligopeptide transport system permease protein oppc) (db:swissprot) OPPC_BACSU P24139 BACILLUS SUBTILIS 1423 -11529318 7000686044 oppc:spo0kc oligopeptide abc transporter permease oppc:sporulation initiation protein spo0kc (cl:oligopeptide permease protein oppb) (db:pir2.dat) A69669 A69669 Bacillus subtilis 1423 -11529318 5000688755 oppc (db:genpept-bct1) (de:b. subtilis opp operon (genes oppa, oppb, oppc, oppd and oppf) foroligopeptide permease.) (le:2760) (re:3677) (di:direct) BSOPPOPER X56347 g40007 Bacillus subtilis 1423 -11529318 7500887196 oppc oligopeptide abc transporter permease (fn:required for initiation of sporulation,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: spo0kc) (le:27615) (re:28532) (di:direct) BSUB0007 Z99110 g2633499 Bacillus subtilis 1423 -11529318 87754 oppc:spo0kc (de:oligopeptide transport system permease protein oppc) (db:swissprot) OPPC_BACSU P24139 BACILLUS SUBTILIS 1423 -11529318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751692	1613	23769	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751694	1614	23770	228	76

Description

6500725461 spo0kd:oppd oligopeptide abc transporter:atp-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) oppD oppD Bacillus subtilis 1423 -11529319 7000694336 spo0kd:oppd oligopeptide transport atp-binding protein oppd:sporulation initiation protein spo0kd (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B69669 B69669 Bacillus subtilis 1423 -11529319 7500955214 oppd oligopeptide abc transporter atp-binding (fn:required for initiation of sporulation,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: spo0kd) (le:28537) (re:29613) (di:direct) BSUB0007 Z99110 g2633500 Bacillus subtilis 1423 -11529319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751700	1615	23771	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751704	1616	23772	462	153

Description

6500725462 spo0ke:oppf oligopeptide abc transporter:atp-binding protein:oligopeptide transport atp-binding protein oppf (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) oppF oppF Bacillus subtilis 1423 -11529320 216863 spo0ke sporulation protein (sr:b.subtilis (strain jh642) dna, clones pdr20/21, pjl2/3 and pjl7) (db:genpept-bct1) (de:bacillus subtilis spo0k operon.) (nt:alternative translation start) (le:5161) (re:6078) (di:direct) BACSPO0K M57689 g551727 Bacillus subtilis 1423 -11529320 7500955195 oppf oligopeptide abc transporter atp-binding (fn:required for initiation of sporulation,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: spo0ke) (le:29615) (re:30532) (di:direct) BSUB0007 Z99110 g2633501 Bacillus subtilis 1423 -11529320 7000694337 oppf oligopeptide abc transporter atp-binding protein initiation of sporulation:competence development oppf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir) C69669 C69669 Bacillus subtilis 1423 -11529320

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751713	1617	23773	621	206

Description

6500725463 dciaa:dppa dipeptide abc transporter:dipeptide transport protein dppa (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) dppA dppA Bacillus subtilis 1423 -11529321 7000692923 dppa dipeptide abc transporter sporulation dppa (db:pir2.dat) C69618 C69618 Bacillus subtilis 1423 -11529321 6000689738 dppa dppa (fn:abc-type dipeptide transport system) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:12528) (re:13352) (di:direct) BSAJ2571 AJ002571 g2632013 Bacillus subtilis 1423 -11529321 7500963941 dppa dipeptide abc transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: dciaa) (le:165477) (re:166301) (di:direct) BSUB0007 Z99110 g2633646 Bacillus subtilis 1423 -11529321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751720	1618	23774	900	300

Description

6500725464 dciab:dppb dipeptide abc transporter:permease:dipeptide transport system permease protein dppb (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) dppB dppB Bacillus subtilis 1423 -11529322 219126 dppb:dciab (de:dipeptide transport system permease protein dppb) (db:swissprot) DPPB_BACSU P26903 BACILLUS SUBTILIS 1423 -11529322 7000685090 dppb:dciab dipeptide transport system permease protein dppb:dciab protein:dipeptide abc transporter permease sporulation dppb (cl:oligopeptide permease protein oppb) (db:pir2.dat) S16648 S16648 Bacillus subtilis 1423 -11529322 6000684675 dppb dppb (fn:abc-type dipeptide transport system) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:13369) (re:14295) (di:direct) BSAJ2571 AJ002571 g2632014 Bacillus subtilis 1423 -11529322 5000688735 dciab (db:genpept-bct1) (de:b.subtilis dcia operon.) (le:1051) (re:1977) (di:direct) BSDCIA X56678 g580850 Bacillus subtilis 1423 -11529322 304098 dppb dipeptide abc transporter permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: dciab) (le:166318) (re:167244) (di:direct) BSUB0007 Z99110 g2633647 Bacillus subtilis 1423 -11529322 69228 dppb:dciab (de:dipeptide transport system permease protein dppb) (db:swissprot) DPPB_BACSU P26903 BACILLUS SUBTILIS 1423 -11529322 153009 dppb:dciab dipeptide abc transporter permease sporulation dppb:dciab protein (cl:oligopeptide permease protein oppb) (db:pir) S16648 S16648 Bacillus subtilis 1423 -11529322

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751886	1619	23775	195	64

Description

6500725465 dciac:dppc dipeptide abc transporter:permease:dipeptide transport system permease protein dppc (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) dppC dppC Bacillus subtilis 1423 -11529323 7000692907 dppc:dciac dipeptide abc transporter permease:dciac protein (cl:oligopeptide permease protein oppb) (db:pir2.dat) S16649 S16649 Bacillus subtilis 1423 -11529323 7500963940 dppc dppc (fn:abc-type dipeptide transport system) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:14301) (re:15263) (di:direct) BSAJ2571 AJ002571 g2632015 Bacillus subtilis 1423 -11529323 6000686183 dppc dipeptide abc transporter permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: dciac) (le:167250) (re:168212) (di:direct) BSUB0007 Z99110 g2633648 Bacillus subtilis 1423 -11529323 169952 dppc:dciac dipeptide abc transporter permease sporulation dppc:dciac protein (db:pir) S16649 S16649 Bacillus subtilis 1423 -11529323

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751890	1620	23776	228	76

Description

6500725466 dciad:dppd dipeptide abc transporter:atp-binding protein:dipeptide transport atp-binding protein dppd (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) dppD dppD Bacillus subtilis 1423 -11529324 219128 dppd:dciad (de:dipeptide transport atp-binding protein dppd) (db:swissprot) DPPD_BACSU P26905 BACILLUS SUBTILIS 1423 -11529324 7000685091 dppd:dciad dipeptide transport atp-binding protein dppd:dipeptide abc transporter atp-binding protein sporulation dppd:dipeptide transport protein dciad (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) S16650 S16650 Bacillus subtilis 1423 -11529324 6000684677 dppd dppd (fn:abc-type dipeptide transport system) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:15268) (re:16275) (di:direct) BSAJ2571 AJ002571 g2632016 Bacillus subtilis 1423 -11529324 5000688737 dciad (db:genpept-bct1) (de:b.subtilis dcia operon.) (le:2950) (re:3957) (di:direct) BSDCIA X56678 g48807 Bacillus subtilis 1423 -11529324 304100 dppd dipeptide abc transporter atp-binding protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: dciad) (le:168217) (re:169224) (di:direct) BSUB0007 Z99110 g2633649 Bacillus subtilis 1423 -11529324 69234 dppd:dciad (de:dipeptide transport atp-binding protein dppd) (db:swissprot) DPPD_BACSU P26905 BACILLUS SUBTILIS 1423 -11529324 153025 dppd:dciad dipeptide abc transporter atp-binding protein sporulation dppd:dipeptide transport protein dciad (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir) S16650 S16650 Bacillus subtilis 1423 -11529324

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751891	1621	23777	258	85

Description

GTC ORF with score 185 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1030.) (nt:similar to saccharomyces cerevisiae orf ynl274c,) (le:276) (re:1280) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751898	1622	23778	963	320

Description

6500725467 dciae:dppe dipeptide abc transporter:dipeptide-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) dppE dppE Bacillus subtilis 1423 -11529325 7000692922 dppe:dciae dipeptide abc transporter dipeptide-binding protein (cl:dipeptide transport protein) (db:pir2.dat) G69618 G69618 Bacillus subtilis 1423 -11529325 6000689740 dppe dppe (fn:abc-type dipeptide transport system) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:16278) (re:17927) (di:direct) BSAJ2571 AJ002571 g2632017 Bacillus subtilis 1423 -11529325 7500955177 dppe dipeptide abc transporter dipeptide-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: dciae) (le:169227) (re:170876) (di:direct) BSUB0007 Z99110 g2633650 Bacillus subtilis 1423 -11529325

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751921	1623	23779	738	246

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751929	1624	23780	474	158

Description

GTC ORF with score 441 to: (sr:european rabbit strain=new zealand) (db:genpept-mam) (de:oryctolagus cuniculus protein phosphatase 2a0 b' regulatory subunitbeta3 isoform mrna, complete cds.) (nt:alternatively spliced form of the b' beta subunit;) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751931	1625	23781	402	133

Description

GTC ORF with score 448 to: (sr:european rabbit strain=new zealand) (db:genpept-mam) (de:oryctolagus cuniculus protein phosphatase 2a0 b' regulatory subunitbeta3 isoform mrna, complete cds.) (nt:alternatively spliced form of the b' beta subunit;) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751932	1626	23782	744	247

Description

6500725468 aminopeptidase:aminopeptidase amps (gtcfc:12.1) (ec:3.4.11.-) (keggfc:14.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) ampS ampS Bacillus subtilis 1423 -11529326 59412 amps (ec:3.4.11.-) (de:aminopeptidase amps,) (db:swissprot) AMPS_BACSU P39762 BACILLUS SUBTILIS 1423 -11529326 7000684576 amps aminopeptidase amps (cl:bacillus aminopeptidase) (db:pir2.dat) C69585 C69585 Bacillus subtilis 1423 -11529326 7500876869 amps aminopeptidase (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to amps gene with genban accession number) (le:20100) (re:21332) (di:complement) AF012285 AF012285 g3282130 Bacillus subtilis 1423 -11529326 220069 amps aminopeptidase (db:genpept-bct1) (ec:3.4.11.-) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:119612) (re:120844) (di:complement) BSUB0008 Z99111 g2633816 Bacillus subtilis 1423 -11529326 5000689454 (de:(amps) (pn:aminopeptidase amps:amps protein:fragment) (gtcfc:13.07) (ec:3.4.11.-) (amps_bacsu) (keggfc:11.1) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ampS ampS Bacillus subtilis 1423 10117825

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751933	1627	23783	285	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751944	1628	23784	960	319

Description

6500725469 amino acid carrier protein:amino acid carrier protein alst (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) alsT alsT Bacillus subtilis 1423 -11529327 7500876783 alst (de:amino acid carrier protein alst) (db:swissprot) ALST_BACSU Q45068 BACILLUS SUBTILIS 1423 -11529327 7000684566 alst amino acid carrier protein alst (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) A69585 A69585 Bacillus subtilis 1423 -11529327 217895 alst alst (fn:aminoacid carrier protein) (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:similar to sodium/proton dependent alanine carrier) (le:20601) (re:21998) (di:direct) BC170DEGR Z73234 g1405464 Bacillus subtilis 1423 -11529327 7502851603 alst amino acid carrier protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:156980) (re:158377) (di:direct) BSUB0010 Z99113 g2634195 Bacillus subtilis 1423 -11529327 4000709754 alst (de:amino acid carrier protein alst) (db:swissprot) ALST_BACSU Q45068 BACILLUS SUBTILIS 1423 -11529327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751950	1629	23785	327	108

Description

GTC ORF with score 122 to: (sr:house mouse) (db:genpept-rod) (de:mus musculus hematopoietic-specific il-2 deubiquitinating enzyme(dub-2) gene, complete cds.) (nt:ubiquitin-specific thiol protease (ubp)) (le:398:1208) (re:425:2817) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751963	1630	23786	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751975	1631	23787	645	214

Description

5000688370 bfmb2:bfmb:bfmbb branched-chain alpha-keto acid dehydrogenase e2 subunit:lipoamide acyltransferase:lipoamide acyltransferase component:e2 of branched-chain alpha-keto acid dehydrogenase complex:dihydrolipoamide branched chain transacylase (gtcfc:12.1) (ec:2.3.1.-) (keggfc:14.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) bfmBB bfmBB Bacillus subtilis 1423 -11529328 87440 bfmbb:bfmb2:bfmb (ec:2.3.1.-) (de:chain transacylase)) (db:swissprot) ODB2_BACSU P37942 BACILLUS SUBTILIS 1423 -11529328 7000686029 bfmbb dihydrolipoamide s-acyltransferase::alpha-oxo acid dehydrogenase complex bfmbb:branched-chain alpha-oxo acid dehydrogenase complex e2 component:dihydrolipoyl acyltransferase (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.-) (db:pir2.dat) S32488 S32488 Bacillus subtilis 1423 -11529328 7500887086 branched chain alpha-keto acid dehydrogenase e2 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis branched chain alpha-keto acid dehydrogenaseel-alpha, branched chain alpha-keto acid dehydrogenase e1-beta, andbranched chain alpha-keto acid dehydrogenase e2, complete cds.) (le:2228) ... BACBRANCH M97391 g142613 Bacillus subtilis 1423 -11529328 215303 bfmbb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:221574) (re:222848) (di:direct) BACJH642 D84432 g1303944 Bacillus subtilis 1423 -11529328 216188 bfmbb branched-chain alpha-keto acid dehydrogenase e2 (db:genpept-bct1) (ec:2.3.1.-) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: bfmb2) (le:100771) (re:102045) (di:complement) BSUB0013 Z99116 g2634837 Bacillus subtilis 1423 -11529328 137906 bfmbb dihydrolipoamide s-acyltransferase::alpha-oxo acid dehydrogenase complex bfmbb:branched-chain alpha-oxo acid dehydrogenase complex e2 component:dihydrolipoyl acyltransferase (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.-) (db:pir) S32488 S32488 Bacillus subtilis 1423 -11529328 6500725470 bfmb2:bfmb branched-chain alpha-keto acid dehydrogenase e2 subunit:lipoamide acyltransferase:lipoamide acyltransferase component:e2 of branched-chain alpha-keto acid dehydrogenase complex:dihydrolipoamide branched chain transacylase (gtcfc:12.1) (ec:2.3.1.-) (keggfc:14.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) bfmBB bfmBB Bacillus subtilis 1423 -11529328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501751985	1632	23788	252	83

Description

6500725471 yrdj:brnq branched-chain amino acid transporter (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) brnQ brnQ Bacillus subtilis 1423 -11529329 7000692294 brnq branched-chain amino acid transporter brnq (cl:branched-chain amino acid transport system ii carrier protein braz) (db:pir2.dat) D69596 D69596 Bacillus subtilis 1423 -11529329 1500692683 yrdj amino acid transporter (db:genpept-bct1) (de:bacillus subtilis aminoglycoside 6-adenylyltransferase (aadk) gene,partial cds, and yrda (yrda), yrdb (yrdb), hypothetical proteinyrdc (yrdc), yrdd (yrdd), hypothetical cytochrome p450 protein yrde(yrde), ribonuclease inhibitor (y... BSU93876 U93876 g1934652 Bacillus subtilis 1423 -11529329 7500963466 brnq branched-chain amino acid transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yrdj) (le:126979) (re:128301) (di:complement) BSUB0014 Z99117 g2635114 Bacillus subtilis 1423 -11529329

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752002	1633	23789	618	206

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752120	1634	23790	372	124

Description

6500725472 aminoglycoside 6-adenylyltransferase:aad:6 (gtcfc:12.1) (ec:2.7.7.-) (keggfc:14.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) aadK aadK Bacillus subtilis 1423 -11529330 57833 aadk (ec:2.7.7.-) (de:aminoglycoside 6-adenylyltransferase, (aad(6))) (db:swissprot) AADK_BACSU P17585 BACILLUS SUBTILIS 1423 -11529330 124056 aadk aminoglycoside 6-adenylyltransferase (cl:aminoglycoside 6-adenylyltransferase) (ec:2.7.7.-) (db:pir1.dat) XXBSG JU0059 Bacillus subtilis 1423 -11529330 215108 aadk aminoglycoside 6-adenylyltransferase (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis (168 marburg) aminoglycoside6-adenylyltransferase (aadk) gene, complete cds.) (le:90) (re:944) (di:direct) BACAADK M26879 g529016 Bacillus subtilis 1423 -11529330 7500876219 aadk aminoglycoside 6-adenylyltransferase (db:genpept-bct1) (ec:2.7.7.-) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:135501) (re:136355) (di:complement) BSUB0014 Z99117 g2635124 Bacillus subtilis 1423 -11529330 5000688488 (de:(aadk) (pn:aminoglycoside 6-adenylyltransferase:aad:aminoglycoside 6-adenylyltransferase :aad:6) (gtcfc:7.01:9.12) (ec:2.7.7.-) (aadk_bacsu) (keggfc:4.4:9.13) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) aadK aadK Bacillus subtilis 1423 10000613

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752132	1635	23791	582	193

Description

GTC ORF with score 445 to: (or:Callithrix sp.) (fn:converts sorbitol to fructose using nad+) (sr:callithrix sp) (db:genpept-pri2) (de:callithrix sp. sorbitol dehydrogenase (sord) mrna, partial cds.) (nt:adh-like protein) (le:1) (re:1071) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752134	1636	23792	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752151	1637	23793	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752165	1638	23794	309	102

Description

GTC ORF with score 273 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana bac t7i23, complete sequence.) (nt:similar to yeast general negative regulator of) (le:23723:23994:24373:24660) (re:23793:24174:24577:24888) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752176	1639	23795	603	200

Description

6500725473 amino acid permease (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) aapA aapA Bacillus subtilis 1423 -11529331 7500876228 aapa (de:amino acid permease aapa) (db:swissprot) AAPA_BACSU O06005 BACILLUS SUBTILIS 1423 -11529331 7000692194 aapa amino acid permease aapa (cl:arginine permease) (db:pir2.dat) B69580 B69580 Bacillus subtilis 1423 -11529331 1500695689 aapa amino acid permease (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:376) (re:1755) (di:complement) BS233DEG X92868 g2108260 Bacillus subtilis 1423 -11529331 7500876231 aapa amino acid permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:166376) (re:167755) (di:direct) BSUB0014 Z99117 g2635155 Bacillus subtilis 1423 -11529331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752178	1640	23796	312	103

Description

6500725474 glutamine abc transporter:atp-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) glnQ glnQ Bacillus subtilis 1423 -11529332 7000693052 glnq glutamine transport protein glnq (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) G69633 G69633 Bacillus subtilis 1423 -11529332 219333 glnq glutamine abc transporter atp-binding protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:202178) (re:202906) (di:direct) BSUB0014 Z99117 g2635188 Bacillus subtilis 1423 -11529332 6000689836 glnq glutamine abc transporter atp-binding protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:6498) (re:7226) (di:direct) BSUB0015 Z99118 g2635206 Bacillus subtilis 1423 -11529332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752181	1641	23797	294	97

Description

6500725475 glutamine abc transporter:glutamine-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) glnH glnH Bacillus subtilis 1423 -11529333 7000693054 glnh glutamine abc transporter glutamine-binding protein glnh (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) D69633 D69633 Bacillus subtilis 1423 -11529333 219334 glnh glutamine abc transporter glutamine-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:202928) (re:203749) (di:direct) BSUB0014 Z99117 g2635189 Bacillus subtilis 1423 -11529333 6000689838 glnh glutamine abc transporter glutamine-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:7248) (re:8069) (di:direct) BSUB0015 Z99118 g2635207 Bacillus subtilis 1423 -11529333

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752198	1642	23798	348	115

Description

6500725476 glutamine abc transporter:integral membrane protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) glnM glnM Bacillus subtilis 1423 -11529334 7000693055 glnm glutamine abc transporter membrane protein glnm (cl:histidine permease protein m) (db:pir2.dat) E69633 E69633 Bacillus subtilis 1423 -11529334 219335 glnm glutamine abc transporter integral membrane (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:203810) (re:204460) (di:direct) BSUB0014 Z99117 g2635190 Bacillus subtilis 1423 -11529334 6000689840 glnm glutamine abc transporter integral membrane (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:8130) (re:8780) (di:direct) BSUB0015 Z99118 g2635208 Bacillus subtilis 1423 -11529334

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752215	1643	23799	795	264

Description

6500725477 glutamine abc transporter:integral membrane protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) glnP glnP Bacillus subtilis 1423 -11529335 7000693056 glnp glutamine abc transporter membrane protein glnp (cl:histidine permease protein m) (db:pir2.dat) F69633 F69633 Bacillus subtilis 1423 -11529335 219336 glnp glutamine abc transporter integral membrane (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:204477) (re:205133) (di:direct) BSUB0014 Z99117 g2635191 Bacillus subtilis 1423 -11529335 6000689842 glnp glutamine abc transporter integral membrane (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:8797) (re:9453) (di:direct) BSUB0015 Z99118 g2635209 Bacillus subtilis 1423 -11529335

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752357	1644	23800	498	165

Description

6500725478 histidine transport protein:atp-binding protein (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) hisP hisP Bacillus subtilis 1423 -11529336 7000693096 hisp histidine transport protein hisp (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) F69641 F69641 Bacillus subtilis 1423 -11529336 4000714243 hisp putative amino acid transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:173999) (re:174778) (di:direct) AF008220 AF008220 g2293251 Bacillus subtilis 1423 -11529336 6000689065 hisp histidine transport protein atp-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:208289) (re:209068) (di:complement) BSUB0015 Z99118 g2635399 Bacillus subtilis 1423 -11529336 7500955212 hisp histidine transport protein atp-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:5649) (re:6428) (di:complement) BSUB0016 Z99119 g2635418 Bacillus subtilis 1423 -11529336

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752358	1645	23801	585	194

Description

6500725479 branched-chain amino acid transporter (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) braB braB Bacillus subtilis 1423 -11529337 7000692293 brab branched-chain amino acid transporter brab (cl:branched-chain amino acid transport system ii carrier protein braz) (db:pir2.dat) C69596 C69596 Bacillus subtilis 1423 -11529337 4000714220 brab branch-chain amino acid transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:149487) (re:150824) (di:complement) AF008220 AF008220 g2293322 Bacillus subtilis 1423 -11529337 7500963465 brab branched-chain amino acid transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:29603) (re:30940) (di:direct) BSUB0016 Z99119 g2635444 Bacillus subtilis 1423 -11529337

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752372	1646	23802	288	95

Description

6500725480 ytfq:opud glycine betaine transporter:glycine betaine transporter opud (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuD opuD Bacillus subtilis 1423 -11529338 87855 opud (de:glycine betaine transporter opud) (db:swissprot) OPUD_BACSU P54417 BACILLUS SUBTILIS 1423 -11529338 7000686057 opud glycine betaine transporter opud (db:pir2.dat) G69670 G69670 Bacillus subtilis 1423 -11529338 220050 opud putative transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:100760) (re:102298) (di:complement) AF008220 AF008220 g2293330 Bacillus subtilis 1423 -11529338 4000707233 opud glycine betaine transporter (fn:osmoprotection) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (nt:alternate gene name: ytfq) (le:78128) (re:79666) (di:direct) BSUB0016 Z99119 g2635491 Bacillus subtilis 1423 -11529338 7500887350 opud glycine betaine transporter opud (db:genpept-bct2) (de:bacillus subtilis glycine betaine transporter opud (opud) gene,complete cds.) (le:460) (re:1998) (di:direct) BSU50082 U50082 g1524397 Bacillus subtilis 1423 -11529338 5000689095 (de:(opud) (pn:glycine betaine transporter opud) (gtcfc:13.07) (ec:) (opud_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) opuD opuD Bacillus subtilis 1423 10029996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752373	1647	23803	345	114

Description

6500725481 proz:opubd choline abc transporter:membrane protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuBD opuBD Bacillus subtilis 1423 -11529339 7000692370 opubd choline abc transporter membrane protein opubd:hypothetical protein spae 5 region (cl:glycine betaine/carnitine/choline abc transporter) (db:pir2.dat) B69670 B69670 Bacillus subtilis 1423 -11529339 4000714282 opubd transmembrane protein (db:genpept-bct1) (de:bacillus subtilis choline transport system including atpase(opuba), transmembrane protein (opubb), choline binding proteinprecursor (opubc) and transmembrane protein (opubd) genes, completecds; and unknown gene.) (nt:opubd; part o... AF008930 AF008930 g2293450 Bacillus subtilis 1423 -11529339 7500963532 opubd choline abc transporter membrane protein (fn:high affinity transport of choline) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: proz) (le:59319) (re:59999) (di:complement) BSUB0018 Z99121 g2635883 Bacillus subtilis 1423 -11529339

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752374	1648	23804	330	109

Description

6500725482 prox:opubc choline abc transporter:choline-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuBC opuBC Bacillus subtilis 1423 -11529340 7000692368 opubc choline abc transporter choline-binding protein opubc (db:pir2.dat) A69670 A69670 Bacillus subtilis 1423 -11529340 4000714281 opubc choline binding protein precursor (db:genpept-bct1) (de:bacillus subtilis choline transport system including atpase(opuba), transmembrane protein (opubb), choline binding proteinprecursor (opubc) and transmembrane protein (opubd) genes, completecds; and unknown gene.) (nt:part of choli... AF008930 AF008930 g2293449 Bacillus subtilis 1423 -11529340 7500963530 opubc choline abc transporter choline-binding (fn:high affinity transport of choline) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: prox) (le:60016) (re:60936) (di:complement) BSUB0018 Z99121 g2635884 Bacillus subtilis 1423 -11529340

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752401	1649	23805	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752424	1650	23806	558	186

Description

6500725483 prow:opubb choline abc transporter:membrane protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuBB opuBB Bacillus subtilis 1423 -11529341 7000692369 opubb choline abc transporter membrane protein opubb (cl:glycine betaine/carnitine/choline abc transporter) (db:pir2.dat) H69669 H69669 Bacillus subtilis 1423 -11529341 4000714280 opubb transmembrane protein (db:genpept-bct1) (de:bacillus subtilis choline transport system including atpase(opuba), transmembrane protein (opubb), choline binding proteinprecursor (opubc) and transmembrane protein (opubd) genes, completecds; and unknown gene.) (nt:opubb; part o... AF008930 AF008930 g2293448 Bacillus subtilis 1423 -11529341 7500963531 opubb choline abc transporter membrane protein (fn:high affinity transport of choline) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: prow) (le:60948) (re:61601) (di:complement) BSUB0018 Z99121 g2635885 Bacillus subtilis 1423 -11529341

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752435	1651	23807	210	69

Description

6500725484 prov:opuba choline abc transporter:atp-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuBA opuBA Bacillus subtilis 1423 -11529342 7000692367 opuba choline abc transporter atp-binding protein opuba (cl:glycine betaine/proline transport protein prov:atp-binding cassette homology:cbs homology) (db:pir2.dat) G69669 G69669 Bacillus subtilis 1423 -11529342 4000714279 opuba atpase (db:genpept-bct1) (de:bacillus subtilis choline transport system including atpase(opuba), transmembrane protein (opubb), choline binding proteinprecursor (opubc) and transmembrane protein (opubd) genes, completecds; and unknown gene.) (nt:opuba; part o... AF008930 AF008930 g2293447 Bacillus subtilis 1423 -11529342 7500963529 opuba choline abc transporter atp-binding protein (fn:high affinity transport of choline) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: prov) (le:61618) (re:62763) (di:complement) BSUB0018 Z99121 g2635886 Bacillus subtilis 1423 -11529342

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752436	1652	23808	414	137

Description

6500725485 yvbb:opucd glycine betaine/carnitine/choline abc transporter:membrane protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuCD opuCD Bacillus subtilis 1423 -11529343 7000693064 opucd glycine betaine/carnitine/choline abc transporter membrane p opucd (cl:glycine betaine/carnitine/choline abc transporter) (db:pir2.dat) F69670 F69670 Bacillus subtilis 1423 -11529343 4000714294 opucd transmembrane protein (db:genpept-bct1) (de:bacillus subtilis osmoprotectant transport system opuc includingatpase (opuca), transmembrane protein (opucb), osmoprotectantbinding protein precursor (opucc) and transmembrane protein (opucd)genes, complete cds.) (nt:opucd; part ... AF009352 AF009352 g2271392 Bacillus subtilis 1423 -11529343 7500964035 opucd glycine betaine/carnitine/choline abc (fn:high affinity transport of glycine betaine,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvbb) (le:67059) (re:67748) (di:complement) BSUB0018 Z99121 g2635893 Bacillus subtilis 1423 -11529343

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752437	1653	23809	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752440	1654	23810	246	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752443	1655	23811	231	76

Description

6500725486 yvbc:opucc osmoprotectant-binding protein:glycine betaine/carnitine/choline abc transporter:osmoprotectant-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuCC opuCC Bacillus subtilis 1423 -11529344 7000693065 opucc glycine betaine/carnitine/choline abc transporter osmoprotec opucc (db:pir2.dat) E69670 E69670 Bacillus subtilis 1423 -11529344 7500964036 opucc glycine betaine/carnitine/choline abc (fn:high affinity transport of glycine betaine,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvbc) (le:67766) (re:68677) (di:complement) BSUB0018 Z99121 g2635894 Bacillus subtilis 1423 -11529344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752446	1656	23812	405	134

Description

6500725487 yvbd:opucb glycine betaine/carnitine/choline abc transporter:membrane protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuCB opuCB Bacillus subtilis 1423 -11529345 7000693063 opucb glycine betaine/carnitine/choline abc transporter membrane p opucb (cl:glycine betaine/carnitine/choline abc transporter) (db:pir2.dat) D69670 D69670 Bacillus subtilis 1423 -11529345 4000714292 opucb transmembrane protein (db:genpept-bct1) (de:bacillus subtilis osmoprotectant transport system opuc includingatpase (opuca), transmembrane protein (opucb), osmoprotectantbinding protein precursor (opucc) and transmembrane protein (opucd)genes, complete cds.) (nt:opucb; part ... AF009352 AF009352 g2271390 Bacillus subtilis 1423 -11529345 7500964034 opucb glycine betaine/carnitine/choline abc (fn:high affinity transport of glycine betaine,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvbd) (le:68697) (re:69350) (di:complement) BSUB0018 Z99121 g2635895 Bacillus subtilis 1423 -11529345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752461	1657	23813	675	224

Description

6500725488 yvbe:opuca glycine betaine/carnitine/choline abc transporter:atp-binding protein (gtcfc:12.1:12.6) (keggfc:11.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) opuCA opuCA Bacillus subtilis 1423 -11529346 7000693062 opuca glycine betaine/carnitine/choline abc transporter atp-bindin opuca (cl:glycine betaine/proline transport protein prov:atp-binding cassette homology:cbs homology) (db:pir2.dat) C69670 C69670 Bacillus subtilis 1423 -11529346 4000714291 opuca atpase (db:genpept-bct1) (de:bacillus subtilis osmoprotectant transport system opuc includingatpase (opuca), transmembrane protein (opucb), osmoprotectantbinding protein precursor (opucc) and transmembrane protein (opucd)genes, complete cds.) (nt:opuca; part ... AF009352 AF009352 g2271389 Bacillus subtilis 1423 -11529346 7500964033 opuca glycine betaine/carnitine/choline abc (fn:high affinity transport of glycine betaine,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvbe) (le:69373) (re:70515) (di:complement) BSUB0018 Z99121 g2635896 Bacillus subtilis 1423 -11529346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752462	1658	23814	435	144

Description

GTC ORF with score 101 to: (db:genpept-bct2) (de:streptomyces hygroscopicus putative pteridine-dependentdioxygenase, pks modules 1,2,3 and 4, and putative regulatoryprotein genes, complete cds and putative hydroxylase gene, partialcds.) (nt:orf8) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752605	1659	23815	366	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752607	1660	23816	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752611	1661	23817	456	152

Description

6500725489 amino acid racemase:probable amino acid racemase (gtcfc:12.1) (ec:5.1.1.-) (keggfc:14.1) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) racX racX Bacillus subtilis 1423 -11529347 7000692199 racx amino acid racemase racx (db:pir2.dat) C69688 C69688 Bacillus subtilis 1423 -11529347 1500694049 racx amino acid racemase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:132929) (re:133612) (di:complement) BSUB0018 Z99121 g2635956 Bacillus subtilis 1423 -11529347 7500963406 racx amino acid racemase (db:genpept-bct1) (de:b.subtilis genomic dna fragment (88 kb).) (nt:putative) (le:48059) (re:48742) (di:direct) BSZ94043 Z94043 g1945684 Bacillus subtilis 1423 -11529347

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752626	1662	23818	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752629	1663	23819	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752641	1664	23820	384	127

Description

6500725490 ipa-78d:rocc amino acid permease:amino-acid permease rocc (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) rocC rocC Bacillus subtilis 1423 -11529348 7500890487 rocc:ipa-78d (de:amino-acid permease rocc) (db:swissprot) ROCC_BACSU P39636 BACILLUS SUBTILIS 1423 -11529348 7000686435 rocc amino acid permease rocc:protein ipa-77d (cl:arginine permease) (db:pir2.dat) S39733 S39733 Bacillus subtilis 1423 -11529348 5000688769 ipa-78d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:80368) (re:81780) (di:direct) BSGENR X73124 g414002 Bacillus subtilis 1423 -11529348 219315 rocc amino acid permease (fn:arginine and ornithine utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-78d) (le:76179) (re:77591) (di:complement) BSUB0020 Z99123 g2636312 Bacillus subtilis 1423 -11529348 95881 rocc:ipa-78d (de:amino-acid permease rocc) (db:swissprot) ROCC_BACSU P39636 BACILLUS SUBTILIS 1423 -11529348 170156 rocc amino acid permease rocc (cl:arginine permease) (db:pir) S39733 S39733 Bacillus subtilis 1423 -11529348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752651	1665	23821	309	102

Description

6500725491 ee57d:hutm histidine permease:putative histidine permease (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) hutM hutM Bacillus subtilis 1423 -11529349 78095 hutm:ee57d (de:putative histidine permease) (db:swissprot) HUTM_BACSU P42087 BACILLUS SUBTILIS 1423 -11529349 7000685573 hutm histidine permease hutm (cl:arginine permease) (db:pir2.dat) E69643 E69643 Bacillus subtilis 1423 -11529349 215860 ee57d::hutm histidine permease (sr:bacillus subtilis (strain:bgsc1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome containing the hut and wapa loci.) (nt:putative) (le:361) (re:1788) (di:complement) BACHUTWAPA D31856 g603766 Bacillus subtilis 1423 -11529349 7500883634 hutm histidine permease (fn:histidine utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:47047) (re:48474) (di:direct) BSUB0021 Z99124 g2636485 Bacillus subtilis 1423 -11529349 5000688748 (de:(hutm) (pn:putative histidine permease) (gn:ee57d) (gtcfc:12.01:12.02:12.03) (ec:) (hutm_bacsu) (keggfc:11.2) (bsorffc:1.0.0) (db:gtc-bacillus subtilis)) hutM hutM Bacillus subtilis 1423 10020434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752652	1666	23822	519	173

Description

5000688770 amino acid permease:amino-acid permease roce (gtcfc:12.1) (keggfc:14.2) (bsorffc:1.1.1) (db:gtc-bacillus subtilis) rocE rocE Bacillus subtilis 1423 -11529350 215785 roce (de:amino-acid permease roce) (db:swissprot) ROCE_BACSU P39137 BACILLUS SUBTILIS 1423 -11529350 169859 roce probable arginine permease roce (cl:arginine permease) (db:pir2.dat) S49268 S55794 Bacillus subtilis 1423 -11529350 302081 roce amino acid permease (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (le:24219) (re:25622) (di:complement) BACGNTZA D78193 g1064806 Bacillus subtilis 1423 -11529350 6500725492 roce amino acid permease (db:genpept-bct1) (de:b.subtilis rocd, roce and rocf genes.) (le:1669) (re:3072) (di:direct) BSROCDEF X81802 g559883 Bacillus subtilis 1423 -11529350 219597 roce amino acid permease (fn:arginine and ornithine utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:142603) (re:144006) (di:complement) BSUB0021 Z99124 g2636580 Bacillus subtilis 1423 -11529350 95882 roce (de:amino-acid permease roce) (db:swissprot) ROCE_BACSU P39137 BACILLUS SUBTILIS 1423 -11529350 7000686436 roce amino acid permease roce (cl:arginine permease) (db:pir) S49268 A69694 Bacillus subtilis 1423 -11529350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752664	1667	23823	750	249

Description

5000688843 preprotein translocase subunit:preprotein translocase sece subunit (gtcfc:12.10) (keggfc:14.2) (bsorffc:6.4.1) (db:gtc-bacillus subtilis) secE secE Bacillus subtilis 1423 -11529351 98309 sece (de:preprotein translocase sece subunit) (db:swissprot) SECE_BACSU Q06799 BACILLUS SUBTILIS 1423 -11529351 7000686585 sece preprotein translocase chain sece (cl:protein-export protein sece) (db:pir2.dat) S39858 S39858 Bacillus subtilis 1423 -11529351 7500891473 orfe e.coli sece homologous protein (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis genes for sigma factor h and ribosomal proteins.) (le:595) (re:774) (di:direct) BACSHRBPNS D13303 g285627 Bacillus subtilis 1423 -11529351 216736 sece preprotein translocase subunit (fn:protein secretion) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:117529) (re:117708) (di:direct) BSUB0001 Z99104 g2632367 Bacillus subtilis 1423 -11529351 154817 sece preprotein translocase chain sece (cl:protein-export protein sece) (db:pir) S39858 S39858 Bacillus subtilis 1423 -11529351 6500725493 preprotein translocase subunit:preprotein translocase sece subunit (gtcfc:12.10) (keggfc:14.2) (bsorffc:6.4.1) (db:gtc-bacillus subtilis) secE secE Bacillus subtilis 1423 -11529351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752671	1668	23824	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752673	1669	23825	672	223

Description

5000688844 preprotein translocase subunit:preprotein translocase secy subunit (gtcfc:12.10) (keggfc:14.2) (bsorffc:6.4.1) (db:gtc-bacillus subtilis) secY secY Bacillus subtilis 1423 -11529352 219618 secy (de:preprotein translocase secy subunit) (db:swissprot) SECY_BACSU P16336 BACILLUS SUBTILIS 1423 -11529352 135227 secy preprotein translocase secy (cl:preprotein translocase secy) (db:pir1.dat) BWBSSY S08629 Bacillus subtilis 1423 -11529352 216627 secy integral membrane protein (db:genpept-bct1) (de:bacillus subtilis ribosomal protein (rplpnxefroq, rpmcdj,rpsqnhemk) genes, integral membrane protein (secy) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infa) gene, rna polymerase al... BACRPLP L47971 g1044984 Bacillus subtilis 1423 -11529352 216841 secy (sr:bacillus subtilis (strain 1a241) dna) (db:genpept-bct1) (de:bacillus subtilis spectinomycin resistance (s5, l30, l15, secy andadk) genes, complete cds.) (le:1215) (re:2510) (di:direct) BACSPCR M31102 g1184273 Bacillus subtilis 1423 -11529352 7500891490 secy protein aa 1-431 (db:genpept-bct1) (de:bacillus subtilis dna for secy protein homologue.) (le:164) (re:1459) (di:direct) BSSECYH X51329 g580926 Bacillus subtilis 1423 -11529352 6500725494 secy preprotein translocase subunit (fn:protein secretion) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:144525) (re:145820) (di:direct) BSUB0001 Z99104 g2632403 Bacillus subtilis 1423 -11529352 98342 secy (de:preprotein translocase secy subunit) (db:swissprot) SECY_BACSU P16336 BACILLUS SUBTILIS 1423 -11529352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752682	1670	23826	1296	431

Description

5000688839 signal recognition particle protein:fifty-four homolog (gtcfc:11.1:12.13) (keggfc:14.2) (bsorffc:6.4.1) (db:gtc-bacillus subtilis) ffh ffh Bacillus subtilis 1423 -11529353 99400 ffh (de:signal recognition particle protein (fifty-four homolog)) (db:swissprot) SR54_BACSU P37105 BACILLUS SUBTILIS 1423 -11529353 7000686672 ffh signal recognition particle chain ffh (cl:signal recognition particle 54k protein) (db:pir2.dat) B47154 B47154 Bacillus subtilis 1423 -11529353 7500892034 ffh signal recognition particle (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:73153) (re:74493) (di:direct) BSUB0009 Z99112 g2633970 Bacillus subtilis 1423 -11529353 4000707343 ffh ffh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis orf1, ffh, rpsp genes for orf1, ffh and 30sribosomal protein s16, complete cds.) (le:711) (re:2051) (di:direct) D14356 D14356 g2309080 Bacillus subtilis 1423 -11529353 170544 ffh signal recognition particle chain ffh (db:pir) B47154 B47154 Bacillus subtilis 1423 -11529353 6500725495 signal recognition particle protein:fifty-four homolog (gtcfc:11.1:12.13) (keggfc:14.2) (bsorffc:6.4.1) (db:gtc-bacillus subtilis) ffh ffh Bacillus subtilis 1423 -11529353

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752693	1671	23827	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752695	1672	23828	747	248

Description

6500725496 type i signal peptidase:signal peptidase i s:spase i:leader peptidase i (gtcfc:11.1) (ec:3.4.21.89) (keggfc:14.1) (bsorffc:6.4.1) (db:gtc-bacillus subtilis) sipS sipS Bacillus subtilis 1423 -11529354 215501 sips (ec:3.4.21.89) (de:signal peptidase i s, (spase i) (leader peptidase i)) (db:swissprot) LEPS_BACSU P28628 BACILLUS SUBTILIS 1423 -11529354 7000685729 sips signal peptidase i:sips:leader peptidase (cl:signal peptidase i sips) (ec:3.4.99.36) (db:pir2.dat) S23381 S23381 Bacillus subtilis 1423 -11529354 7500884929 sips signal peptidase (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (le:6740) (re:7294) (di:direct) BACDIA L09228 g410122 Bacillus subtilis 1423 -11529354 5000688845 sips sips (fn:signal peptidase i) (db:genpept-bct1) (de:b.subtilis sips gene for sips signal peptidase i.) (nt:the putative protein shows similarities with other) (le:239) (re:793) (di:direct) BSSIPSG Z11847 g580928 Bacillus subtilis 1423 -11529354 364565 sips type i signal peptidase (fn:modulation of the capacity and specificity for) (db:genpept-bct1) (ec:3.4.21.89) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:36289) (re:36843) (di:complement) BSUB0013 Z99116 g2634766 Bacillus subtilis 1423 -11529354 81897 sips (ec:3.4.21.89) (de:signal peptidase i s, (spase i) (leader peptidase i)) (db:swissprot) LEPS_BACSU P28628 BACILLUS SUBTILIS 1423 -11529354 170533 sips signal peptidase i:sips:leader peptidase (ec:3.4.99.36) (db:pir) S23381 S23381 Bacillus subtilis 1423 -11529354 219626 sips type i signal peptidase (fn:modulation of the capacity and specificity for) (db:genpept-bct1) (ec:3.4.21.89) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:36289) (re:36843) (di:complement) BSUB0013 Z99116 g2634766 Bacillus subtilis 1423 -11529354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752844	1673	23829	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752853	1674	23830	501	166

Description

6500725497 div-341:ts-341:div:seca translocase binding subunit:atpase::preprotein translocase seca subunit (gtcfc:12.10) (keggfc:14.2) (bsorffc:6.4.1) (db:gtc-bacillus subtilis) secA secA Bacillus subtilis 1423 -11529355 98290 seca:div+ (de:preprotein translocase seca subunit) (db:swissprot) SECA_BACSU P28366 BACILLUS SUBTILIS 1423 -11529355 7000686582 seca:div preprotein translocase seca:div protein:seca protein homolog (cl:preprotein translocase seca:dead/h box helicase homology) (db:pir2.dat) JQ0647 JQ0647 Bacillus subtilis 1423 -11529355 7500891445 seca seca protein (sr:bacillus subtilis (strain:marburg 168t) dna) (db:genpept-bct1) (de:b.subutilis gene for seca protein.) (le:544) (re:3069) (di:direct) BACSECA D10279 g216334 Bacillus subtilis 1423 -11529355 216692 seca translocase binding subunit atpase (fn:protein secretion) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: div, div-341, ts-341) (le:30280) (re:32805) (di:complement) BSUB0019 Z99122 g2636056 Bacillus subtilis 1423 -11529355 298113 seca (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762349 Bacillus subtilis 1423 -11529355 153237 seca:div preprotein translocase seca:div protein:seca protein homolog (cl:preprotein translocase seca:dead/h box helicase homology) (db:pir) JQ0647 JQ0647 Bacillus subtilis 1423 -11529355 220130 seca (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762349 Bacillus subtilis 1423 -11529355 5000688842 (de:(seca) (pn:) (gn:div) (gtcfc:12.10) (ec:) (seca_bacsu) (keggfc:11.2) (bsorffc:6.4.0) (db:gtc-bacillus subtilis)) secA secA Bacillus subtilis 1423 10040169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752881	1675	23831	1014	337

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752898	1676	23832	1095	365

Description

6500725498 superoxide dismutase (gtcfc:12.12) (keggfc:14.2) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) sodF sodF Bacillus subtilis 1423 -11529356 7000694661 sodf superoxide dismutase:fe/mn sodf (cl:superoxide dismutase (mn)) (ec:1.15.1.1) (db:pir2.dat) C69709 C69709 Bacillus subtilis 1423 -11529356 5500701921 sodf superoxide dismutase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to propionibacterium shermanii superoxide) (le:84050) (re:84895) (di:direct) AF027868 AF027868 g2619018 Bacillus subtilis 1423 -11529356 7500965243 sodf superoxide dismutase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:103141) (re:103986) (di:direct) BSUB0011 Z99114 g2634326 Bacillus subtilis 1423 -11529356

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752911	1677	23833	201	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752918	1678	23834	612	204

Description

6500725499 yqgd:soda superoxide dismutase:mn:general stress protein 24:gsp24 (gtcfc:12.12) (ec:1.15.1.1) (keggfc:14.1) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) sodA sodA Bacillus subtilis 1423 -11529357 7000694660 soda superoxide dismutase:mn soda (cl:superoxide dismutase (mn)) (ec:1.15.1.1) (db:pir2.dat) B69709 B69709 Bacillus subtilis 1423 -11529357 216095 yqgd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:133564) (re:134244) (di:direct) BACJH642 D84432 g1303851 Bacillus subtilis 1423 -11529357 7500953945 soda superoxide dismutase (db:genpept-bct1) (ec:1.15.1.1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqgd) (le:189377) (re:190057) (di:complement) BSUB0013 Z99116 g2634935 Bacillus subtilis 1423 -11529357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752924	1679	23835	411	136

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752928	1680	23836	651	216

Description

6500725500 perr:ahpc alkyl hydroperoxide reductase:small subunit:alkyl hydroperoxide reductase c22 protein:general stress protein 22 (gtcfc:12.12) (ec:1.6.4.-) (keggfc:14.1) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) ahpC ahpC Bacillus subtilis 1423 -11529358 58991 ahpc (ec:1.6.4.-) (de:protein 22)) (db:swissprot) AHPC_BACSU P80239 BACILLUS SUBTILIS 1423 -11529358 7000684544 ahpc alkyl hydroperoxide reductase:small chain:54k protein:alkyl hydroperoxide reductase chain c22 homolog:nadh dehydrogenase ahpc:nadh oxidase hydrogen peroxide-forming (cl:alkyl hydroperoxide reductase c22 protein:alkyl hydroperoxidase c22 protein homology) (ec:1.6.4.-) (db:pir2.dat) F69583 F69583 Bacillus subtilis 1423 -11529358 215761 ahpc alkyl hydroperoxide reductase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (nt:induced by hydrogen peroxide) (le:496) (re:1059) (di:direct) BACGNTZA D78193 g1064782 Bacillus subtilis 1423 -11529358 302057 ahpc alkyl hydroperoxide reductase small subunit (db:genpept-bct1) (ec:1.6.4.-) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: perr) (le:118878) (re:119441) (di:direct) BSUB0021 Z99124 g2636556 Bacillus subtilis 1423 -11529358 5000689430 (de:(ahpc) (pn:alkyl hydroperoxide reductase c22 protein:general stress protein 22) (gtcfc:13.07) (ec:1.6.4.-) (ahpc_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) ahpC ahpC Bacillus subtilis 1423 10001735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501752931	1681	23837	561	186

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753116	1682	23838	1776	592

Description

6500725501 ndh:ahpf large subunit and nadh dehydrogenase:nadh dehydrogenase:alkyl hydroperoxide reductase (gtcfc:12.12) (keggfc:14.1) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) ahpF ahpF Bacillus subtilis 1423 -11529359 68553 ahpf:ndh (ec:1.6.99.3) (de:nadh dehydrogenase, (alkyl hydroperoxide reductase)) (db:swissprot) DHNA_BACSU P42974 BACILLUS SUBTILIS 1423 -11529359 7000685044 ahpf alkyl hydroperoxide reductase:large chain:54k protein:nadh dehydrogenase ahpf:nadh oxidase hydrogen peroxide-forming (cl:nadh oxidase (hydrogen peroxide-forming):thioredoxin reductase homology) (ec:1.6.-.-) (db:pir2.dat) G69583 G69583 Bacillus subtilis 1423 -11529359 215762 ahpf alkyl hydroperoxide reductase (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis 36kb sequence between gntz and trny genesencoding 34 orfs.) (nt:induced by hydrogen peroxide) (le:1073) (re:2602) (di:direct) BACGNTZA D78193 g1064783 Bacillus subtilis 1423 -11529359 302058 ahpf alkyl hydroperoxide reductase large subunit (db:genpept-bct1) (ec:1.6.99.3) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: ndh) (le:119455) (re:120984) (di:direct) BSUB0021 Z99124 g2636557 Bacillus subtilis 1423 -11529359 5000689431 (de:(ahpf) (pn:nadh dehydrogenase:alkyl hydroperoxide reductase) (gn:ndh) (gtcfc:13.07) (ec:1.6.99.3) (dhna_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) ahpF ahpF Bacillus subtilis 1423 10011145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753129	1683	23839	516	171

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753140	1684	23840	540	179

Description

5000688846 hypothetical protein:possible thiophene and furan oxidation protein thdf (gtcfc:12.12) (keggfc:14.2) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) thdF thdF Bacillus subtilis 1423 -11529360 214986 thdf (de:possible thiophene and furan oxidation protein thdf) (db:swissprot) THDF_BACSU P25811 BACILLUS SUBTILIS 1423 -11529360 170627 thdf thiophen / furan oxidation protein thdf:50k protein homolog (cl:thiophen / furan oxidation protein:translation elongation factor tu homology) (db:pir2.dat) JQ1215 I40439 Bacillus subtilis 1423 -11529360 7500893020 tdhf thiophen and furan oxidation (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:59506) (re:60885) (di:complement) BAC180K D26185 g467386 Bacillus subtilis 1423 -11529360 219461 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:homologous to e.coli 50k) (le:2515) (re:3894) (di:direct) BSORIGS X62539 g40025 Bacillus subtilis 1423 -11529360 7502851604 thdf (fn:thiophen and furan oxidation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:211438) (re:212817) (di:complement) BSUB0021 Z99124 g2636649 Bacillus subtilis 1423 -11529360 101283 thdf (de:possible thiophene and furan oxidation protein thdf) (db:swissprot) THDF_BACSU P25811 BACILLUS SUBTILIS 1423 -11529360 7000686783 thdf thiophen / furan oxidation protein thdf:50k protein homolog (db:pir) JQ1215 S66026 Bacillus subtilis 1423 -11529360 6500725502 hypothetical protein:possible thiophene and furan oxidation protein thdf (gtcfc:12.12) (keggfc:14.2) (bsorffc:7.2.1) (db:gtc-bacillus subtilis) thdF thdF Bacillus subtilis 1423 -11529360

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753150	1685	23841	510	170

Description

6500725503 yflr:cits two-component sensor histidine kinase (gtcfc:12.13) (keggfc:12.1) (bsorffc:6.1.2:6.1.2) (db:gtc-bacillus subtilis) citS citS Bacillus subtilis 1423 -11529361 7000694859 cits two-component sensor histidine kinase cits (cl:two-component sensor histidine kinase:sensor histidine kinase homology) (db:pir2.dat) E69600 E69600 Bacillus subtilis 1423 -11529361 5500687911 cits two-component sensor histidine kinase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yflr) (le:27633) (re:29261) (di:direct) BSUB0005 Z99108 g2633082 Bacillus subtilis 1423 -11529361 7500955342 yflr (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:19260) (re:20888) (di:complement) D86417 D86417 g2443240 Bacillus subtilis 1423 -11529361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753153	1686	23842	363	120

Description

6500725504 yflq:citt two-component response regulator (gtcfc:12.13) (keggfc:12.1) (bsorffc:6.1.2:6.1.2) (db:gtc-bacillus subtilis) citT citT Bacillus subtilis 1423 -11529362 7000694836 citt two-component response regulator citt (cl:transcription regulator crir:response regulator homology) (db:pir2.dat) F69600 F69600 Bacillus subtilis 1423 -11529362 5500687910 citt two-component response regulator (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yflq) (le:29233) (re:29913) (di:direct) BSUB0005 Z99108 g2633083 Bacillus subtilis 1423 -11529362 7500965385 yflq (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:18608) (re:19288) (di:complement) D86417 D86417 g2443239 Bacillus subtilis 1423 -11529362

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753172	1687	23843	285	94

Description

GTC ORF with score 125 to: (sr:thale cress) (db:genpept-pln1) (de:genomic sequence of arabidopsis bac f8a5, complete sequence.) (nt:highly similar to auxin-induced protein (aldo/keto) (le:82317:82757:82928) (re:82655:82850:83100) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753173	1688	23844	303	100

Description

GTC ORF with score 107 to: (fn:gel formation, gastric epithelial protection) (sr:pig) (db:genpept-mam) (de:sus scrofa yorkshire/chester white/hampshire clone pgm-ss-2agastric mucin mrna, partial cds.) (nt:bases 1-105 encode a cysteine rich, non-repeat)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753177	1689	23845	591	196

Description

6500725505 spoiif:spoiij:gsic:scob:scod:kina two-component sensor histidine kinase:sporulation kinase a:stage ii sporulation protein j (gtcfc:12.13) (ec:2.7.3.-) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) kinA kinA Bacillus subtilis 1423 -11529363 7500884624 kina:spoiij:spoiif:scod:gsic (ec:2.7.3.-) (de:sporulation kinase a, (stage ii sporulation protein j)) (db:swissprot) KINA_BACSU P16497 BACILLUS SUBTILIS 1423 -11529363 170521 kina sensory kinase:kina:sporulation initiation-related sensor histidine kinase kina (ec:2.7.1.-) (db:pir2.dat) A33496 A33496 Bacillus subtilis 1423 -11529363 216479 (sr:b.subtilis dna, clones pjm8(100-106,110-113,115-116,122)) (db:genpept-bct1) (de:b.subtilis protein kinase (kina) gene, complete cds.) (nt:protein kinase kina) (le:371) (re:2191) (di:direct) BACPKSP M31067 g143333 Bacillus subtilis 1423 -11529363 6000686194 kina kina protein (fn:sporulation kinase) (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:4382) (re:6202) (di:direct) BS16829KB AJ222587 g2632220 Bacillus subtilis 1423 -11529363 7500884625 kina two-component sensor histidine kinase (fn:involved in the initiation of sporulation) (db:genpept-bct1) (ec:2.7.3.-) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: spoiif, spoiij, gsic, scob,) (le:74638) (re:76458) (di:direct) BSUB0008 Z99111 g2633770 Bacillus subtilis 1423 -11529363 7000694575 kina sensory kinase:kina:sporulation initiation-related sensor histidine kinase kina (ec:2.7.1.-) (db:pir) A33496 A33496 Bacillus subtilis 1423 -11529363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753188	1690	23846	384	127

Description

6500725506 ssb:mska:kinc two-component sensor histidine kinase:sporulation kinase c (gtcfc:12.13) (ec:2.7.3.-) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) kinC kinC Bacillus subtilis 1423 -11529364 80714 kinc:mska:ssb (ec:2.7.3.-) (de:sporulation kinase c,) (db:swissprot) KINC_BACSU P39764 BACILLUS SUBTILIS 1423 -11529364 7000685687 kinc:mska:ssb sensor kinase:kinc:protein-histidine kinase ssb:sporulation initiation two-component sensor histidine kinase kinc (ec:2.7.3.-) (db:pir2.dat) I39871 I39871 Bacillus subtilis 1423 -11529364 220073 kinc histidine protein kinase (fn:phosphorylase-independent kinase for spooa) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to kinc, encoded by genbank accession) (le:23436) (re:24722) (di:direct) AF012285 AF012285 g3282134 Bacillus subtilis 1423 -11529364 7500884626 kinc (sr:bacillus subtilis (sub_species:marburg, strain:168) (db:genpept-bct1) (de:bacillus subtilis genes for amps, mrebh, orf1, kinc, orf3, orf4 andorf5.) (le:2977) (re:4263) (di:direct) BACAMOKOOO D37799 g520842 Bacillus subtilis 1423 -11529364 215164 kinc sensor kinase (fn:phosphorylation of spo0a) (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis sensor kinase (kinc) gene, complete cds andcomplete orf.) (nt:homologous to kina and kinb genes) (le:183) (re:1469) (di:direct) BACKINC L34803 g514330 Bacillus subtilis 1423 -11529364 216263 ssb kinc (sr:bacillus subtilis (sub_species marburg) (sub_strain jh642,strai) (db:genpept-bct1) (de:bacillus subtilis genes for orf1 and kinc.) (le:911) (re:2197) (di:direct) BACORFKINC D37798 g520577 Bacillus subtilis 1423 -11529364 216418 kinc two-component sensor histidine kinase (fn:involved in the initiation of sporulation) (db:genpept-bct1) (ec:2.7.3.-) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ssb) (le:122948) (re:124234) (di:direct) BSUB0008 Z99111 g2633820 Bacillus subtilis 1423 -11529364 170520 kinc:mska:ssb sensor kinase:kinc:protein-histidine kinase ssb:sporulation initiation two-component sensor histidine kinase kinc (ec:2.7.3.-) (db:pir) I39871 I39871 Bacillus subtilis 1423 -11529364 5000688854 (de:(kinc) (pn:sporulation kinase c) (gn:mska:ssb) (gtcfc:12.13) (ec:2.7.3.-) (kinc_bacsu) (keggfc:11.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) kinC kinC Bacillus subtilis 1423 10022955

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753213	1691	23847	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753312	1692	23848	1518	506

Description

6500725507 ypxe:rese two-component sensor histidine kinase:sensor protein rese (gtcfc:12.13) (ec:2.7.3.-) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) resE resE Bacillus subtilis 1423 -11529365 93988 rese (ec:2.7.3.-) (de:sensor protein rese,) (db:swissprot) RESE_BACSU P35164 BACILLUS SUBTILIS 1423 -11529365 7000686302 rese two-component sensor histidine kinase rese (db:pir2.dat) H69691 H69691 Bacillus subtilis 1423 -11529365 7500889645 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx18) (le:22425) (re:24194) (di:direct) BACDIA L09228 g410142 Bacillus subtilis 1423 -11529365 215521 rese two-component sensor histidine kinase (fn:involved in global regulation of aerobic and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypxe) (le:19389) (re:21158) (di:complement) BSUB0013 Z99116 g2634746 Bacillus subtilis 1423 -11529365 170273 rese two-component sensor histidine kinase rese (db:pir) H69691 H69691 Bacillus subtilis 1423 -11529365 5000688856 (de:(rese) (pn:sensor protein rese) (gtcfc:12.13) (ec:2.7.3.-) (rese_bacsu) (keggfc:11.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) resE resE Bacillus subtilis 1423 10035972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753323	1693	23849	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753328	1694	23850	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753336	1695	23851	960	319

Description

6500725508 ypxd:resd two-component response regulator:transcriptional regulatory protein resd (gtcfc:12.13) (keggfc:12.1) (bsorffc:6.1.2:6.1.2) (db:gtc-bacillus subtilis) resD resD Bacillus subtilis 1423 -11529366 93987 resd (de:transcriptional regulatory protein resd) (db:swissprot) RESD_BACSU P35163 BACILLUS SUBTILIS 1423 -11529366 7000686301 resd two-component response regulator involved in aerobic and anaer resd (cl:ompr protein:response regulator homology) (db:pir2.dat) G69691 G69691 Bacillus subtilis 1423 -11529366 7500889644 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx17) (le:21706) (re:22428) (di:direct) BACDIA L09228 g410141 Bacillus subtilis 1423 -11529366 215520 resd two-component response regulator (fn:activation role in global regulation of aerobic) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypxd) (le:21155) (re:21877) (di:complement) BSUB0013 Z99116 g2634747 Bacillus subtilis 1423 -11529366 170272 resd two-component response regulator involved in aerobic and anaer resd (cl:ompr protein:response regulator homology) (db:pir) G69691 G69691 Bacillus subtilis 1423 -11529366 5000688913 (de:(resd) (pn:transcriptional regulatory protein resd:resd protein) (gtcfc:12.13) (ec:) (resd_bacsu) (keggfc:11.2) (bsorffc:6.1.3) (db:gtc-bacillus subtilis)) resD resD Bacillus subtilis 1423 10035971

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753339	1696	23852	480	159

Description

5000688957 spo0c:spo0g:spoiil:sof-1:spo0a two-component response regulator:stage 0 sporulation protein a (gtcfc:12.13:12.15) (keggfc:12.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spo0A spo0A Bacillus subtilis 1423 -11529367 99072 spo0a:spo0c:spo0g (de:stage 0 sporulation protein a) (db:swissprot) SP0A_BACSU P06534 BACILLUS SUBTILIS 1423 -11529367 131100 spo0a stage 0 sporulation protein spo0a:sporulation initiation two-component response regulator spo0a (cl:stage 0 sporulation protein a:response regulator homology) (db:pir1.dat) (mp:215 (degrees)) SZBS0A A94036 Bacillus subtilis 1423 -11529367 7500891891 spo0a (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:200777) (re:201580) (di:direct) BACJH642 D84432 g1303925 Bacillus subtilis 1423 -11529367 216169 (sr:b.subtilis dna, clone pbbc1 (3); (strain w168), clone pjh101 (2)) (db:genpept-bct1) (de:b.subtilis spo0a (sporulation) gene, complete cds.) (nt:spo0a sporulation protein (gtg start codon)) (le:309) (re:1112) (di:direct) BACSP00AA M10082 g143585 Bacillus subtilis 1423 -11529367 216846 spo0a two-component response regulator (fn:central role in the initiation of sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: spo0c, spo0g, spoiil, sof-1) (le:122041) (re:122844) (di:complement) BSUB0013 Z99116 g2634856 Bacillus subtilis 1423 -11529367 7000686622 spo0a stage 0 sporulation protein spo0a:sporulation initiation two-component response regulator spo0a (cl:stage 0 sporulation protein a:response regulator homology) (db:pir) (mp:215 (degrees)) SZBS0A A22665 Bacillus subtilis 1423 -11529367 6500725509 spo0c:spo0g:spoiil:sof-1 two-component response regulator:stage 0 sporulation protein a (gtcfc:12.13:12.15) (keggfc:12.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spo0A spo0A Bacillus subtilis 1423 -11529367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753343	1697	23853	780	259

Description

6500725510 spo0d:spo0b sporulation initiation phosphoprotein:stage 0 sporulation protein b (gtcfc:12.13:12.15) (keggfc:12.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spo0B spo0B Bacillus subtilis 1423 -11529368 219652 spo0b:spo0d (de:stage 0 sporulation protein b) (db:swissprot) SP0B_BACSU P06535 BACILLUS SUBTILIS 1423 -11529368 131101 spo0b stage 0 sporulation protein b:spo0b protein b:sporulation initiation phosphoprotein spo0b (cl:stage 0 sporulation protein b) (db:pir1.dat) (mp:245 (degrees)) SZBS0B A22974 Bacillus subtilis 1423 -11529368 215815 spoob sporulation protein (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtillis sporulation protein (spoob), gtp-binding protein(obg), phenylalanine biosynthesis associated protein (pheb), andmonofunctional prephenate dehydratase (phea) genes, complete cds.) (le:5... BACGTPBP M24537 g508978 Bacillus subtilis 1423 -11529368 216847 (sr:b. subtilis dna, clone pgs0b10) (db:genpept-bct1) (de:b. subtilis, spo0b locus, early sporulation gene spo0b, completecoding sequence.) (nt:spo0b protein) (le:462) (re:1040) (di:direct) BACSPO0B K02664 g143587 Bacillus subtilis 1423 -11529368 216850 spoob (sr:bacillus subtilis (clone pbag1, sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis spo0b early sporulation gene, complete cds.) (le:106) (re:684) (di:direct) BACSPO0B2 K02666 g143593 Bacillus subtilis 1423 -11529368 5000688958 spoob spoob polypeptide (db:genpept-bct1) (de:bacillus subtilis spoob gene and flanking regions.) (le:106) (re:684) (di:direct) BSSPOOB X02655 g40179 Bacillus subtilis 1423 -11529368 7500891892 spo0b sporulation initiation phosphoprotein (fn:stage 0 sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: spo0d) (le:58112) (re:58690) (di:complement) BSUB0015 Z99118 g2635258 Bacillus subtilis 1423 -11529368 99079 spo0b:spo0d (de:stage 0 sporulation protein b) (db:swissprot) SP0B_BACSU P06535 BACILLUS SUBTILIS 1423 -11529368

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753349	1698	23854	435	144

Description

6500725511 two-component response regulator (gtcfc:12.13) (keggfc:12.1) (bsorffc:6.1.2:6.1.2) (db:gtc-bacillus subtilis) lytT lytT Bacillus subtilis 1423 -11529369 7000694838 lytt two-component response regulator involved in the rate of autol lytt (cl:yeht protein:response regulator homology) (db:pir2.dat) B69655 B69655 Bacillus subtilis 1423 -11529369 220278 lytt two-component response regulator (fn:involved in controlling the rate of autolysis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:159728) (re:160453) (di:complement) BSUB0015 Z99118 g2635357 Bacillus subtilis 1423 -11529369 304151 lytt autolysin response regulator (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to lytr of staphylococcus aureus;) (le:9454) (re:10179) (di:direct) BSZ75208 Z75208 g1770002 Bacillus subtilis 1423 -11529369

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753350	1699	23855	918	306

Description

6500725512 two-component sensor histidine kinase (gtcfc:12.13) (keggfc:12.1) (bsorffc:6.1.2:6.1.2) (db:gtc-bacillus subtilis) lytS lytS Bacillus subtilis 1423 -11529370 7000694866 lyts two-component sensor histidine kinase involved in the rate of lyts (cl:hypothetical protein b2380) (db:pir2.dat) A69655 A69655 Bacillus subtilis 1423 -11529370 220277 lyts two-component sensor histidine kinase (fn:involved in controlling the rate of autolysis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:160431) (re:162212) (di:complement) BSUB0015 Z99118 g2635358 Bacillus subtilis 1423 -11529370 304150 lyts autolysin sensor kinase (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology with lyts of staphyloccous aureus;) (le:7695) (re:9476) (di:direct) BSZ75208 Z75208 g1770001 Bacillus subtilis 1423 -11529370

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753356	1700	23856	255	84

Description

6500725513 two-component sensor histidine kinase:alkaline phosphatase synthesis sensor protein phor (gtcfc:12.13) (ec:2.7.3.-) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) phoR phoR Bacillus subtilis 1423 -11529371 89645 phor (ec:2.7.3.-) (de:alkaline phosphatase synthesis sensor protein phor,) (db:swissprot) PHOR_BACSU P23545 BACILLUS SUBTILIS 1423 -11529371 7000686138 phor phosphate response regulator histidine kinase phor (db:pir2.dat) A27650 A27650 Bacillus subtilis 1423 -11529371 7500888059 phor signal transduction protein kinase (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:201317) (re:203056) (di:direct) AF008220 AF008220 g2293271 Bacillus subtilis 1423 -11529371 216472 phor alkaline phosphatase regulatory protein (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis alkaline phosphatase regulatory protein (phopgene, 3' end and phor gene, complete cds).) (le:85) (re:1824) (di:direct) BACPHORP M23549 g143331 Bacillus subtilis 1423 -11529371 4000707249 phor two-component sensor histidine kinase (fn:involved in phosphate regulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:180011) (re:181750) (di:complement) BSUB0015 Z99118 g2635375 Bacillus subtilis 1423 -11529371 170487 phor phosphate regulation two-component sensor histidine kinase phor (db:pir) A27650 A27650 Bacillus subtilis 1423 -11529371 5000688855 (de:(phor) (pn:alkaline phosphatase synthesis sensor protein phor) (gtcfc:12.13) (ec:2.7.3.-) (phor_bacsu) (keggfc:11.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) phoR phoR Bacillus subtilis 1423 10031767

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753357	1701	23857	441	147

Description

6500725514 two-component response regulator:alkaline phosphatase synthesis transcriptional regulatory protein phop (gtcfc:12.13) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) phoP phoP Bacillus subtilis 1423 -11529372 7000694837 phop phosphate response regulator protein phop:alkaline phosphatase regulatory protein:regulatory protein phop (cl:ompr protein:response regulator homology) (db:pir1.dat) (mp:71 min) RGBSAP F69676 Bacillus subtilis 1423 -11529372 4000714263 phop signal transduction regulator (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:200602) (re:201324) (di:direct) AF008220 AF008220 g2293270 Bacillus subtilis 1423 -11529372 7500965386 phop two-component response regulator (fn:involved in phosphate regulation (phoa, phob,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:181743) (re:182465) (di:complement) BSUB0015 Z99118 g2635376 Bacillus subtilis 1423 -11529372

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753367	1702	23858	1119	372

Description

6500725515 two-component sensor histidine kinase:sporulation kinase b (gtcfc:12.13) (ec:2.7.3.-) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) kinB kinB Bacillus subtilis 1423 -11529373 1500694332 kinb two-component sensor histidine kinase (fn:involved in the initiation of sporulation) (db:genpept-bct1) (ec:2.7.3.-) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:32144) (re:33433) (di:direct) BSUB0017 Z99120 g2635641 Bacillus subtilis 1423 -11529373 7500965425 kinb sporulation-specific atp-dependent protein (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuga to yugd.) (le:1577) (re:2866) (di:direct) BSZ93933 Z93933 g1934780 Bacillus subtilis 1423 -11529373 7000694865 kinb two-component sensor histidine kinase involved in the initiati kinb (db:pir) G69648 G69648 Bacillus subtilis 1423 -11529373

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753374	1703	23859	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753387	1704	23860	501	166

Description

GTC ORF with score 238 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:o302; this 302 aa orf is 34 pct identical (2 gaps)) (le:7159) (re:8067) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753388	1705	23861	396	131

Description

6500725516 two-component sensor histidine kinase:sensor protein comp (gtcfc:12.13) (ec:2.7.1.-) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) comP comP Bacillus subtilis 1423 -11529374 7000694864 comp two-component sensor histidine kinase involved in early compet comp (db:pir2.dat) B69604 B69604 Bacillus subtilis 1423 -11529374 1500694328 comp two-component sensor histidine kinase (fn:involved in early competence) (db:genpept-bct1) (ec:2.7.1.-) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:55605) (re:57914) (di:complement) BSUB0017 Z99120 g2635664 Bacillus subtilis 1423 -11529374 7500965424 histidine kinase (fn:competence; effector transduction protein) (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufa to yufe.) (le:3614) (re:5923) (di:direct) BSZ93932 Z93932 g1934771 Bacillus subtilis 1423 -11529374

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753392	1706	23862	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753556	1707	23863	963	321

Description

6500725517 sacu:iep:degu two-component response regulator:transcriptional regulatory protein degu:protease production enhancer protein (gtcfc:12.13:10.11) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) degU degU Bacillus subtilis 1423 -11529375 68239 degu:iep (de:protein)) (db:swissprot) DEGU_BACSU P13800 BACILLUS SUBTILIS 1423 -11529375 130892 degu:iep extracellular proteinase response regulator degu:extracellular proteinase regulatory protein iep (cl:regulatory protein coma:response regulator homology) (db:pir1.dat) RGBSXD C30191 Bacillus subtilis 1423 -11529375 7500880154 (sr:b.subtilis (strain 168) dna, clone picm1) (db:genpept-bct1) (de:b.subtilis iep gene encoding a protease production enhancerprotein, complete cds, and sacu enhancer protein gene, 3' end.) (nt:iep protein) (le:486) (re:1175) (di:direct) BACIEP M21658 g143089 Bacillus subtilis 1423 -11529375 215901 (sr:b.subtilis dna, clones pdh(49,51,54,55,59,64)) (db:genpept-bct1) (de:b.subtilis sacu region, degs and degu genes, complete cds.) (nt:degu protein (gtg start codon)) (le:1972) (re:2661) (di:direct) BACSACU M23558 g143499 Bacillus subtilis 1423 -11529375 216669 (sr:b.subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:b.subtilis transcriptional activator protein (degu) gene andprotein kinase (degs) gene, complete cds.) (nt:protein kinase (put.); putative) (le:1460) (re:2149) (di:direct) BACSACUL M23649 g143502 Bacillus subtilis 1423 -11529375 324984 degu two-component response regulator (fn:essential for degradative enzyme (sacb and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: sacu, iep) (le:46577) (re:47266) (di:complement) BSUB0019 Z99122 g2636075 Bacillus subtilis 1423 -11529375 298094 degu transcriptional regulator of degradation (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762330 Bacillus subtilis 1423 -11529375 5000688890 sacu s2 (db:genpept-pat) (de:b.subtilis sacu gene.) (le:1461) (re:2150) (di:direct) A08709 A08709 g580656 Bacillus subtilis 1423 -11529375 7000685005 degu:iep extracellular proteinase response regulator degu:extracellular proteinase regulatory protein iep (cl:regulatory protein coma:response regulator homology) (db:pir) RGBSXD B30190 Bacillus subtilis 1423 -11529375 216671 degu two-component response regulator (fn:essential for degradative enzyme (sacb and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: sacu, iep) (le:46577) (re:47266) (di:complement) BSUB0019 Z99122 g2636075 Bacillus subtilis 1423 -11529375 220111 degu transcriptional regulator of degradation (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762330 Bacillus subtilis 1423 -11529375

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753561	1708	23864	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753573	1709	23865	675	224

Description

6500725518 sacu:degs two-component sensor histidine kinase:sensor protein degs (gtcfc:12.13) (ec:2.7.3.-) (keggfc:12.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) degS degS Bacillus subtilis 1423 -11529376 68236 degs:sacu (ec:2.7.3.-) (de:sensor protein degs,) (db:swissprot) DEGS_BACSU P13799 BACILLUS SUBTILIS 1423 -11529376 131461 degs degradative enzyme regulator / competence regulator degs:two-component sensor histidine kinase degs (cl:regulatory protein degs) (db:pir1.dat) RGBSDS B30191 Bacillus subtilis 1423 -11529376 7500880151 (sr:b.subtilis dna, clones pdh(49,51,54,55,59,64)) (db:genpept-bct1) (de:b.subtilis sacu region, degs and degu genes, complete cds.) (nt:degs protein) (le:732) (re:1889) (di:direct) BACSACU M23558 g143498 Bacillus subtilis 1423 -11529376 216668 (sr:b.subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:b.subtilis transcriptional activator protein (degu) gene andprotein kinase (degs) gene, complete cds.) (nt:transcriptional activator protein) (le:220) (re:1377) (di:direct) BACSACUL M23649 g143501 Bacillus subtilis 1423 -11529376 216670 degs two-component sensor histidine kinase (fn:degradative enzyme and competence regulation) (db:genpept-bct1) (ec:2.7.3.-) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: sacu) (le:47349) (re:48506) (di:complement) BSUB0019 Z99122 g2636076 Bacillus subtilis 1423 -11529376 298093 degs histidine kinase (fn:phosphorylates degu) (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flag... BSU56901 U56901 g1762329 Bacillus subtilis 1423 -11529376 7000685004 degs degradative enzyme regulator / competence regulator degs:two-component sensor histidine kinase degs (cl:regulatory protein degs) (db:pir) RGBSDS A30190 Bacillus subtilis 1423 -11529376 220110 degs histidine kinase (fn:phosphorylates degu) (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flag... BSU56901 U56901 g1762329 Bacillus subtilis 1423 -11529376 5000688851 (de:(degs) (pn:sensor protein degs) (gn:sacu) (gtcfc:12.13) (ec:2.7.3.-) (degs_bacsu) (keggfc:11.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) degS degS Bacillus subtilis 1423 10010829

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753578	1710	23866	252	83

Description

5000688960 two-component response regulator:stage 0 sporulation protein f (gtcfc:12.13:12.15) (keggfc:12.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spo0F spo0F Bacillus subtilis 1423 -11529377 304113 spo0f (de:stage 0 sporulation protein f) (db:swissprot) SP0F_BACSU P06628 BACILLUS SUBTILIS 1423 -11529377 130886 spo0f stage 0 sporulation protein spo0f:sporulation initiation two-component response regulator spo0f (cl:chemotaxis chey protein:response regulator homology) (db:pir1.dat) (mp:323 (degrees)) SZBS0F A24737 Bacillus subtilis 1423 -11529377 7500891894 spo0f (sr:bacillus subtilis (strains jh642 and uot0550) dna) (db:genpept-bct1) (de:bacillus subtillis spo0f, ctp synthetase (ctra), andfructose-bisphosphate aldolase (orfy-tsr) genes, complete cds.) (le:2715) (re:3089) (di:direct) BACSPO0FA M22039 g143598 Bacillus subtilis 1423 -11529377 216854 (sr:b.subtilis (168t) dna, clones pjh4122 and pjh4133) (db:genpept-bct1) (de:b.subtilis spo0f 2 gene coding for early sporulation protein spo0f.) (nt:spo0f protein) (le:32) (re:406) (di:direct) BACSPO0FG M11081 g143601 Bacillus subtilis 1423 -11529377 6000685182 spo0f (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 320-321 degrees).) (nt:protein that belongs to the receiver class of) (le:11856) (re:12230) (di:direct) BSDNA320D Z49782 g853764 Bacillus subtilis 1423 -11529377 216856 (db:genpept-bct1) (de:bacillus subtilis spoof gene.) (nt:spoof protein (aa 1-124)) (le:247) (re:621) (di:direct) BSSPO0F X03497 g40157 Bacillus subtilis 1423 -11529377 219141 spo0f two-component response regulator (fn:initiation of sporulation (stage 0) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:211513) (re:211887) (di:complement) BSUB0019 Z99122 g2636238 Bacillus subtilis 1423 -11529377 219636 spo0f two-component response regulator (fn:initiation of sporulation (stage 0) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:10203) (re:10577) (di:complement) BSUB0020 Z99123 g2636250 Bacillus subtilis 1423 -11529377 99081 spo0f (de:stage 0 sporulation protein f) (db:swissprot) SP0F_BACSU P06628 BACILLUS SUBTILIS 1423 -11529377 7000686624 spo0f stage 0 sporulation protein spo0f:sporulation initiation two-component response regulator spo0f (cl:chemotaxis chey protein:response regulator homology) (db:pir) (mp:323 (degrees)) SZBS0F B32354 Bacillus subtilis 1423 -11529377 6500725519 two-component response regulator:stage 0 sporulation protein f (gtcfc:12.13:12.15) (keggfc:12.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spo0F spo0F Bacillus subtilis 1423 -11529377

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753581	1711	23867	276	91

Description

6500725520 cheb:chey two-component response regulator:chemotaxis protein chey homolog (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) cheY cheY Bacillus subtilis 1423 -11529378 7000692360 chey:cheb chemotactic tumbling protein chey:flagellar switch bias-modulating two-component response regulator chey (cl:chemotaxis chey protein:response regulator homology) (db:pir2.dat) A40874 A40874 Bacillus subtilis 1423 -11529378 7500963523 cheb chemotactic response protein (sr:b.subtilis dna) (db:genpept-bct1) (de:b.subtilis chemotactic response protein (cheb) gene, complete cds.) (le:24) (re:386) (di:direct) BACCHEBQ M59781 g142682 Bacillus subtilis 1423 -11529378 215350 chey two-component response regulator (fn:modulation of flagellar switch bias) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: cheb) (le:104809) (re:105171) (di:direct) BSUB0009 Z99112 g2634005 Bacillus subtilis 1423 -11529378 169911 chey:cheb chemotactic tumbling protein chey:flagellar switch bias-modulating two-component response regulator chey (cl:response regulator homology) (db:pir) A40874 A40874 Bacillus subtilis 1423 -11529378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753582	1712	23868	285	94

Description

6500725521 chel:cheb methyl-accepting chemotaxis proteins:mcp-glutamate methylesterase and two-component response regulator-like:protein-glutamate methylesterase (gtcfc:12.13) (ec:3.1.1.61) (keggfc:14.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) cheB cheB Bacillus subtilis 1423 -11529379 7500878638 cheb:chel (ec:3.1.1.61) (de:protein-glutamate methylesterase,) (db:swissprot) CHEB_BACSU Q05522 BACILLUS SUBTILIS 1423 -11529379 7000684807 cheb protein-glutamate methylesterase:cheb:chemotactic methylesterase:mcp-glutamate methylesterase cheb (cl:protein-glutamate methylesterase:response regulator homology) (ec:3.1.1.61) (db:pir2.dat) A48511 A48511 Bacillus subtilis 1423 -11529379 5000688848 cheb cheb (db:genpept-bct1) (de:b.subtilis cheb gene.) (le:39) (re:1112) (di:direct) BSCHEB X67806 g580836 Bacillus subtilis 1423 -11529379 219059 cheb methyl-accepting chemotaxis proteins (fn:chemotaxis receptor demethylation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: chel) (le:112711) (re:113784) (di:direct) BSUB0009 Z99112 g2634014 Bacillus subtilis 1423 -11529379 64229 cheb:chel (ec:3.1.1.61) (de:protein-glutamate methylesterase,) (db:swissprot) CHEB_BACSU Q05522 BACILLUS SUBTILIS 1423 -11529379 139620 cheb protein-glutamate methylesterase:cheb:chemotactic methylesterase:mcp-glutamate methylesterase cheb (cl:protein-glutamate methylesterase:response regulator homology) (ec:3.1.1.61) (db:pir) A48511 A48511 Bacillus subtilis 1423 -11529379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753590	1713	23869	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753594	1714	23870	909	303

Description

GTC ORF with score 144 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid k08h10, complete sequence.) (nt:cdna est embl:d26945 comes from this gene; cdna est) (le:33555:33695:34526:35188) (re:33650:34477:35092:35526) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753608	1715	23871	606	201

Description

6500725522 chen:chea two-component sensor histidine kinase:chemotaxis protein chea (gtcfc:12.13) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) cheA cheA Bacillus subtilis 1423 -11529380 64225 chea:chen (ec:2.7.3.-) (de:chemotaxis protein chea,) (db:swissprot) CHEA_BACSU P29072 BACILLUS SUBTILIS 1423 -11529380 130881 chea:chen two-component sensor histidine kinase chemotactic signal modululator chea:chemotaxis protein chen (cl:chemotaxis protein chea) (db:pir1.dat) QRBSCN A41653 Bacillus subtilis 1423 -11529380 7500878637 chen histidine kinase chemotactic signal modulator (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:b.subtilis histidine kinase chemotactic signal modulator (chen)gene, complete cds; orf1 3' end;orf2 5' end.) (le:54) (re:2069) (di:direct) BACCHEN M57894 g142685 Bacillus subtilis 1423 -11529380 215352 chea two-component sensor histidine kinase (fn:chemotactic signal modulator (chemotaxis)) (db:genpept-bct1) (ec:2.7.3.-) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: chen) (le:113790) (re:115805) (di:direct) BSUB0009 Z99112 g2634015 Bacillus subtilis 1423 -11529380 7000684805 chea:chen two-component sensor histidine kinase chemotactic signal modululator chea:chemotaxis protein chen (cl:chemotaxis protein chea) (db:pir) QRBSCN E69598 Bacillus subtilis 1423 -11529380 5000688847 (de:(chea) (pn:chemotaxis protein chea) (gn:chen) (gtcfc:12.13) (ec:2.7.3.-) (chea_bacsu) (keggfc:11.1) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) cheA cheA Bacillus subtilis 1423 10006889

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753611	1716	23872	606	201

Description

6500725523 srfb:comaa:coma1:coma two-component response regulator:coma operon protein 1 (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.2:6.1.2) (db:gtc-bacillus subtilis) comA comA Bacillus subtilis 1423 -11529381 64864 comaa:coma1 (de:coma operon protein 1) (db:swissprot) CMA1_BACSU P14204 BACILLUS SUBTILIS 1423 -11529381 130893 coma regulatory protein coma:late competence genes response regulator coma (cl:regulatory protein coma:response regulator homology) (db:pir1.dat) RGBSCA A33591 Bacillus subtilis 1423 -11529381 215363 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis comp and coma genes encoding competence proteins,complete cds.) (nt:a competence protein 1) (le:2725) (re:3369) (di:direct) BACCOMBA2 M22856 g142701 Bacillus subtilis 1423 -11529381 1500685153 coma two-component response regulator (fn:positive regulation of late competence genes) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (nt:alternate gene name: srfb, comaa) (le:54880) (re:55524) (di:complement) BSUB0017 Z99120 g2635663 Bacillus subtilis 1423 -11529381 7500878892 comaa (fn:competence; early block effector signal) (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufa to yufe.) (le:6004) (re:6648) (di:direct) BSZ93932 Z93932 g1934772 Bacillus subtilis 1423 -11529381 5000689907 (de:(comaa) (pn:coma operon protein 1:coma operon protein 1) (gn:coma1) (gtcfc:13.12) (ec:) (cma1_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comAA comAA Bacillus subtilis 1423 10007525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753619	1717	23873	1182	393

Description

GTC ORF with score 108 to: (db:genpept-pln1) (de:aspergillus niger putative dna binding protein facb (facb) gene,complete cds.) (nt:description: homologue of the emericella nidulans) (le:1186:1778:2143:2482) (re:1669:2085:2423:2839) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753635	1718	23874	1137	379

Description

5000688850 transcriptional regulator:competence regulatory protein comq (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) comQ comQ Bacillus subtilis 1423 -11529382 65417 comq (de:competence regulatory protein comq) (db:swissprot) COMQ_BACSU P33690 BACILLUS SUBTILIS 1423 -11529382 7000684868 comq transcription regulator comq (db:pir2.dat) A38111 A38111 Bacillus subtilis 1423 -11529382 7500879081 comq (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis comq gene, complete cds, and degq and comp,partial cds's.) (nt:competence regulation) (le:206) (re:1105) (di:direct) BACCOMQP M71283 g142714 Bacillus subtilis 1423 -11529382 215381 comq transcriptional regulator (fn:regulation of late competence operon (comg) and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:58084) (re:58983) (di:complement) BSUB0017 Z99120 g2635666 Bacillus subtilis 1423 -11529382 1500685159 comq (fn:competence; competence regulatory gene) (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yufa to yufe.) (le:2545) (re:3444) (di:direct) BSZ93932 Z93932 g1934770 Bacillus subtilis 1423 -11529382 170483 comq transcriptional regulator comq (db:pir) A38111 A38111 Bacillus subtilis 1423 -11529382 6500725524 transcriptional regulator:competence regulatory protein comq (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.2) (db:gtc-bacillus subtilis) comQ comQ Bacillus subtilis 1423 -11529382

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753652	1719	23875	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753803	1720	23876	609	203

Description

GTC ORF with score 108 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid f58a3, complete sequence.) (nt:cdna est embl:d72059 comes from this gene; cdna est) (le:23588:31283:31466:31638) (re:23676:31391:31589:31942) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753808	1721	23877	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753812	1722	23878	843	281

Description

GTC ORF with score 1085 to: (sr:neurospora crassa (individual_isolate 740r231a) (library: lambd) (db:genpept-pln1) (ec:4.1.1.1) (de:neurospora crassa pyruvate decarboxylase (cfp) mrna, complete cds.) (nt:59 kda) (le:76) (re:1788) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753815	1723	23879	585	194

Description

6500725525 yqfh:bex gtp-binding protein:bex protein (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.5) (db:gtc-bacillus subtilis) bex bex Bacillus subtilis 1423 -11529383 61597 era:bex (de:gtp-binding protein era homolog (bex protein)) (db:swissprot) ERA_BACSU P42182 BACILLUS SUBTILIS 1423 -11529383 7000684697 bex gtp-binding protein bex (cl:translation elongation factor tu homology) (db:pir2.dat) B69593 B69593 Bacillus subtilis 1423 -11529383 216070 yqfh (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:108658) (re:109563) (di:direct) BACJH642 D84432 g1303826 Bacillus subtilis 1423 -11529383 219854 bex bex (db:genpept-bct1) (de:bacillus subtilis cytidine deaminase (cdd) gene and g-protein bex(bex) gene, complete cds.) (nt:similar to era, an essential small g-protein in e.) (le:503) (re:1408) (di:direct) BSU18532 U18532 g606745 Bacillus subtilis 1423 -11529383 6000684530 bex gtp-binding protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqfh; gtp-binding protein) (le:214057) (re:214962) (di:complement) BSUB0013 Z99116 g2634961 Bacillus subtilis 1423 -11529383 7500881103 bex gtp-binding protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqfh; gtp-binding protein) (le:9867) (re:10772) (di:complement) BSUB0014 Z99117 g2634975 Bacillus subtilis 1423 -11529383 5000688936 (de:(bex) (pn:bex protein) (gtcfc:12.13) (ec:) (bex_bacsu) (keggfc:11.2) (bsorffc:6.1.5) (db:gtc-bacillus subtilis)) bex bex Bacillus subtilis 1423 10004306

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753820	1724	23880	228	75

Description

6500725526 yqxb:yqeq:lepa gtp-binding protein:gtp-binding protein lepa (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.5) (db:gtc-bacillus subtilis) lepA lepA Bacillus subtilis 1423 -11529384 81888 lepa (de:gtp-binding protein lepa) (db:swissprot) LEPA_BACSU P37949 BACILLUS SUBTILIS 1423 -11529384 7000685727 lepa gtp-binding protein lepa (cl:gtp-binding membrane protein lepa:translation elongation factor tu homology) (db:pir2.dat) G69649 G69649 Bacillus subtilis 1423 -11529384 216048 yqeq (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:86866) (re:88704) (di:direct) BACJH642 D84432 g1303804 Bacillus subtilis 1423 -11529384 219369 lepa (db:genpept-bct1) (de:b.subtilis lepa and hemn genes.) (le:128) (re:1966) (di:direct) BSLEPORF X91655 g1122398 Bacillus subtilis 1423 -11529384 7500884918 lepa gtp-binding protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqxb, yqeq) (le:30726) (re:32564) (di:complement) BSUB0014 Z99117 g2634997 Bacillus subtilis 1423 -11529384 5000688840 (de:(lepa) (pn:gtp-binding protein lepa:gtp-binding protein lepa homolog:fragment) (gtcfc:12.10) (ec:) (lepa_bacsu) (keggfc:11.2) (bsorffc:6.4.0) (db:gtc-bacillus subtilis)) lepA lepA Bacillus subtilis 1423 10024122

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753821	1725	23881	243	80

Description

5000688937 gtpase activity:spo0b-associated gtp-binding protein (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.5) (db:gtc-bacillus subtilis) obg obg Bacillus subtilis 1423 -11529385 87389 obg (de:spo0b-associated gtp-binding protein) (db:swissprot) OBG_BACSU P20964 BACILLUS SUBTILIS 1423 -11529385 7000686026 obg gtp-binding protein obg:spo0b-associated gtp-binding protein (cl:gtp-binding protein obg:translation elongation factor tu homology) (db:pir1.dat) B32804 B32804 Bacillus subtilis 1423 -11529385 7500887066 obg gtp-binding protein (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtillis sporulation protein (spoob), gtp-binding protein(obg), phenylalanine biosynthesis associated protein (pheb), andmonofunctional prephenate dehydratase (phea) genes, complete cds.) (nt:t... BACGTPBP M24537 g508979 Bacillus subtilis 1423 -11529385 215816 obg gtpase activity (fn:may be required to stimulate activity of the) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:56792) (re:58078) (di:complement) BSUB0015 Z99118 g2635257 Bacillus subtilis 1423 -11529385 131478 obg gtp-binding protein obg:spo0b 3-region (cl:spo0b 3'-region gtp-binding protein) (db:pir) B32804 B32804 Bacillus subtilis 1423 -11529385 6500725527 gtpase activity:spo0b-associated gtp-binding protein (gtcfc:12.13) (keggfc:14.2) (bsorffc:6.1.5) (db:gtc-bacillus subtilis) obg obg Bacillus subtilis 1423 -11529385

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753828	1726	23882	327	108

Description

5000689014 small acid-soluble spore protein:alpha/beta-type sasp:sspf protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspF sspF Bacillus subtilis 1423 -11529386 303676 sspf (de:sspf protein) (db:swissprot) SSPF_BACSU P37549 BACILLUS SUBTILIS 1423 -11529386 7000686687 sspf small acid-soluble spore protein minor alpha/beta-type sasp sspf:hypothetical protein 0.3 kb gene region (db:pir2.dat) I40472 I40472 Bacillus subtilis 1423 -11529386 7500892145 sspf similar product to sspa (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:116783) (re:116968) (di:direct) BAC180K D26185 g467434 Bacillus subtilis 1423 -11529386 219658 orf (db:genpept-bct1) (de:bacillus subtilis 0.3 kb gene.) (nt:0.3 kb gene) (le:176) (re:361) (di:direct) BSSPOR01 X00847 g580935 Bacillus subtilis 1423 -11529386 6500725528 sspf small acid-soluble spore protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:53181) (re:53366) (di:direct) BSUB0001 Z99104 g2632312 Bacillus subtilis 1423 -11529386 99582 sspf (de:sspf protein) (db:swissprot) SSPF_BACSU P37549 BACILLUS SUBTILIS 1423 -11529386 170600 sspf small acid-soluble spore protein minor alpha/beta-type sasp sspf:hypothetical protein 0.3 kb gene region (db:pir) I40472 I40472 Bacillus subtilis 1423 -11529386 215034 orf (db:genpept-bct1) (de:bacillus subtilis 0.3 kb gene.) (nt:0.3 kb gene) (le:176) (re:361) (di:direct) BSSPOR01 X00847 g580935 Bacillus subtilis 1423 -11529386

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753832	1727	23883	768	255

Description

5000688992 hypothetical protein:stage v sporulation protein g (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVG spoVG Bacillus subtilis 1423 -11529387 215038 spovg (de:stage v sporulation protein g) (db:swissprot) SP5G_BACSU P28015 BACILLUS SUBTILIS 1423 -11529387 7000686648 spovg stage v sporulation protein spovg:spore cortex synthesis protein spovg (cl:stage v sporulation protein spovg) (db:pir2.dat) S18902 S18902 Bacillus subtilis 1423 -11529387 7500891953 spovg stage v sporulation (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:119466) (re:119759) (di:direct) BAC180K D26185 g467438 Bacillus subtilis 1423 -11529387 219674 spovg (db:genpept-bct1) (de:b.subtilis spovg and tms genes.) (nt:startcodon gtg) (le:133) (re:426) (di:direct) BSSPOVG X62378 g580939 Bacillus subtilis 1423 -11529387 7502851605 spovg (fn:required for spore cortex synthesis (stage v) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:55864) (re:56157) (di:direct) BSUB0001 Z99104 g2632316 Bacillus subtilis 1423 -11529387 99160 spovg (de:stage v sporulation protein g) (db:swissprot) SP5G_BACSU P28015 BACILLUS SUBTILIS 1423 -11529387 170592 spovg stage v sporulation protein spovg:spore cortex synthesis protein spovg (db:pir) S18902 S18902 Bacillus subtilis 1423 -11529387 6500725529 hypothetical protein:stage v sporulation protein g (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVG spoVG Bacillus subtilis 1423 -11529387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753834	1728	23884	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753838	1729	23885	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753839	1730	23886	444	147

Description

5000688987 pth:spovc hypothetical protein:probable peptidyl-trna hydrolase:stage v sporulation protein c (gtcfc:10.6) (ec:3.1.1.29) (keggfc:14.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVC spoVC Bacillus subtilis 1423 -11529388 99156 spovc:pth (ec:3.1.1.29) (de:sporulation protein c)) (db:swissprot) SP5C_BACSU P37470 BACILLUS SUBTILIS 1423 -11529388 7000686646 spovc stage v sporulation protein spovc:spore coat formation protein spovc (cl:peptidyl-trna hydrolase) (db:pir2.dat) C69715 C69715 Bacillus subtilis 1423 -11529388 7500891950 spovc stage v sporulation (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:123104) (re:123670) (di:direct) BAC180K D26185 g467442 Bacillus subtilis 1423 -11529388 215042 spovc (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:thermosensitive mutant blocks spore coat formation) (le:59502) (re:60068) (di:direct) BSUB0001 Z99104 g2632320 Bacillus subtilis 1423 -11529388 206290 spovc stage v sporulation protein spovc:spore coat formation protein spovc (db:pir) C69715 C69715 Bacillus subtilis 1423 -11529388 6500725530 pth hypothetical protein:probable peptidyl-trna hydrolase:stage v sporulation protein c (gtcfc:10.6) (ec:3.1.1.29) (keggfc:14.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVC spoVC Bacillus subtilis 1423 -11529388

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753847	1731	23887	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753848	1732	23888	567	188

Description

6500725531 spoiih:spoiik:spoiie serine phosphatase:stage ii sporulation protein e (gtcfc:12.15) (ec:3.1.3.16) (keggfc:14.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIE spoIIE Bacillus subtilis 1423 -11529389 99127 spoiie:spoiih (ec:3.1.3.16) (de:stage ii sporulation protein e,) (db:swissprot) SP2E_BACSU P37475 BACILLUS SUBTILIS 1423 -11529389 7000686629 spoiie stage ii sporulation protein spoiie:asymmetric septum formation protein spoiie:sigma-f activation serine phosphatase spoiie (cl:stage ii sporulation protein e) (db:pir1.dat) S66094 S66094 Bacillus subtilis 1423 -11529389 7500891932 spoiie stage ii sporulation (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:134138) (re:136621) (di:direct) BAC180K D26185 g467453 Bacillus subtilis 1423 -11529389 215053 spoiie spoiie (db:genpept-bct1) (de:bacillus subtilis spoiie (spoiie) gene, complete cds.) (le:300) (re:2783) (di:direct) BSU26835 U26835 g857493 Bacillus subtilis 1423 -11529389 219894 spoiie serine phosphatase (fn:dephosphorylates spoiiaa-p and overcomes) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: spoiih, spoiik) (le:70536) (re:73019) (di:direct) BSUB0001 Z99104 g2632331 Bacillus subtilis 1423 -11529389 206287 spoiie stage ii sporulation protein spoiie:asymmetric septum formation protein spoiie:sigma-f activation serine phosphatase spoiie (cl:stage ii sporulation protein e) (db:pir) S66094 S66094 Bacillus subtilis 1423 -11529389 5000688966 (de:(spoiie) (pn:stage ii sporulation protein e:stage ii sporulation protein e) (gn:spoiih) (gtcfc:12.15) (ec:3.1.3.16) (sp2e_bacsu) (keggfc:11.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis)) spoIIE spoIIE Bacillus subtilis 1423 10040986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753850	1733	23889	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753855	1734	23890	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753862	1735	23891	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753868	1736	23892	408	135

Description

5000689071 sporulation-specific sasp protein:sigma-g-dependent sporulation specific sasp protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) csgA csgA Bacillus subtilis 1423 -11529390 219100 csga (de:sigma-g-dependent sporulation specific sasp protein) (db:swissprot) CSGA_BACSU P54379 BACILLUS SUBTILIS 1423 -11529390 4000707007 csgaa:csga sporulation-specific sasp protein csga (db:pir2.dat) JC6187 JC6187 Bacillus subtilis 1423 -11529390 7500879450 csga sasp protein (db:genpept-bct1) (de:b.subtilis orf1, csga, orf2, orf3, and orf4 genes.) (nt:sigmag-dependent; sporulation specific; putative) (le:488) (re:736) (di:direct) BSCSGAORF X92859 g1212789 Bacillus subtilis 1423 -11529390 6500725532 csga sporulation-specific sasp protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:33405) (re:33653) (di:direct) BSUB0002 Z99105 g2632493 Bacillus subtilis 1423 -11529390 7500879451 csga (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:31056) (re:31304) (di:direct) AB006424 AB006424 g3599630 Bacillus subtilis 1423 -11529390 66627 csga (de:sigma-g-dependent sporulation specific sasp protein) (db:swissprot) CSGA_BACSU P54379 BACILLUS SUBTILIS 1423 -11529390 7000684913 csga sporulation-specific sasp protein csga (db:pir) B69608 B69608 Bacillus subtilis 1423 -11529390

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753871	1737	23893	360	119

Description

6500725533 pig:cota spore coat protein:outer (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotA cotA Bacillus subtilis 1423 -11529391 7000694606 cota:pig spore coat protein outer cota (db:pir2.dat) F69604 F69604 Bacillus subtilis 1423 -11529391 7500965203 cota spore coat protein outer (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: pig) (le:82479) (re:84020) (di:complement) BSUB0004 Z99107 g2632943 Bacillus subtilis 1423 -11529391

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753875	1738	23894	201	66

Description

6500725534 polypeptide c...:cotja:coat hypothetical protein:required for the assembly of cotjc (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotJA cotJA Bacillus subtilis 1423 -11529392 7000684935 cotja (de:cotja protein) (db:swissprot) CTJA_BACSU Q45536 BACILLUS SUBTILIS 1423 -11529392 7000684936 cotja polypeptide composition of the spore coat cotja (db:pir2.dat) F69605 F69605 Bacillus subtilis 1423 -11529392 215383 cotja (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis cotjabc operon, polypeptide(s) affecting sporecoat composition, cds.) (nt:putative) (le:326) (re:574) (di:direct) BACCOTJABC L38014 g1377749 Bacillus subtilis 1423 -11529392 7500879536 cotja (fn:polypeptide composition of the spore coat;) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:154715) (re:154963) (di:direct) BSUB0004 Z99107 g2633002 Bacillus subtilis 1423 -11529392

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753878	1739	23895	273	90

Description

6500725535 hypothetical protein:polypeptide composition of the spore coat (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotJB cotJB Bacillus subtilis 1423 -11529393 7000684937 cotjb (de:cotjb protein) (db:swissprot) CTJB_BACSU Q45537 BACILLUS SUBTILIS 1423 -11529393 7000684938 cotjb polypeptide composition of the spore coat cotjb (db:pir2.dat) G69605 G69605 Bacillus subtilis 1423 -11529393 215384 cotjb (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis cotjabc operon, polypeptide(s) affecting sporecoat composition, cds.) (nt:putative) (le:519) (re:821) (di:direct) BACCOTJABC L38014 g1377750 Bacillus subtilis 1423 -11529393 7500879537 cotjb (fn:polypeptide composition of the spore coat) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:154908) (re:155210) (di:direct) BSUB0004 Z99107 g2633003 Bacillus subtilis 1423 -11529393

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501753879	1740	23896	558	185

Description

6500725536 hypothetical protein:polypeptide composition of the spore coat (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotJC cotJC Bacillus subtilis 1423 -11529394 7000684939 cotjc (de:cotjc protein) (db:swissprot) CTJC_BACSU Q45538 BACILLUS SUBTILIS 1423 -11529394 7000684940 cotjc polypeptide composition of the spore coat cotjc (db:pir2.dat) H69605 H69605 Bacillus subtilis 1423 -11529394 215385 cotjc (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis cotjabc operon, polypeptide(s) affecting sporecoat composition, cds.) (nt:putative) (le:836) (re:1405) (di:direct) BACCOTJABC L38014 g1377751 Bacillus subtilis 1423 -11529394 7500879538 cotjc (fn:polypeptide composition of the spore coat) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:155225) (re:155794) (di:direct) BSUB0004 Z99107 g2633004 Bacillus subtilis 1423 -11529394

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754063	1741	23897	375	124

Description

5000689013 small acid-soluble spore protein:gamma-type sasp:small:acid-soluble spore protein gamma-type:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspE sspE Bacillus subtilis 1423 -11529395 7000686563 sspe (de:small, acid-soluble spore protein gamma-type (sasp)) (db:swissprot) SASG_BACSU P07784 BACILLUS SUBTILIS 1423 -11529395 131071 sspe small acid-soluble spore protein major gamma-type sasp sspe:sasp-delta (cl:gamma-type small acid-soluble spore protein) (db:pir1.dat) A26873 A26873 Bacillus subtilis 1423 -11529395 216933 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis sspe gene encoding small acid-soluble spore proteingamma (sasp-gamma), complete cds.) (nt:small acid-soluble protein gamma) (le:97) (re:351) (di:direct) BACSSPE M16184 g143712 Bacillus subtilis 1423 -11529395 220372 sspe small acid-soluble spore protein gamma-type (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:134586) (re:134840) (di:direct) BSUB0005 Z99108 g2633189 Bacillus subtilis 1423 -11529395 7500891329 sspe small acid soluble protein gamma (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:1436) (re:1690) (di:direct) BSZ82044 Z82044 g1673389 Bacillus subtilis 1423 -11529395 7502851606 sspe (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:27477) (re:27731) (di:direct) D85082 D85082 g2804549 Bacillus subtilis 1423 -11529395 97979 sspe (de:small, acid-soluble spore protein gamma-type (sasp)) (db:swissprot) SASG_BACSU P07784 BACILLUS SUBTILIS 1423 -11529395 6500725537 small acid-soluble spore protein:gamma-type sasp:small:acid-soluble spore protein gamma-type:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspE sspE Bacillus subtilis 1423 -11529395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754064	1742	23898	399	133

Description

5000688996 hypothetical protein:stage v sporulation protein r (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVR spoVR Bacillus subtilis 1423 -11529396 99163 spovr (de:stage v sporulation protein r) (db:swissprot) SP5R_BACSU P37875 BACILLUS SUBTILIS 1423 -11529396 7000686650 spovr involved in spore cortex synthesis spovr (db:pir2.dat) D69716 D69716 Bacillus subtilis 1423 -11529396 4000707339 spovr (fn:involved in spore cortex synthesis (stage v) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:15599) (re:17005) (di:direct) BSUB0006 Z99109 g2633275 Bacillus subtilis 1423 -11529396 7500891955 spovr (fn:appears to be involved in spore cortex) (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:see subtilist bg10182, embl l26337 and swiss prot) (le:2247) (re:3653) (di:direct) BSY14082 Y14082 g2226196 Bacillus subtilis 1423 -11529396 6500725538 hypothetical protein:stage v sporulation protein r (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVR spoVR Bacillus subtilis 1423 -11529396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754080	1743	23899	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754084	1744	23900	195	64

Description

5000689010 small acid-soluble spore protein:beta-type sasp:small:acid-soluble spore protein b:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspB sspB Bacillus subtilis 1423 -11529397 97960 sspb (de:small, acid-soluble spore protein b (sasp)) (db:swissprot) SAS2_BACSU P04832 BACILLUS SUBTILIS 1423 -11529397 7000686561 sspb small acid-soluble spore protein major beta-type sasp sspb (cl:alpha/beta-type small acid-soluble spore protein) (db:pir2.dat) H69718 H69718 Bacillus subtilis 1423 -11529397 7500891325 (sr:b.subtilis 168 dna) (db:genpept-bct1) (de:bacillus subtilis sspb gene coding for small, acid-soluble sporeprotein (sasp), complete cds.) (nt:small, acid-soluble spore protein (sspb)) (le:370) (re:573) (di:direct) BACSSPB M12621 g143708 Bacillus subtilis 1423 -11529397 216931 sspb small acid-soluble spore protein beta-type (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:50011) (re:50214) (di:complement) BSUB0006 Z99109 g2633310 Bacillus subtilis 1423 -11529397 4000707323 sspb small:acid-soluble spore protein b sasp (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:see embl m12621) (le:11516) (re:11719) (di:direct) BSY14080 Y14080 g2226162 Bacillus subtilis 1423 -11529397 131049 sspb small acid-soluble spore protein major beta-type sasp sspb (cl:alpha/beta-type small acid-soluble spore protein) (db:pir) H69718 H69718 Bacillus subtilis 1423 -11529397 6500725539 small acid-soluble spore protein:beta-type sasp:small:acid-soluble spore protein b:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspB sspB Bacillus subtilis 1423 -11529397

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754087	1745	23901	342	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754092	1746	23902	393	130

Description

5000688953 spore coat protein:insoluble fraction:spore coat protein z (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotZ cotZ Bacillus subtilis 1423 -11529398 65531 cotz (de:spore coat protein z) (db:swissprot) COTZ_BACSU Q08312 BACILLUS SUBTILIS 1423 -11529398 7000684884 cotz spore coat protein insoluble fraction cotz (db:pir2.dat) E47119 E47119 Bacillus subtilis 1423 -11529398 7500879162 coty spore coat protein (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis insoluble spore coat protein (cotv, cotw, cotz,cotx, coty) genes, complete cds's.) (le:2280) (re:2726) (di:direct) BACCOTVZ L10116 g304149 Bacillus subtilis 1423 -11529398 215392 cotz spore coat protein insoluble fraction (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:54523) (re:54969) (di:complement) BSUB0007 Z99110 g2633528 Bacillus subtilis 1423 -11529398 170568 cotz spore coat protein insoluble fraction cotz (db:pir) E47119 E47119 Bacillus subtilis 1423 -11529398 6500725540 spore coat protein:insoluble fraction:spore coat protein z (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotZ cotZ Bacillus subtilis 1423 -11529398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754095	1747	23903	327	109

Description

5000688952 spore coat protein:insoluble fraction:spore coat protein y (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotY cotY Bacillus subtilis 1423 -11529399 65530 coty (de:spore coat protein y) (db:swissprot) COTY_BACSU Q08311 BACILLUS SUBTILIS 1423 -11529399 7000684883 coty spore coat protein insoluble fraction coty (db:pir2.dat) D47119 D47119 Bacillus subtilis 1423 -11529399 7500879161 cotx spore coat protein (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis insoluble spore coat protein (cotv, cotw, cotz,cotx, coty) genes, complete cds's.) (le:1664) (re:2152) (di:direct) BACCOTVZ L10116 g304148 Bacillus subtilis 1423 -11529399 215391 coty spore coat protein insoluble fraction (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:55097) (re:55585) (di:complement) BSUB0007 Z99110 g2633529 Bacillus subtilis 1423 -11529399 170567 coty spore coat protein insoluble fraction coty (db:pir) D47119 D47119 Bacillus subtilis 1423 -11529399 6500725541 spore coat protein:insoluble fraction:spore coat protein y (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotY cotY Bacillus subtilis 1423 -11529399

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754110	1748	23904	390	129

Description

5000688951 spore coat protein:insoluble fraction:spore coat protein x (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotX cotX Bacillus subtilis 1423 -11529400 65529 cotx (de:spore coat protein x) (db:swissprot) COTX_BACSU Q08313 BACILLUS SUBTILIS 1423 -11529400 7000684882 cotx spore coat protein insoluble fraction cotx (db:pir2.dat) C47119 C47119 Bacillus subtilis 1423 -11529400 7500879160 cotz spore coat protein (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis insoluble spore coat protein (cotv, cotw, cotz,cotx, coty) genes, complete cds's.) (le:994) (re:1512) (di:direct) BACCOTVZ L10116 g304147 Bacillus subtilis 1423 -11529400 215390 cotx spore coat protein insoluble fraction (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:55737) (re:56255) (di:complement) BSUB0007 Z99110 g2633530 Bacillus subtilis 1423 -11529400 170566 cotx spore coat protein insoluble fraction cotx (db:pir) C47119 C47119 Bacillus subtilis 1423 -11529400 6500725542 spore coat protein:insoluble fraction:spore coat protein x (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotX cotX Bacillus subtilis 1423 -11529400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754112	1749	23905	921	307

Description

5000688950 spore coat protein:insoluble fraction:spore coat protein w (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotW cotW Bacillus subtilis 1423 -11529401 65528 cotw (de:spore coat protein w) (db:swissprot) COTW_BACSU Q08310 BACILLUS SUBTILIS 1423 -11529401 7000684881 cotw spore coat protein insoluble fraction cotw:spore coat protein:38k (db:pir2.dat) (mp:107 (degrees)) B47119 B47119 Bacillus subtilis 1423 -11529401 7500879159 cotw spore coat protein (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis insoluble spore coat protein (cotv, cotw, cotz,cotx, coty) genes, complete cds's.) (le:578) (re:895) (di:direct) BACCOTVZ L10116 g304146 Bacillus subtilis 1423 -11529401 215389 cotw spore coat protein insoluble fraction (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:56354) (re:56671) (di:complement) BSUB0007 Z99110 g2633531 Bacillus subtilis 1423 -11529401 170565 cotw spore coat protein insoluble fraction cotw:spore coat protein:38k (db:pir) (mp:107 (degrees)) B47119 B47119 Bacillus subtilis 1423 -11529401 6500725543 spore coat protein:insoluble fraction:spore coat protein w (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotW cotW Bacillus subtilis 1423 -11529401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754144	1750	23906	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754151	1751	23907	492	163

Description

5000688949 spore coat protein:insoluble fraction:spore coat protein v (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotV cotV Bacillus subtilis 1423 -11529402 65527 cotv (de:spore coat protein v) (db:swissprot) COTV_BACSU Q08309 BACILLUS SUBTILIS 1423 -11529402 7000684880 cotv spore coat protein insoluble fraction cotv (db:pir2.dat) A47119 A47119 Bacillus subtilis 1423 -11529402 7500879158 cotv spore coat protein (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis insoluble spore coat protein (cotv, cotw, cotz,cotx, coty) genes, complete cds's.) (le:151) (re:537) (di:direct) BACCOTVZ L10116 g304145 Bacillus subtilis 1423 -11529402 215388 cotv spore coat protein insoluble fraction (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:56712) (re:57098) (di:complement) BSUB0007 Z99110 g2633532 Bacillus subtilis 1423 -11529402 170564 cotv spore coat protein insoluble fraction cotv (db:pir) A47119 A47119 Bacillus subtilis 1423 -11529402 6500725544 spore coat protein:insoluble fraction:spore coat protein v (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotV cotV Bacillus subtilis 1423 -11529402

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754163	1752	23908	387	128

Description

5000688948 spore coat protein:inner:spore coat protein t precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotT cotT Bacillus subtilis 1423 -11529403 219094 cott (de:spore coat protein t precursor) (db:swissprot) COTT_BACSU P11863 BACILLUS SUBTILIS 1423 -11529403 7500879157 (db:genpept-bct1) (de:bacillus subtilis cott gene for spore coat protein t.) (nt:spore coat protein t precursor) (le:209) (re:532) (di:direct) BSCOTT X13740 g39865 Bacillus subtilis 1423 -11529403 7502851607 cott spore coat protein inner (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:85706) (re:86029) (di:complement) BSUB0007 Z99110 g2633563 Bacillus subtilis 1423 -11529403 65526 cott (de:spore coat protein t precursor) (db:swissprot) COTT_BACSU P11863 BACILLUS SUBTILIS 1423 -11529403 7000684879 cott spore coat protein inner cott (db:pir) F69606 F69606 Bacillus subtilis 1423 -11529403 6500725545 spore coat protein:inner:spore coat protein t precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotT cotT Bacillus subtilis 1423 -11529403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754164	1753	23909	747	249

Description

6500725546 hypothetical protein:disruption blocks sporulation after septum formation (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIISB spoIISB Bacillus subtilis 1423 -11529404 7000692924 spoiisb disruption blocks sporulation after septum formation spoiisb (db:pir2.dat) E69713 E69713 Bacillus subtilis 1423 -11529404 6000689718 ykad ykad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:574) (re:744) (di:complement) BSAJ2571 AJ002571 g2632003 Bacillus subtilis 1423 -11529404 7500963942 spoiisb (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:disruption blocks sporulation after septum) (le:153523) (re:153693) (di:complement) BSUB0007 Z99110 g2633636 Bacillus subtilis 1423 -11529404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754174	1754	23910	309	102

Description

6500725547 ykac:spoiisa hypothetical protein:lethal when synthesized during vegetative growth in the absence of spoiisb (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIISA spoIISA Bacillus subtilis 1423 -11529405 7000694159 spoiisa lethal when synthesized during vegetative growth in the abs spoiisa (db:pir2.dat) D69713 D69713 Bacillus subtilis 1423 -11529405 6000689720 ykac ykac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:744) (re:1490) (di:complement) BSAJ2571 AJ002571 g2632004 Bacillus subtilis 1423 -11529405 7500964892 spoiisa (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykac; lethal when synthesized) (le:153693) (re:154439) (di:complement) BSUB0007 Z99110 g2633637 Bacillus subtilis 1423 -11529405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754176	1755	23911	1503	501

Description

5000689012 small acid-soluble spore protein:alpha/beta-type sasp:small:acid-soluble spore protein d:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspD sspD Bacillus subtilis 1423 -11529406 97969 sspd (de:small, acid-soluble spore protein d (sasp)) (db:swissprot) SAS4_BACSU P04833 BACILLUS SUBTILIS 1423 -11529406 131055 sspd small acid-soluble spore protein minor alpha/beta-type sasp sspd (cl:alpha/beta-type small acid-soluble spore protein) (db:pir1.dat) D24546 D24546 Bacillus subtilis 1423 -11529406 216932 (sr:b.subtilis 168 dna) (db:genpept-bct1) (de:bacillus subtilis sspd gene coding for small, acid-soluble sporeprotein (sasp), complete cds.) (nt:small, acid-soluble spore protein (sspd)) (le:295) (re:489) (di:direct) BACSSPD M12622 g143710 Bacillus subtilis 1423 -11529406 7500891328 sspd small acid-soluble spore protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:18476) (re:18670) (di:complement) BSUB0008 Z99111 g2633718 Bacillus subtilis 1423 -11529406 6500725548 small acid-soluble spore protein:alpha/beta-type sasp:small:acid-soluble spore protein d:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspD sspD Bacillus subtilis 1423 -11529406

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754181	1756	23912	468	155

Description

5000688959 negative sporulation regulatory phosphatase:stage 0 sporulation regulatory protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spo0E spo0E Bacillus subtilis 1423 -11529407 7500891893 spo0e (de:stage 0 sporulation regulatory protein) (db:swissprot) SP0E_BACSU P05043 BACILLUS SUBTILIS 1423 -11529407 7000686623 spo0e negative sporulation regulatory phosphatase spo0e (db:pir2.dat) S03746 S03746 Bacillus subtilis 1423 -11529407 219654 (db:genpept-bct1) (de:bacillus subtilis spooe gene for sporulation regulatory protein andunidentified reading frame (3' to spooe gene).) (nt:sporulation regulatory protein (aa 1-85)) (le:187) (re:444) (di:direct) BSSPOOE Y00526 g40182 Bacillus subtilis 1423 -11529407 6500725549 spo0e negative sporulation regulatory phosphatase (fn:specific dephosphorylation of spo0a-p (stage 0) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:35360) (re:35617) (di:direct) BSUB0008 Z99111 g2633735 Bacillus subtilis 1423 -11529407 99080 spo0e (de:stage 0 sporulation regulatory protein) (db:swissprot) SP0E_BACSU P05043 BACILLUS SUBTILIS 1423 -11529407 170089 spo0e negative sporulation regulatory phosphatase spo0e (db:pir) S03746 S03746 Bacillus subtilis 1423 -11529407

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754184	1757	23913	339	112

Description

6500725550 spl:splb spore photoproduct lyase (gtcfc:12.15) (ec:4.1.99.-) (keggfc:14.1) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) splB splB Bacillus subtilis 1423 -11529408 99288 splb:spl (ec:4.1.99.-) (de:spore photoproduct lyase,) (db:swissprot) SPL_BACSU P37956 BACILLUS SUBTILIS 1423 -11529408 7000686654 splb spore photoproduct lyase splb (db:pir2.dat) C47084 C47084 Bacillus subtilis 1423 -11529408 7500891979 spore photoproduct lyase (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis 168 enzyme i of the pep:phototransferase systemgene, 3' end, and spore photoproduct lyase gene, complete cds.) (le:930) (re:1958) (di:direct) BACENZYMEI L08809 g289270 Bacillus subtilis 1423 -11529408 215572 splb spore photoproduct lyase (fn:repair of uv radiation-induced dna damage) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: spl) (le:66387) (re:67415) (di:direct) BSUB0008 Z99111 g2633764 Bacillus subtilis 1423 -11529408 170583 splb spore photoproduct lyase splb (db:pir) C47084 C47084 Bacillus subtilis 1423 -11529408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754190	1758	23914	273	90

Description

5000688989 hypothetical protein:stage v sporulation protein e (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVE spoVE Bacillus subtilis 1423 -11529409 219672 spove (de:stage v sporulation protein e) (db:swissprot) SP5E_BACSU P07373 BACILLUS SUBTILIS 1423 -11529409 131644 spove stage v sporulation protein e:spore cortex synthesis protein spove (cl:rod shape-determining protein) (db:pir1.dat) (mp:133 (degrees)) SZBS5E S10243 Bacillus subtilis 1423 -11529409 7500891952 (db:genpept-bct1) (de:bacillus subtilis spove gene.) (nt:spove gene product (aa 1-366)) (le:61) (re:1161) (di:direct) BSSPOVE1 X51419 g580937 Bacillus subtilis 1423 -11529409 7502851608 spove (fn:required for spore cortex synthesis (stage v) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:194927) (re:196027) (di:direct) BSUB0008 Z99111 g2633892 Bacillus subtilis 1423 -11529409 99158 spove (de:stage v sporulation protein e) (db:swissprot) SP5E_BACSU P07373 BACILLUS SUBTILIS 1423 -11529409 6500725551 hypothetical protein:stage v sporulation protein e (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVE spoVE Bacillus subtilis 1423 -11529409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754191	1759	23915	228	75

Description

5000688995 hypothetical protein:stage v sporulation protein m (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVM spoVM Bacillus subtilis 1423 -11529410 216889 spovm (de:stage v sporulation protein m) (db:swissprot) SP5M_BACSU P37817 BACILLUS SUBTILIS 1423 -11529410 7000686649 spovm spore cortex and coat synthesis protein spovm (db:pir2.dat) S39981 S39981 Bacillus subtilis 1423 -11529410 7500891954 spovm (fn:required for normal spore cortex and coat) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:56425) (re:56505) (di:direct) BSUB0009 Z99112 g2633953 Bacillus subtilis 1423 -11529410 5500684735 spovm spovm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:18197) (re:18277) (di:direct) BSY13937 Y13937 g2337810 Bacillus subtilis 1423 -11529410 7502851609 spovm (sr:bacillus subtilis (sub_strain py79, strain w168) sporulation dna) (db:genpept-bct2) (de:bacillus subtilis sporulation factor (spovm) gene and ribosomalprotein l28 gene, complete cds's.) (le:144) (re:224) (di:direct) BACSPORLG L12244 g143647 Bacillus subtilis 1423 -11529410 99162 spovm (de:stage v sporulation protein m) (db:swissprot) SP5M_BACSU P37817 BACILLUS SUBTILIS 1423 -11529410 170594 spovm spore cortex and coat synthesis protein spovm (db:pir) S39981 S39981 Bacillus subtilis 1423 -11529410 6500725552 hypothetical protein:stage v sporulation protein m (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVM spoVM Bacillus subtilis 1423 -11529410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754194	1760	23916	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754339	1761	23917	546	181

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754347	1762	23918	675	225

Description

6500725553 dpaa:spovfa dipicolinate synthase subunit a:dipicolinate synthase:a chain (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVFA spoVFA Bacillus subtilis 1423 -11529411 219177 spovfa:dpaa (de:dipicolinate synthase, a chain) (db:swissprot) SVFA_BACSU Q04809 BACILLUS SUBTILIS 1423 -11529411 125598 spovfa dipicolinate synthase chain a (cl:dipicolinate synthase chain a) (db:pir1.dat) G46665 G46665 Bacillus subtilis 1423 -11529411 215477 spovfa dipicolinate synthase subunit a (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis protease, 3' end, dipicolinate synthase subunitsa and b (spovfa and spovfb), aspartate semialdehyde dehydrogenase(asd), aspartokinase i (dapg), dihydrodipicolinate synthas... BACDAP L08471 g142826 Bacillus subtilis 1423 -11529411 5000688990 dpaa dpaa (fn:dipicolinic acid synthesis) (db:genpept-bct1) (de:b.subtilis dpaa, dpab, and asd genes.) (le:247) (re:1140) (di:direct) BSDPAGNA Z22554 g296145 Bacillus subtilis 1423 -11529411 7500892282 spovfa dipicolinate synthase subunit a (fn:stage v sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: dpaa) (le:145338) (re:146231) (di:direct) BSUB0009 Z99112 g2634045 Bacillus subtilis 1423 -11529411 99922 spovfa:dpaa (de:dipicolinate synthase, a chain) (db:swissprot) SVFA_BACSU Q04809 BACILLUS SUBTILIS 1423 -11529411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754355	1763	23919	273	91

Description

GTC ORF with score 119 to: (fn:catalyzes the first methylation step from pe to) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe phosphatidylethanolaminemethyltransferase (cho2+) gene, complete cds.) (nt:cho2p) (le:1018) (re:3348) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754356	1764	23920	816	271

Description

6500725554 dpab:spovfb dipicolinate synthase subunit b:dipicolinate synthase:b chain (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVFB spoVFB Bacillus subtilis 1423 -11529412 219178 spovfb:dpab (de:dipicolinate synthase, b chain) (db:swissprot) SVFB_BACSU Q04810 BACILLUS SUBTILIS 1423 -11529412 125599 spovfb dipicolinate synthase chain b (cl:dipicolinate synthase chain b) (db:pir1.dat) F46665 F46665 Bacillus subtilis 1423 -11529412 215478 spovfb dipicolinate synthase subunit b (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis protease, 3' end, dipicolinate synthase subunitsa and b (spovfa and spovfb), aspartate semialdehyde dehydrogenase(asd), aspartokinase i (dapg), dihydrodipicolinate synthas... BACDAP L08471 g142827 Bacillus subtilis 1423 -11529412 5000688991 dpab dpab protein (fn:dipicolinic acid synthesis) (db:genpept-bct1) (de:b.subtilis dpaa, dpab, and asd genes.) (le:1143) (re:1745) (di:direct) BSDPAGNA Z22554 g296146 Bacillus subtilis 1423 -11529412 7500892283 spovfb dipicolinate synthase subunit b (fn:stage v sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: dpab) (le:146234) (re:146836) (di:direct) BSUB0009 Z99112 g2634046 Bacillus subtilis 1423 -11529412 99923 spovfb:dpab (de:dipicolinate synthase, b chain) (db:swissprot) SVFB_BACSU Q04810 BACILLUS SUBTILIS 1423 -11529412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754362	1765	23921	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754371	1766	23922	984	328

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754378	1767	23923	261	86

Description

5000688971 dna translocase:stage iii sporulation protein e (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIE spoIIIE Bacillus subtilis 1423 -11529413 99137 spoiiie (de:stage iii sporulation protein e) (db:swissprot) SP3E_BACSU P21458 BACILLUS SUBTILIS 1423 -11529413 7000686635 spoiiie dna translocase spoiiie (db:pir2.dat) S09411 S09411 Bacillus subtilis 1423 -11529413 7500891938 spoiiie dna translocase (fn:required for chromosome partitioning through) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:153248) (re:155611) (di:direct) BSUB0009 Z99112 g2634052 Bacillus subtilis 1423 -11529413 170560 spoiiie dna translocase spoiiie (db:pir) S09411 S09411 Bacillus subtilis 1423 -11529413 6500725555 dna translocase:stage iii sporulation protein e (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIE spoIIIE Bacillus subtilis 1423 -11529413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754379	1768	23924	444	147

Description

5000688997 hypothetical protein:stage v sporulation protein s (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVS spoVS Bacillus subtilis 1423 -11529414 99164 spovs (de:stage v sporulation protein s) (db:swissprot) SP5S_BACSU P45693 BACILLUS SUBTILIS 1423 -11529414 7000686651 spovs required for dehydratation of the spore core and assembly of t spovs (db:pir2.dat) E69716 E69716 Bacillus subtilis 1423 -11529414 219899 spovs spovs (db:genpept-bct1) (de:bacillus subtilis spovs (spovs) gene, complete cds.) (nt:wildtype) (le:327) (re:587) (di:direct) BSU27501 U27501 g862985 Bacillus subtilis 1423 -11529414 7500891956 spovs (fn:required for dehydratation of the spore core) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:170883) (re:171143) (di:direct) BSUB0009 Z99112 g2634070 Bacillus subtilis 1423 -11529414 6500725556 hypothetical protein:stage v sporulation protein s (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVS spoVS Bacillus subtilis 1423 -11529414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754380	1769	23925	537	178

Description

5000688944 morphogenic protein:spore coat protein e (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotE cotE Bacillus subtilis 1423 -11529415 7500879153 cote (de:spore coat protein e) (db:swissprot) COTE_BACSU P14016 BACILLUS SUBTILIS 1423 -11529415 7000684875 cote outer spore coat protein cote (db:pir2.dat) A31245 A31245 Bacillus subtilis 1423 -11529415 219092 cote coat protein (db:genpept-bct1) (de:bacillus subtilis cote gene for 21kd coat protein.) (le:390) (re:935) (di:direct) BSCOTE X13009 g1200225 Bacillus subtilis 1423 -11529415 6500725557 cote morphogenic protein (fn:outer coat assembly) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:176015) (re:176560) (di:direct) BSUB0009 Z99112 g2634075 Bacillus subtilis 1423 -11529415 65519 cote (de:spore coat protein e) (db:swissprot) COTE_BACSU P14016 BACILLUS SUBTILIS 1423 -11529415 169923 cote outer spore coat protein cote (db:pir) A31245 A31245 Bacillus subtilis 1423 -11529415

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754392	1770	23926	450	150

Description

6500725558 spovj:spovk hypothetical protein:stage v sporulation protein k (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVK spoVK Bacillus subtilis 1423 -11529416 220161 spovk spovk (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750107 Bacillus subtilis 1423 -11529416 7500965219 spovk (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: spovj; disruption leads to the) (le:92244) (re:93212) (di:direct) BSUB0010 Z99113 g2634126 Bacillus subtilis 1423 -11529416 7000694624 spovk spore formation protein spovk (db:pir) B69716 B69716 Bacillus subtilis 1423 -11529416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754393	1771	23927	255	84

Description

6500725559 spore coat protein:outer (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotC cotC Bacillus subtilis 1423 -11529417 7000694607 cotc spore coat protein outer cotc (db:pir2.dat) H69604 H69604 Bacillus subtilis 1423 -11529417 7500965204 cotc spore coat protein outer (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:123050) (re:123406) (di:complement) BSUB0010 Z99113 g2634154 Bacillus subtilis 1423 -11529417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754394	1772	23928	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754397	1773	23929	765	255

Description

6500725560 ynel:cotm spore coat protein:outer (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotM cotM Bacillus subtilis 1423 -11529418 7502851610 cotm (de:spore coat protein m) (db:swissprot) COTM_BACSU Q45058 BACILLUS SUBTILIS 1423 -11529418 7000694608 cotm spore coat protein outer cotm (db:pir2.dat) C69606 C69606 Bacillus subtilis 1423 -11529418 7500965205 ynel ynel (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:similar to heat shock proteins) (le:7331) (re:7723) (di:complement) BC170DEGR Z73234 g1405453 Bacillus subtilis 1423 -11529418 217884 cotm spore coat protein outer (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: ynel) (le:143710) (re:144102) (di:complement) BSUB0010 Z99113 g2634181 Bacillus subtilis 1423 -11529418

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754407	1774	23930	594	197

Description

6500725561 spore coat protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotL cotL Bacillus subtilis 1423 -11529419 7000694610 cotl spore coat protein cotl (db:pir2.dat) B69606 B69606 Bacillus subtilis 1423 -11529419 220192 cotl spore coat protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:144183) (re:144329) (di:complement) BSUB0010 Z99113 g2634182 Bacillus subtilis 1423 -11529419 298586 cotl cotl (db:genpept-bct2) (de:bacillus subtilis cotklm cluster, cotk (cotk), cotl (cotl), andspore coat protein cotm (cotm) genes, complete cds.) (le:431) (re:577) (di:direct) BSU72073 U72073 g1621448 Bacillus subtilis 1423 -11529419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754411	1775	23931	624	207

Description

6500725562 spore coat protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotK cotK Bacillus subtilis 1423 -11529420 7000694609 cotk spore coat protein cotk (db:pir2.dat) A69606 A69606 Bacillus subtilis 1423 -11529420 220191 cotk spore coat protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:144361) (re:144507) (di:complement) BSUB0010 Z99113 g2634183 Bacillus subtilis 1423 -11529420 298585 cotk cotk (db:genpept-bct2) (de:bacillus subtilis cotklm cluster, cotk (cotk), cotl (cotl), andspore coat protein cotm (cotm) genes, complete cds.) (le:253) (re:399) (di:direct) BSU72073 U72073 g1621447 Bacillus subtilis 1423 -11529420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754415	1776	23932	402	133

Description

5000689011 small acid-soluble spore protein:alpha/beta-type sasp:small:acid-soluble spore protein c:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspC sspC Bacillus subtilis 1423 -11529421 97967 sspc (de:small, acid-soluble spore protein c (sasp)) (db:swissprot) SAS3_BACSU P02958 BACILLUS SUBTILIS 1423 -11529421 131044 sspc:sasp-1 small acid-soluble spore protein minor alpha/beta-type sasp sspc:sasp-1:sasp-c:small acid-soluble spore protein beta (cl:alpha/beta-type small acid-soluble spore protein) (db:pir1.dat) USBS1 A03476 Bacillus subtilis 1423 -11529421 216678 yoka unknown (db:genpept-bct1) (de:bacillus subtilis yojp gene, partial cds; yojq/s, yojr, yojt,yoju, yojv, yojw, yojx, yojy, yojz, and yoka genes, complete cds.) (nt:small, acid-soluble spore protein (sspc)) (le:7637) (re:7855) (di:complement) AF012906 AF012906 g2522415 Bacillus subtilis 1423 -11529421 5500684730 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis small, acid-soluble spore protein (saspl) gene, completecds.) (nt:small, acid-soluble spore protein) (le:264) (re:482) (di:direct) BACSASP1 K02968 g143510 Bacillus subtilis 1423 -11529421 7000686562 sspc small acid-soluble spore protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:155312) (re:155530) (di:direct) BSUB0011 Z99114 g2634387 Bacillus subtilis 1423 -11529421 7500891327 sspc small acid-soluble spore protein c (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:129990) (re:130208) (di:complement) AF020713 AF020713 g3025650 Bacteriophage SPBc2 66797 -11529421 6500725563 small acid-soluble spore protein:alpha/beta-type sasp:small:acid-soluble spore protein c:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspC sspC Bacillus subtilis 1423 -11529421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754416	1777	23933	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754434	1778	23934	738	245

Description

GTC ORF with score 248 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754439	1779	23935	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754440	1780	23936	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754583	1781	23937	186	61

Description

5000688943 spore coat protein:inner:spore coat protein d (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotD cotD Bacillus subtilis 1423 -11529422 216499 cotd (de:spore coat protein d) (db:swissprot) COTD_BACSU P07791 BACILLUS SUBTILIS 1423 -11529422 7000684874 cotd 11k inner spore coat protein cotd (db:pir2.dat) D27393 D27393 Bacillus subtilis 1423 -11529422 7500879152 cotd spore coat protein (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (le:11256) (re:11483) (di:direct) BACPONAYPP L47838 g1146180 Bacillus subtilis 1423 -11529422 219091 cotd coat protein (db:genpept-bct1) (de:bacillus subtilis cotd gene for spore coat protein.) (le:258) (re:485) (di:direct) BSCOTDG X05681 g1200224 Bacillus subtilis 1423 -11529422 7502851611 cotd spore coat protein inner (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:136486) (re:136713) (di:complement) BSUB0012 Z99115 g2634639 Bacillus subtilis 1423 -11529422 65518 cotd (de:spore coat protein d) (db:swissprot) COTD_BACSU P07791 BACILLUS SUBTILIS 1423 -11529422 170572 cotd 11k inner spore coat protein cotd (db:pir) D27393 D27393 Bacillus subtilis 1423 -11529422 6500725564 spore coat protein:inner:spore coat protein d (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotD cotD Bacillus subtilis 1423 -11529422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754589	1782	23938	1122	374

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754607	1783	23939	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754629	1784	23940	195	64

Description

6500725565 spovp:spoiva hypothetical protein:stage iv sporulation protein a (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIVA spoIVA Bacillus subtilis 1423 -11529423 99141 spoiva:spovp (de:stage iv sporulation protein a) (db:swissprot) SP4A_BACSU P35149 BACILLUS SUBTILIS 1423 -11529423 7000686636 spoiva coat morphogenesis sporulation protein spoiva:spore cortex formation and coat assembly protein spoiva:stage iv sporulation protein spoiva (db:pir2.dat) A41970 A41970 Bacillus subtilis 1423 -11529423 7500891940 spoiva sporulation protein (sr:bacillus subtilis (strain marburg 168) (library: phage phi105j106) (db:genpept-bct1) (de:bacillus subtilis sporulation protein (spoiva) gene, complete cds.) (le:307) (re:1785) (di:direct) BACSPOIVA M81169 g143636 Bacillus subtilis 1423 -11529423 216883 spoiva (fn:required for proper spore coat morphogenesis in) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:b.subtilis spoiva gene, complete cds; hbsu gene, 5' end; orf1 gene,3' end.) (le:407) (re:1885) (di:direct) BACSPORUL M80926 g143651 Bacillus subtilis 1423 -11529423 216892 spoiva (fn:required for proper spore cortex formation and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: spovp) (le:189892) (re:191370) (di:complement) BSUB0012 Z99115 g2634698 Bacillus subtilis 1423 -11529423 169922 spoiva coat morphogenesis sporulation protein spoiva:spore cortex formation and coat assembly protein spoiva:stage iv sporulation protein spoiva (db:pir) A41970 A41970 Bacillus subtilis 1423 -11529423 5000688976 (de:(spoiva) (pn:stage iv sporulation protein a:stage iv sporulation protein a) (gn:spovp) (gtcfc:12.15) (ec:) (sp4a_bacsu) (keggfc:11.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis)) spoIVA spoIVA Bacillus subtilis 1423 10041000

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754639	1785	23941	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754641	1786	23942	732	244

Description

5000689216 ypea:sleb spore cortex-lytic enzyme:spore-cortex-lytic enzyme prepeptide precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sleB sleB Bacillus subtilis 1423 -11529424 115553 sleb (de:spore-cortex-lytic enzyme prepeptide precursor) (db:swissprot) SLEB_BACSU P50739 BACILLUS SUBTILIS 1423 -11529424 7000686605 sleb spore cortex-lytic enzyme sleb (db:pir2.dat) C69708 C69708 Bacillus subtilis 1423 -11529424 222815 sleb spore cortex-lytic enzyme (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: ypea) (le:202849) (re:203766) (di:complement) BSUB0012 Z99115 g2634711 Bacillus subtilis 1423 -11529424 6000685533 sleb spore cortex-lytic enzyme (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypea) (le:3129) (re:4046) (di:complement) BSUB0013 Z99116 g2634728 Bacillus subtilis 1423 -11529424 7500891683 sleb spore-cortex-lytic enzyme prepeptide (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for spore-cortex-lytic enzyme, complete cds.) (le:610) (re:1527) (di:direct) D79978 D79978 g1688023 Bacillus subtilis 1423 -11529424 216716 sleb spore cortex lytic enzyme (fn:l-alanine-mediated germination) (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzym... BACSERA L47648 g1146210 Bacillus subtilis 1423 -11529424 6500725566 sleb spore cortex lytic enzyme (fn:l-alanine-mediated germination) (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sl... BACSERA L47648 g1146210 Bacillus subtilis 1423 -11529424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754644	1787	23943	384	127

Description

6500725567 ypuk:spmb spore maturation protein:spore maturation protein b (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spmB spmB Bacillus subtilis 1423 -11529425 99290 spmb (de:spore maturation protein b) (db:swissprot) SPMB_BACSU P35158 BACILLUS SUBTILIS 1423 -11529425 7000686657 spmb spore maturation protein spore core dehydratation spmb (cl:spore maturation protein spmb) (db:pir2.dat) S45554 S45554 Bacillus subtilis 1423 -11529425 7500891983 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx12) (le:16809) (re:17348) (di:direct) BACDIA L09228 g410136 Bacillus subtilis 1423 -11529425 215515 spmb spore maturation protein (fn:required for spore core dehydratation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypuk) (le:26235) (re:26774) (di:complement) BSUB0013 Z99116 g2634752 Bacillus subtilis 1423 -11529425 170172 spmb spore maturation protein spore core dehydratation spmb (db:pir) S45554 S45554 Bacillus subtilis 1423 -11529425 5000688956 (de:(spmb) (pn:spore maturation protein b:spore maturation protein b) (gtcfc:12.15) (ec:) (spmb_bacsu) (keggfc:11.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis)) spmB spmB Bacillus subtilis 1423 10041149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754646	1788	23944	642	213

Description

6500725568 ypuj:spma spore maturation protein:spore maturation protein a (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spmA spmA Bacillus subtilis 1423 -11529426 99289 spma (de:spore maturation protein a) (db:swissprot) SPMA_BACSU P35157 BACILLUS SUBTILIS 1423 -11529426 7000686656 spma spore maturation protein spore core dehydratation spma (cl:spore maturation protein spma) (db:pir2.dat) S45553 S45553 Bacillus subtilis 1423 -11529426 7500891982 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx11) (le:16214) (re:16804) (di:direct) BACDIA L09228 g410135 Bacillus subtilis 1423 -11529426 215514 spma spore maturation protein (fn:required for spore core dehydratation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: ypuj) (le:26779) (re:27369) (di:complement) BSUB0013 Z99116 g2634753 Bacillus subtilis 1423 -11529426 170267 spma spore maturation protein spore core dehydratation spma (db:pir) S45553 S45553 Bacillus subtilis 1423 -11529426 5000688955 (de:(spma) (pn:spore maturation protein a:spore maturation protein a) (gtcfc:12.15) (ec:) (spma_bacsu) (keggfc:11.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis)) spmA spmA Bacillus subtilis 1423 10041148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754649	1789	23945	432	143

Description

6500725569 hypothetical protein:stage v sporulation protein af (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAF spoVAF Bacillus subtilis 1423 -11529427 7000694623 spovaf spore formation protein spovaf:stage v sporulation protein af (db:pir2.dat) A69715 A69715 Bacillus subtilis 1423 -11529427 216250 spovaf (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:279797) (re:281275) (di:direct) BACJH642 D84432 g1304006 Bacillus subtilis 1423 -11529427 7500965218 spovaf (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:mutants lead to the production of immature spores) (le:42344) (re:43822) (di:complement) BSUB0013 Z99116 g2634774 Bacillus subtilis 1423 -11529427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754653	1790	23946	462	153

Description

5000688984 hypothetical protein:stage v sporulation protein ae (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAE spoVAE Bacillus subtilis 1423 -11529428 99153 spovae (de:stage v sporulation protein ae) (db:swissprot) SP55_BACSU P40870 BACILLUS SUBTILIS 1423 -11529428 7000686644 spovae spore formation protein spovae (db:pir2.dat) H69714 H69714 Bacillus subtilis 1423 -11529428 216249 spovae (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:278875) (re:279846) (di:direct) BACJH642 D84432 g1304005 Bacillus subtilis 1423 -11529428 7500891948 spovae (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:mutants lead to the production of immature spores) (le:43773) (re:44744) (di:complement) BSUB0013 Z99116 g2634775 Bacillus subtilis 1423 -11529428 6500725570 hypothetical protein:stage v sporulation protein ae (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAE spoVAE Bacillus subtilis 1423 -11529428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754657	1791	23947	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754659	1792	23948	507	168

Description

5000688983 hypothetical protein:stage v sporulation protein ad (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAD spoVAD Bacillus subtilis 1423 -11529429 99152 spovad (de:stage v sporulation protein ad) (db:swissprot) SP54_BACSU P40869 BACILLUS SUBTILIS 1423 -11529429 7000686643 spovad spore formation protein spovad (db:pir2.dat) G69714 G69714 Bacillus subtilis 1423 -11529429 216248 spovad (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:277857) (re:278873) (di:direct) BACJH642 D84432 g1304004 Bacillus subtilis 1423 -11529429 7500891947 spovad (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:mutants lead to the production of immature spores) (le:44746) (re:45762) (di:complement) BSUB0013 Z99116 g2634776 Bacillus subtilis 1423 -11529429 6500725571 hypothetical protein:stage v sporulation protein ad (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAD spoVAD Bacillus subtilis 1423 -11529429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754669	1793	23949	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754673	1794	23950	1155	385

Description

GTC ORF with score 732 to: (fn:controls entry into the asexual developmental) (db:genpept-pln2) (de:neurospora crassa mapkk kinase (nrc-1) gene, complete cds.) (nt:nrc-1; similar to ste11 of saccharomyces) (le:232) (re:2232) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754675	1795	23951	450	149

Description

5000688982 hypothetical protein:stage v sporulation protein ac (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAC spoVAC Bacillus subtilis 1423 -11529430 99151 spovac (de:stage v sporulation protein ac) (db:swissprot) SP53_BACSU P40868 BACILLUS SUBTILIS 1423 -11529430 7000686642 spovac spore formation protein spovac (db:pir2.dat) F69714 F69714 Bacillus subtilis 1423 -11529430 216247 spovac (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:277392) (re:277844) (di:direct) BACJH642 D84432 g1304003 Bacillus subtilis 1423 -11529430 7500891946 spovac (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:mutants lead to the production of immature spores) (le:45775) (re:46227) (di:complement) BSUB0013 Z99116 g2634777 Bacillus subtilis 1423 -11529430 6500725572 hypothetical protein:stage v sporulation protein ac (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAC spoVAC Bacillus subtilis 1423 -11529430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754689	1796	23952	768	255

Description

5000688981 hypothetical protein:stage v sporulation protein ab (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAB spoVAB Bacillus subtilis 1423 -11529431 99150 spovab (de:stage v sporulation protein ab) (db:swissprot) SP52_BACSU P40867 BACILLUS SUBTILIS 1423 -11529431 7000686641 spovab spore formation protein spovab (db:pir2.dat) E69714 E69714 Bacillus subtilis 1423 -11529431 216246 spovab (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:276955) (re:277380) (di:direct) BACJH642 D84432 g1304002 Bacillus subtilis 1423 -11529431 7500891945 spovab (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:mutants lead to the production of immature spores) (le:46239) (re:46664) (di:complement) BSUB0013 Z99116 g2634778 Bacillus subtilis 1423 -11529431 6500725573 hypothetical protein:stage v sporulation protein ab (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAB spoVAB Bacillus subtilis 1423 -11529431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754798	1797	23953	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754809	1798	23954	759	252

Description

GTC ORF with score 201 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c31g5.) (nt:spac31g5.15, anomoly: splicing may be incorrectly) (le:24696:24950:25237:25745) (re:24893:25177:25702:26790) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754812	1799	23955	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754813	1800	23956	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754815	1801	23957	216	71

Description

GTC ORF with score 129 to: (sr:grape powdery mildew) (db:genpept-pln2) (ec:1.14.14.1) (de:uncinula necator eburicol c14-alpha-demethylase (cyp51) gene,complete cds.) (nt:unspecific monooxygenase; cytochrome p450 sterol) (le:203:504:755) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754821	1802	23958	534	177

Description

5000688980 hypothetical protein:stage v sporulation protein aa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAA spoVAA Bacillus subtilis 1423 -11529432 99149 spovaa (de:stage v sporulation protein aa) (db:swissprot) SP51_BACSU P40866 BACILLUS SUBTILIS 1423 -11529432 7000686640 spovaa spore formation protein spovaa (db:pir2.dat) D69714 D69714 Bacillus subtilis 1423 -11529432 216245 spovaa (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:276343) (re:276945) (di:direct) BACJH642 D84432 g1304001 Bacillus subtilis 1423 -11529432 7500891944 spovaa (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:mutants lead to the production of immature spores) (le:46674) (re:47276) (di:complement) BSUB0013 Z99116 g2634779 Bacillus subtilis 1423 -11529432 6500725574 hypothetical protein:stage v sporulation protein aa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVAA spoVAA Bacillus subtilis 1423 -11529432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754833	1803	23959	492	163

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754834	1804	23960	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754854	1805	23961	450	149

Description

5000688963 anti-sigma factor:antagonist of sigma-f and serine kinase:anti-sigma f factor:stage ii sporulation protein ab (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIAB spoIIAB Bacillus subtilis 1423 -11529433 99112 spoiiab (de:anti-sigma f factor (stage ii sporulation protein ab)) (db:swissprot) SP22_BACSU P10728 BACILLUS SUBTILIS 1423 -11529433 7000686626 spoiiab anti-sigma factor / serine kinase spoiiab:sigma factor f inhibitor spoiiab:stage ii sporulation protein spoiiab (db:pir2.dat) B55646 B55646 Bacillus subtilis 1423 -11529433 7500891926 spoiiab (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:275002) (re:275442) (di:direct) BACJH642 D84432 g1303999 Bacillus subtilis 1423 -11529433 216243 (sr:b.subtilis dna, clones phm2 and ppp33) (db:genpept-bct1) (de:b.subtilis spoiia locus sporulation genes.) (nt:sporulation protein orf2 (put.); putative) (le:736) (re:1176) (di:direct) BACSPO2AB M17643 g143614 Bacillus subtilis 1423 -11529433 216866 spoiiab anti-sigma factor antagonist of sigma-f and (fn:binding to sigma-f (spoiiac) in the presence of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:48177) (re:48617) (di:complement) BSUB0013 Z99116 g2634781 Bacillus subtilis 1423 -11529433 170530 spoiiab anti-sigma factor / serine kinase spoiiab:sigma factor f inhibitor spoiiab:stage ii sporulation protein spoiiab (db:pir) B55646 B55646 Bacillus subtilis 1423 -11529433 6500725575 anti-sigma factor:antagonist of sigma-f and serine kinase:anti-sigma f factor:stage ii sporulation protein ab (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIAB spoIIAB Bacillus subtilis 1423 -11529433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754862	1806	23962	516	171

Description

GTC ORF with score 115 to: (fn:dna repair) (sr:neurospora crassa (strain:74-or23-1a) germinating conidia cdna t) (db:genpept-pln1) (de:neurospora crassa mrna for uv-endonuclease.) (nt:start codon putative) (le:148) (re:2118) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501754864	1807	23963	441	147

Description

GTC ORF with score 515 to: (fn:dna repair) (sr:neurospora crassa (strain:74-or23-1a) germinating conidia cdna t) (db:genpept) (de:neurospora crassa mrna for uv-endonuclease, complete cds.) (nt:start codon putative) (le:148) (re:2118) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755058	1808	23964	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755065	1809	23965	603	200

Description

7000692211 anti-anti-sigma factor:antagonist of spoiiab:anti-sigma f factor antagonist:stage ii sporulation protein aa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIAA spoIIAA Bacillus subtilis 1423 -11529434 7500974584 spoiiaa (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:274652) (re:275005) (di:direct) BACJH642 D84432 g1303998 Bacillus subtilis 1423 -11529434 216242 spoiiaa anti-anti-sigma factor antagonist of spoiiab (fn:binding to spoiiab in the presence of adp) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:48614) (re:48967) (di:complement) BSUB0013 Z99116 g2634782 Bacillus subtilis 1423 -11529434 6500725576 anti-anti-sigma factor:antagonist of spoiiab:anti-sigma f factor antagonist:stage ii sporulation protein aa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIAA spoIIAA Bacillus subtilis 1423 -11529434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755088	1810	23966	513	170

Description

5000688973 hypothetical protein:stage ii sporulation protein m (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIM spoIIM Bacillus subtilis 1423 -11529435 99130 spoiim (de:stage ii sporulation protein m) (db:swissprot) SP2M_BACSU P37873 BACILLUS SUBTILIS 1423 -11529435 7000686631 spoiim septal cell wall dissolution factor spoiim:sporulation protein spoiim (db:pir2.dat) A47581 A47581 Bacillus subtilis 1423 -11529435 7500891934 spoiim (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:268604) (re:269248) (di:direct) BACJH642 D84432 g1303992 Bacillus subtilis 1423 -11529435 216236 spoiim (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis spoiim gene, complete cds.) (le:448) (re:1092) (di:direct) BACSPOIIMA L06664 g143634 Bacillus subtilis 1423 -11529435 216882 spoiim (fn:required for dissolution of the septal cell) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:54371) (re:55015) (di:complement) BSUB0013 Z99116 g2634788 Bacillus subtilis 1423 -11529435 170585 spoiim septal cell wall dissolution factor spoiim:sporulation protein spoiim (db:pir) A47581 A47581 Bacillus subtilis 1423 -11529435 6500725577 hypothetical protein:stage ii sporulation protein m (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIM spoIIM Bacillus subtilis 1423 -11529435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755091	1811	23967	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755094	1812	23968	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755103	1813	23969	969	323

Description

5000688977 hypothetical protein:stage iv sporulation protein b (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIVB spoIVB Bacillus subtilis 1423 -11529436 99142 spoivb (de:stage iv sporulation protein b) (db:swissprot) SP4B_BACSU P17896 BACILLUS SUBTILIS 1423 -11529436 7000686637 spoivb stage iv sporulation protein spoivb:intercompartmental pro-sigma-k activation signalling protein spoivb (db:pir2.dat) C35128 C35128 Bacillus subtilis 1423 -11529436 7500891941 spoivb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:199224) (re:200501) (di:direct) BACJH642 D84432 g1303924 Bacillus subtilis 1423 -11529436 216168 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis recombination and sporulation protein (recn, spoivb)genes , complete cds, arginine hydroximate resistance (ahrc) gene,3' end.) (nt:sporulation protein ivb) (le:2036) (re:3313) (di:direct) BACRECN M30297 g143403 Bacillus subtilis 1423 -11529436 216576 spoivb (fn:intercompartmental signalling of pro-sigma-k) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:123120) (re:124397) (di:complement) BSUB0013 Z99116 g2634857 Bacillus subtilis 1423 -11529436 170606 spoivb stage iv sporulation protein spoivb:intercompartmental pro-sigma-k activation signalling protein spoivb (db:pir) C35128 C35128 Bacillus subtilis 1423 -11529436 6500725578 hypothetical protein:stage iv sporulation protein b (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIVB spoIVB Bacillus subtilis 1423 -11529436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755108	1814	23970	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755122	1815	23971	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755126	1816	23972	600	200

Description

6500725579 hypothetical protein:stage iii sporulation protein ah (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAH spoIIIAH Bacillus subtilis 1423 -11529437 7000694268 spoiiiah mutants block sporulation after engulfment spoiiiah (db:pir2.dat) C69712 C69712 Bacillus subtilis 1423 -11529437 216155 spoiiiah (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:186597) (re:187253) (di:direct) BACJH642 D84432 g1303911 Bacillus subtilis 1423 -11529437 7500964985 spoiiiah (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:136368) (re:137024) (di:complement) BSUB0013 Z99116 g2634870 Bacillus subtilis 1423 -11529437

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755131	1817	23973	480	159

Description

GTC ORF with score 270 to: (gtcfc:6.16:6.4:6.5:8.2:9.2) (ec:2.3.2.2) (keggfc:6.4:6.5:6.9:8.6) (rileyfc:1.7.9) (db:gtc-escherichia coli) (gtcfc:metabolism of other amino acids-glutathione metabolism:metabolism of other amino acids-selenoamino acid ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755134	1818	23974	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755137	1819	23975	375	124

Description

6500725580 hypothetical protein:stage iii sporulation protein ag (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAG spoIIIAG Bacillus subtilis 1423 -11529438 7000694267 spoiiiag mutants block sporulation after engulfment spoiiiag (db:pir2.dat) B69712 B69712 Bacillus subtilis 1423 -11529438 216154 spoiiiag (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:185907) (re:186596) (di:direct) BACJH642 D84432 g1303910 Bacillus subtilis 1423 -11529438 7500964984 spoiiiag (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:137025) (re:137714) (di:complement) BSUB0013 Z99116 g2634871 Bacillus subtilis 1423 -11529438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755138	1820	23976	507	169

Description

5000689106 hypothetical protein:stage iii sporulation protein af (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAF spoIIIAF Bacillus subtilis 1423 -11529439 97783 spoiiiaf (de:stage iii sporulation protein af) (db:swissprot) S3AF_BACSU P49783 BACILLUS SUBTILIS 1423 -11529439 7000686540 spoiiiaf mutants block sporulation after engulfment spoiiiaf (db:pir2.dat) A69712 A69712 Bacillus subtilis 1423 -11529439 216153 spoiiiaf (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:185294) (re:185914) (di:direct) BACJH642 D84432 g1303909 Bacillus subtilis 1423 -11529439 219979 spoiiiaf spoiiiaf (db:genpept-bct1) (de:bacillus subtilis spoiiia locus, complete cds.) (nt:spoiiia orf6) (le:3948) (re:4568) (di:direct) BSU35252 U35252 g1000364 Bacillus subtilis 1423 -11529439 7500891265 spoiiiaf (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:137707) (re:138327) (di:complement) BSUB0013 Z99116 g2634872 Bacillus subtilis 1423 -11529439 6500725581 hypothetical protein:stage iii sporulation protein af (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAF spoIIIAF Bacillus subtilis 1423 -11529439

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755159	1821	23977	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755161	1822	23978	441	147

Description

5000689105 hypothetical protein:stage iii sporulation protein ae (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAE spoIIIAE Bacillus subtilis 1423 -11529440 97782 spoiiiae (de:stage iii sporulation protein ae) (db:swissprot) S3AE_BACSU P49782 BACILLUS SUBTILIS 1423 -11529440 7000686539 spoiiiae mutants block sporulation after engulfment spoiiiae (db:pir2.dat) H69711 H69711 Bacillus subtilis 1423 -11529440 216152 spoiiiae (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:184080) (re:185297) (di:direct) BACJH642 D84432 g1303908 Bacillus subtilis 1423 -11529440 7500891264 spoiiiae (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:138324) (re:139541) (di:complement) BSUB0013 Z99116 g2634873 Bacillus subtilis 1423 -11529440 6500725582 hypothetical protein:stage iii sporulation protein ae (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAE spoIIIAE Bacillus subtilis 1423 -11529440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755162	1823	23979	537	178

Description

5000689104 hypothetical protein:stage iii sporulation protein ad (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAD spoIIIAD Bacillus subtilis 1423 -11529441 97776 spoiiiad (de:stage iii sporulation protein ad) (db:swissprot) S3AD_BACSU P49781 BACILLUS SUBTILIS 1423 -11529441 7000686538 spoiiiad mutants block sporulation after engulfment spoiiiad (db:pir2.dat) G69711 G69711 Bacillus subtilis 1423 -11529441 216151 spoiiiad (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:183660) (re:184061) (di:direct) BACJH642 D84432 g1303907 Bacillus subtilis 1423 -11529441 219977 spoiiiad spoiiiad (db:genpept-bct1) (de:bacillus subtilis spoiiia locus, complete cds.) (nt:spoiiia orf4) (le:2315) (re:2716) (di:direct) BSU35252 U35252 g1000362 Bacillus subtilis 1423 -11529441 7500891261 spoiiiad (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:139560) (re:139961) (di:complement) BSUB0013 Z99116 g2634874 Bacillus subtilis 1423 -11529441 6500725583 hypothetical protein:stage iii sporulation protein ad (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAD spoIIIAD Bacillus subtilis 1423 -11529441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755168	1824	23980	768	256

Description

5000689103 hypothetical protein:stage iii sporulation protein ac (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAC spoIIIAC Bacillus subtilis 1423 -11529442 97774 spoiiiac (de:stage iii sporulation protein ac) (db:swissprot) S3AC_BACSU P49780 BACILLUS SUBTILIS 1423 -11529442 7000686537 spoiiiac mutants block sporulation after engulfment spoiiiac (db:pir2.dat) F69711 F69711 Bacillus subtilis 1423 -11529442 216150 spoiiiac (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:183447) (re:183653) (di:direct) BACJH642 D84432 g1303906 Bacillus subtilis 1423 -11529442 219976 spoiiiac spoiiiac (db:genpept-bct1) (de:bacillus subtilis spoiiia locus, complete cds.) (nt:spoiiia orf3) (le:2102) (re:2308) (di:direct) BSU35252 U35252 g1000361 Bacillus subtilis 1423 -11529442 7500891260 spoiiiac (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:139968) (re:140174) (di:complement) BSUB0013 Z99116 g2634875 Bacillus subtilis 1423 -11529442 6500725584 hypothetical protein:stage iii sporulation protein ac (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAC spoIIIAC Bacillus subtilis 1423 -11529442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755169	1825	23981	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755170	1826	23982	423	140

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755177	1827	23983	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755195	1828	23984	654	217

Description

5000688969 hypothetical protein:stage iii sporulation protein ab (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAB spoIIIAB Bacillus subtilis 1423 -11529443 97773 spoiiiab (de:stage iii sporulation protein ab) (db:swissprot) S3AB_BACSU Q01368 BACILLUS SUBTILIS 1423 -11529443 7000686536 spoiiiab stage iii sporulation protein spoiiiab (db:pir2.dat) E69711 E69711 Bacillus subtilis 1423 -11529443 216149 spoiiiab (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:182909) (re:183424) (di:direct) BACJH642 D84432 g1303905 Bacillus subtilis 1423 -11529443 219975 spoiiiab spoiiiab (db:genpept-bct1) (de:bacillus subtilis spoiiia locus, complete cds.) (nt:spoiiia orf2) (le:1564) (re:2079) (di:direct) BSU35252 U35252 g1000360 Bacillus subtilis 1423 -11529443 7500891259 spoiiiab (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:140197) (re:140712) (di:complement) BSUB0013 Z99116 g2634876 Bacillus subtilis 1423 -11529443 6500725585 hypothetical protein:stage iii sporulation protein ab (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAB spoIIIAB Bacillus subtilis 1423 -11529443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755209	1829	23985	687	228

Description

GTC ORF with score 236 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c04g6.) (nt:coded for by c. elegans cdna yk32d5.3; coded for by) (le:2522:2781:3279) (re:2622:2904:3419) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755210	1830	23986	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755367	1831	23987	912	303

Description

5000688968 hypothetical protein:stage iii sporulation protein aa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAA spoIIIAA Bacillus subtilis 1423 -11529444 261378 spoiiiaa (de:stage iii sporulation protein aa) (db:swissprot) S3AA_BACSU Q01367 BACILLUS SUBTILIS 1423 -11529444 7000686535 spoiiiaa stage iii sporulation protein spoiiiaa (db:pir2.dat) S16622 S16622 Bacillus subtilis 1423 -11529444 7500891258 spoiiiaa (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:181992) (re:182915) (di:direct) BACJH642 D84432 g1303904 Bacillus subtilis 1423 -11529444 216148 spoiiiaa spoiiiaa (db:genpept-bct1) (de:bacillus subtilis spoiiia locus, complete cds.) (nt:spoiiia orf1) (le:647) (re:1570) (di:direct) BSU35252 U35252 g1000359 Bacillus subtilis 1423 -11529444 219974 spoiiiaa (fn:mutants block sporulation after engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:140706) (re:141629) (di:complement) BSUB0013 Z99116 g2634877 Bacillus subtilis 1423 -11529444 7502851612 spoiiiaa spoiiiaa protein (fn:sporulation,stage iii) (db:genpept-bct1) (de:b.subtilis spoiiiaa and spoiiiab genes.) (le:199) (re:1122) (di:direct) SPO3A X61962 g581722 Bacillus subtilis 1423 -11529444 97772 spoiiiaa (de:stage iii sporulation protein aa) (db:swissprot) S3AA_BACSU Q01367 BACILLUS SUBTILIS 1423 -11529444 170604 spoiiiaa stage iii sporulation protein spoiiiaa (db:pir) S16622 S16622 Bacillus subtilis 1423 -11529444 6500725586 hypothetical protein:stage iii sporulation protein aa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIAA spoIIIAA Bacillus subtilis 1423 -11529444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755368	1832	23988	522	173

Description

5000689329 yqhf:cotn spore coat-associated protein:hypothetical 28.3 kd protein in comgg-sinr intergenic region (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotN cotN Bacillus subtilis 1423 -11529445 115929 yqhf (de:hypothetical 28.3 kd protein in comgg-sinr intergenic region) (db:swissprot) YQHF_BACSU P54507 BACILLUS SUBTILIS 1423 -11529445 7000688422 cotn spore coat-associated protein cotn (db:pir2.dat) D69606 D69606 Bacillus subtilis 1423 -11529445 216129 yqhf (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:165739) (re:166524) (di:direct) BACJH642 D84432 g1303885 Bacillus subtilis 1423 -11529445 7500952477 cotn spore coat-associated protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqhf) (le:157097) (re:157882) (di:complement) BSUB0013 Z99116 g2634896 Bacillus subtilis 1423 -11529445 6500725587 yqhf spore coat-associated protein:hypothetical 28.3 kd protein in comgg-sinr intergenic region (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotN cotN Bacillus subtilis 1423 -11529445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755369	1833	23989	192	63

Description

5000688974 hypothetical protein:stage ii sporulation protein p (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIP spoIIP Bacillus subtilis 1423 -11529446 99131 spoiip (de:stage ii sporulation protein p) (db:swissprot) SP2P_BACSU P37968 BACILLUS SUBTILIS 1423 -11529446 7000686632 spoiip required for dissolution of the septal cell wall spoiip (db:pir2.dat) A69713 A69713 Bacillus subtilis 1423 -11529446 215796 orf78 protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis gpr gene for spore protease partial sequence and 3'downstream region.) (nt:spoiip (ref. seventh international conference on) (le:741) (re:1946) (di:direct) BACGPR D17650 g403482 Bacillus subtilis 1423 -11529446 216046 spoiip (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:85172) (re:86377) (di:direct) BACJH642 D84432 g1303802 Bacillus subtilis 1423 -11529446 7500891935 spoiip (fn:required for dissolution of the septal cell) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:33053) (re:34258) (di:complement) BSUB0014 Z99117 g2634999 Bacillus subtilis 1423 -11529446 6500725588 hypothetical protein:stage ii sporulation protein p (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIP spoIIP Bacillus subtilis 1423 -11529446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755399	1834	23990	222	73

Description

6500725589 cisb:sigk:spoivcb n-terminal half:rna polymerase sporulation-specific sigma factor:sigma-k:n-terminal half (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIVCB spoIVCB Bacillus subtilis 1423 -11529447 215356 (sr:b.subtilis (strain jh642) dna) (db:genpept-bct1) (de:b.subtilis site-specific dna recombinase (cisa) and rna polymerasesigma-k subunit (cisb; spoivcb) genes, complete cds.) (nt:rna polymerase sigma-k subunit (cisb)) (le:1544) (re:2014) (di:complement) BACCISAB M29040 g455127 Bacillus subtilis 1423 -11529447 216024 spoivcb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:66148) (re:66618) (di:complement) BACJH642 D84432 g1303780 Bacillus subtilis 1423 -11529447 7500954156 spoivcb rna polymerase sporulation-specific sigma factor (fn:late mother cell-specific gene expression) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: cisb, sigk) (le:52812) (re:53282) (di:direct) BSUB0014 Z99117 g2635021 Bacillus subtilis 1423 -11529447 7000694565 spoivcb rna polymerase sporulation mother cell-specific late sigm spoivcb (cl:transcription initiation factor sigma k) (db:pir) A69714 A69714 Bacillus subtilis 1423 -11529447

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755401	1835	23991	648	215

Description

5000688939 cisa:spoivca site-specific dna recombinase:putative dna recombinase (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIVCA spoIVCA Bacillus subtilis 1423 -11529448 64650 cisa:spoivca (de:putative dna recombinase) (db:swissprot) CISA_BACSU P17867 BACILLUS SUBTILIS 1423 -11529448 7000684820 spoivca:spoivc:cisa sigk-creating site-specific dna recombinase cisa/spoivca (db:pir2.dat) A43656 A43656 Bacillus subtilis 1423 -11529448 7500878756 (sr:b.subtilis (strain jh642) dna) (db:genpept-bct1) (de:b.subtilis site-specific dna recombinase (cisa) and rna polymerasesigma-k subunit (cisb; spoivcb) genes, complete cds.) (nt:dna recombinase (cisa) (gtg start codon)) (le:134) (re:1636) (di:direct) BACCISAB M29040 g142690 Bacillus subtilis 1423 -11529448 215355 spoivca (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:64738) (re:66240) (di:direct) BACJH642 D84432 g1303779 Bacillus subtilis 1423 -11529448 216023 spoivca site-specific recombinase (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (le:46493) (re:47995) (di:direct) BACSKIN D32216 g1217886 Bacillus subtilis 1423 -11529448 216810 spoivca site-specific dna recombinase (fn:required for the chromosomal rearrangement that) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: cisa) (le:53190) (re:54692) (di:complement) BSUB0014 Z99117 g2635022 Bacillus subtilis 1423 -11529448 169968 spoivca:spoivc:cisa sigk-creating site-specific dna recombinase cisa/spoivca (db:pir) A43656 A43656 Bacillus subtilis 1423 -11529448 6500725590 cisa site-specific dna recombinase:putative dna recombinase (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIVCA spoIVCA Bacillus subtilis 1423 -11529448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755402	1836	23992	354	117

Description

6500725591 sigk:spoivd:spoive:spoiiic c-terminal half:rna polymerase sporulation-specific sigma factor:sigma-k:c-terminal half (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIC spoIIIC Bacillus subtilis 1423 -11529449 7500954157 spoiiic (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:17857) (re:18273) (di:complement) BACJH642 D84432 g1303719 Bacillus subtilis 1423 -11529449 215963 (sr:b.subtilis (strain 168) dna, (library of e.ferrari, d.j.henner an) (db:genpept-bct1) (de:b.subtilis spoiic gene, complete cds.) (nt:spoiiic peptide) (le:364) (re:780) (di:direct) BACSPOKB M19299 g143644 Bacillus subtilis 1423 -11529449 216888 spoiiic rna polymerase sporulation-specific sigma factor (fn:late mother cell-specific gene expression) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: sigk, spoivd, spoive) (le:101157) (re:101573) (di:direct) BSUB0014 Z99117 g2635084 Bacillus subtilis 1423 -11529449 139177 spoiiic transcription initiation factor sigma k:unrearranged form:spoiiic region:sporulation mother cell-specific late rna polymerase sigma factor spoiiic (cl:transcription initiation factor sigma k) (db:pir) C55249 A28627 Bacillus subtilis 1423 -11529449 7000689107 spoiiic transcription initiation factor sigma k:unrearranged form:spoiiic region:sporulation mother cell-specific late rna polymerase sigma factor spoiiic (cl:transcription initiation factor sigma k) (db:pir) C55249 S02441 Bacillus subtilis 1423 -11529449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755404	1837	23993	267	89

Description

6500725592 spoiiif:spovb hypothetical protein:stage v sporulation protein b (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVB spoVB Bacillus subtilis 1423 -11529450 99155 spovb:spoiiif (de:stage v sporulation protein b) (db:swissprot) SP5B_BACSU Q00758 BACILLUS SUBTILIS 1423 -11529450 7000686645 spovb spore cortex synthesis protein spovb (db:pir2.dat) (mp:239 deg) I39989 I39989 Bacillus subtilis 1423 -11529450 7500891949 spovb sporulation protein (sr:bacillus subtilis (sub_strain jh642, strain 168, sub_specie) (db:genpept-bct1) (de:bacillus subtilis sporulation protein (spovb, stage v) gene,complete cds.) (le:350) (re:1906) (di:direct) BACSPOVBA M76666 g143655 Bacillus subtilis 1423 -11529450 216894 spovb (fn:involved in spore cortex synthesis (stage v) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: spoiiif) (le:33695) (re:35251) (di:direct) BSUB0015 Z99118 g2635232 Bacillus subtilis 1423 -11529450 170587 spovb spore cortex synthesis protein spovb (db:pir) (mp:239 deg) I39989 I39989 Bacillus subtilis 1423 -11529450 5000688986 (de:(spovb) (pn:stage v sporulation protein b:stage v sporulation protein b) (gn:spoiiif) (gtcfc:12.15) (ec:) (sp5b_bacsu) (keggfc:11.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis)) spoVB spoVB Bacillus subtilis 1423 10041014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755411	1838	23994	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755416	1839	23995	192	63

Description

6500725593 bofb:spovl:spoivfa inhibitor of spoivfb:stage iv sporulation protein fa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIVFA spoIVFA Bacillus subtilis 1423 -11529451 7500891942 spoivfa:bofb (de:stage iv sporulation protein fa) (db:swissprot) SP4F_BACSU P26936 BACILLUS SUBTILIS 1423 -11529451 7000686638 spoivfa sporulation protein spoivfa:spoivfb inhibitor spoivfa (db:pir2.dat) S18437 S18437 Bacillus subtilis 1423 -11529451 5000688978 spoivfa sporulation protein (fn:hypothesised to stabilize but inhibit spoivfb) (db:genpept-bct1) (de:b.subtilis spoivfa, spoivfb, l20, orfx and l24 genes.) (le:159) (re:953) (di:direct) BSSPOIVFO X59528 g40171 Bacillus subtilis 1423 -11529451 219646 spoivfa inhibitor of spoivfb (fn:hypothesised to stabilize the thermolabile) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: bofb, spovl) (le:60963) (re:61757) (di:complement) BSUB0015 Z99118 g2635263 Bacillus subtilis 1423 -11529451 99143 spoivfa:bofb (de:stage iv sporulation protein fa) (db:swissprot) SP4F_BACSU P26936 BACILLUS SUBTILIS 1423 -11529451 170589 spoivfa sporulation protein spoivfa:spoivfb inhibitor spoivfa (db:pir) S18437 S18437 Bacillus subtilis 1423 -11529451

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755417	1840	23996	255	84

Description

5000688964 hypothetical protein:stage ii sporulation protein b (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIB spoIIB Bacillus subtilis 1423 -11529452 99120 spoiib (de:stage ii sporulation protein b) (db:swissprot) SP2B_BACSU P37575 BACILLUS SUBTILIS 1423 -11529452 7000686627 spoiib endospore development protein spoiib:stage ii sporulation protein spoiib (db:pir2.dat) C40646 C40646 Bacillus subtilis 1423 -11529452 7500891930 spoiib (fn:involved in endospore development) (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis comc gene, 5' end cds; spoiib gene, complete cds;orfa gene, 3' end cds.) (le:343) (re:1341) (di:direct) BACSPOIIB L04519 g143624 Bacillus subtilis 1423 -11529452 216875 spoiib (fn:endospore development (stage ii sporulation)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:67425) (re:68423) (di:complement) BSUB0015 Z99118 g2635271 Bacillus subtilis 1423 -11529452 170603 spoiib endospore development protein spoiib:stage ii sporulation protein spoiib (db:pir) C40646 C40646 Bacillus subtilis 1423 -11529452 6500725594 hypothetical protein:stage ii sporulation protein b (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIB spoIIB Bacillus subtilis 1423 -11529452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755418	1841	23997	234	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755434	1842	23998	369	122

Description

5000688993 hypothetical protein:stage vi sporulation protein d (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVID spoVID Bacillus subtilis 1423 -11529453 99168 spovid (de:stage vi sporulation protein d) (db:swissprot) SP6D_BACSU P37963 BACILLUS SUBTILIS 1423 -11529453 7000686653 spovid spore coat assembly protein spovid (db:pir2.dat) A69716 A69716 Bacillus subtilis 1423 -11529453 216897 spovid sporulation protein (sr:bacillus subtilis (strain w168) library made from vegetative cell) (db:genpept-bct1) (de:bacillus subtilis sporulation protein (spovid) gene, complete cds.) (le:296) (re:2023) (di:direct) BACSPOVID L07792 g143661 Bacillus subtilis 1423 -11529453 7500891958 spovid (fn:required for assembly of the spore coat (stage) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:74992) (re:76719) (di:complement) BSUB0015 Z99118 g2635276 Bacillus subtilis 1423 -11529453 6500725595 hypothetical protein:stage vi sporulation protein d (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoVID spoVID Bacillus subtilis 1423 -11529453

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755435	1843	23999	399	132

Description

5000689009 small acid-soluble spore protein:alpha-type sasp:small:acid-soluble spore protein a:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspA sspA Bacillus subtilis 1423 -11529454 97951 sspa (de:small, acid-soluble spore protein a (sasp)) (db:swissprot) SAS1_BACSU P04831 BACILLUS SUBTILIS 1423 -11529454 131050 sspa small acid-soluble spore protein major alpha-type sasp sspa (cl:alpha/beta-type small acid-soluble spore protein) (db:pir1.dat) A24546 A24546 Bacillus subtilis 1423 -11529454 216929 sspa dna-binding protein (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:153471) (re:153680) (di:direct) AF008220 AF008220 g2293231 Bacillus subtilis 1423 -11529454 4000707322 (sr:b.subtilis 168 dna) (db:genpept-bct1) (de:bacillus subtilis sspa gene coding for small, acid-soluble sporeprotein (sasp), complete cds.) (nt:small, acid-soluble spore protein (sspa)) (le:262) (re:471) (di:direct) BACSSPA M12620 g143704 Bacillus subtilis 1423 -11529454 7500891324 sspa small acid-soluble spore protein alpha-type (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:26747) (re:26956) (di:complement) BSUB0016 Z99119 g2635441 Bacillus subtilis 1423 -11529454 6500725596 small acid-soluble spore protein:alpha-type sasp:small:acid-soluble spore protein a:sasp (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) sspA sspA Bacillus subtilis 1423 -11529454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755438	1844	24000	540	179

Description

5000688947 spore coat protein:spore coat protein s:coat protein 40 kd component 2:cot40-2 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotS cotS Bacillus subtilis 1423 -11529455 65525 cots (de:spore coat protein s (coat protein 40 kd component 2) (cot40-2)) (db:swissprot) COTS_BACSU P46914 BACILLUS SUBTILIS 1423 -11529455 7000684878 cots spore coat protein cots (db:pir2.dat) I39808 I39808 Bacillus subtilis 1423 -11529455 7500879156 cots spore-coat protein (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:18373) (re:19428) (di:direct) AF008220 AF008220 g2293142 Bacillus subtilis 1423 -11529455 215387 cots spore coat protein cots (sr:bacillus subtilis (strain:60015) dna) (db:genpept-bct1) (de:bacillus subtilis cots gene for spore coat protein cots, completecds.) (le:1388) (re:2443) (di:direct) BACCOTS D31847 g976223 Bacillus subtilis 1423 -11529455 4000706996 cots spore coat protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:160999) (re:162054) (di:complement) BSUB0016 Z99119 g2635574 Bacillus subtilis 1423 -11529455 170570 cots spore coat protein cots (db:pir) I39808 I39808 Bacillus subtilis 1423 -11529455 6500725597 spore coat protein:spore coat protein s:coat protein 40 kd component 2:cot40-2 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotS cotS Bacillus subtilis 1423 -11529455

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755441	1845	24001	600	199

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755447	1846	24002	681	226

Description

6500725598 spore coat protein:outer (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotB cotB Bacillus subtilis 1423 -11529456 7500879151 cotb (de:spore coat protein b) (db:swissprot) COTB_BACSU P07789 BACILLUS SUBTILIS 1423 -11529456 7000684873 cotb spore coat protein outer cotb:spore coat protein:59k (db:pir2.dat) G69604 G69604 Bacillus subtilis 1423 -11529456 1500693626 cotb spore coat protein outer (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:116706) (re:117848) (di:complement) BSUB0019 Z99122 g2636130 Bacillus subtilis 1423 -11529456 7502851613 cotb spore coat protein b:cotb (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:7323) (re:8465) (di:direct) BSZ93767 Z93767 g1929336 Bacillus subtilis 1423 -11529456 65516 cotb (de:spore coat protein b) (db:swissprot) COTB_BACSU P07789 BACILLUS SUBTILIS 1423 -11529456

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755449	1847	24003	270	89

Description

6500725599 ywrh:coth spore coat protein:inner:spore coat protein h (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotH cotH Bacillus subtilis 1423 -11529457 7000694605 coth spore coat protein inner coth (db:pir2.dat) E69605 E69605 Bacillus subtilis 1423 -11529457 1500693625 coth spore coat protein inner (fn:involved in the assembly of several proteins in) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ywrh) (le:117976) (re:119064) (di:complement) BSUB0019 Z99122 g2636131 Bacillus subtilis 1423 -11529457 7500965202 ywrh (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:6107) (re:7195) (di:direct) BSZ93767 Z93767 g1929335 Bacillus subtilis 1423 -11529457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755450	1848	24004	354	117

Description

5000688946 morphogenetic protein:spore coat protein g (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotG cotG Bacillus subtilis 1423 -11529458 1500685164 cotg (de:spore coat protein g) (db:swissprot) COTG_BACSU P39801 BACILLUS SUBTILIS 1423 -11529458 7000684877 cotg spore coat protein cotg (db:pir2.dat) I40534 I40534 Bacillus subtilis 1423 -11529458 7500879155 cotg spore coat protein (db:genpept-bct1) (de:bacillus subtilis spore coat protein (cotg) gene, complete cds.) (nt:cotg) (le:245) (re:832) (di:direct) BSU14964 U14964 g555937 Bacillus subtilis 1423 -11529458 219823 cotg morphogenetic protein (fn:required for the incorporation of cotb into the) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:119205) (re:119792) (di:direct) BSUB0019 Z99122 g2636132 Bacillus subtilis 1423 -11529458 7502851614 cotg spore coat protein g:cotg (db:genpept-bct1) (de:b.subtilis dna; 15.2 kb fragment, from ywqn gene to ywro gene.) (le:5379) (re:5966) (di:complement) BSZ93767 Z93767 g1929334 Bacillus subtilis 1423 -11529458 65522 cotg (de:spore coat protein g) (db:swissprot) COTG_BACSU P39801 BACILLUS SUBTILIS 1423 -11529458 170569 cotg spore coat protein cotg (db:pir) I40534 I40534 Bacillus subtilis 1423 -11529458 6500725600 morphogenetic protein:spore coat protein g (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotG cotG Bacillus subtilis 1423 -11529458

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755471	1849	24005	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755475	1850	24006	747	248

Description

5000688970 transcriptional regulator:stage iii sporulation protein d:14 kd transcription factor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIID spoIIID Bacillus subtilis 1423 -11529459 217959 spoiiid (de:stage iii sporulation protein d (14 kd transcription factor)) (db:swissprot) SP3D_BACSU P15281 BACILLUS SUBTILIS 1423 -11529459 7000686634 spoiiid transcription regulator of sigma-e/sigma-k-dependent gene spoiiid:14k mother cell stage iv--stage v transcription switch factor (db:pir2.dat) A33472 A33472 Bacillus subtilis 1423 -11529459 306303 (db:genpept-bct1) (de:bacillus subtilis spoiiid gene for '14 kda protein' transcriptionfactor.) (nt:transcription factor (aa 1-93)) (le:235) (re:516) (di:direct) BCSPO3D X15520 g580763 Bacillus subtilis 1423 -11529459 219637 (db:genpept-bct1) (de:bacillus subtilis spoiiid sporulation specific gene.) (nt:spoiiid protein (aa 1-93)) (le:102) (re:383) (di:direct) BSSPO3D X52076 g580931 Bacillus subtilis 1423 -11529459 6500725601 spoiiid transcriptional regulator (fn:regulation of genes controlled by mother) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:150385) (re:150666) (di:complement) BSUB0019 Z99122 g2636167 Bacillus subtilis 1423 -11529459 220398 spoiiid spoiiid (db:genpept-bct1) (de:b.subtilis ywo(a,b,c,d,e,f,g,h), nrg(a,b), spoiiid and mb1 genes.) (le:10637) (re:10918) (di:direct) BSZ82987 Z82987 g1684653 Bacillus subtilis 1423 -11529459 99136 spoiiid (de:stage iii sporulation protein d (14 kd transcription factor)) (db:swissprot) SP3D_BACSU P15281 BACILLUS SUBTILIS 1423 -11529459 170638 spoiiid sigma-e-and sigma-k-dependent gene transcriptional regulator spoiiid:14k mother cell stage iv--stage v transcription switch factor (db:pir) A33472 A33472 Bacillus subtilis 1423 -11529459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755476	1851	24007	360	119

Description

6500725602 ywni:spoiiq hypothetical protein:required for completion of engulfment (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIQ spoIIQ Bacillus subtilis 1423 -11529460 7000694491 spoiiq required for completion of engulfment spoiiq (db:pir2.dat) B69713 B69713 Bacillus subtilis 1423 -11529460 220228 spoiiq (fn:required for completion of engulfment) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ywni) (le:161666) (re:162517) (di:complement) BSUB0019 Z99122 g2636180 Bacillus subtilis 1423 -11529460 7500965130 ywni unknown (db:genpept-bct1) (de:b.subtilis urease operon and downstream dna.) (le:8714) (re:9565) (di:direct) BSUEROP Y08559 g1592705 Bacillus subtilis 1423 -11529460

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755643	1852	24008	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755657	1853	24009	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755665	1854	24010	213	70

Description

6500725603 spoiic:spoiid hypothetical protein:stage ii sporulation protein d (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIID spoIID Bacillus subtilis 1423 -11529461 99124 spoiid:spoiic (de:stage ii sporulation protein d) (db:swissprot) SP2D_BACSU P07372 BACILLUS SUBTILIS 1423 -11529461 131103 spoiid stage ii sporulation protein spoiid (cl:stage ii sporulation protein d) (db:pir1.dat) (mp:316 (degrees)) SZBS2D A26083 Bacillus subtilis 1423 -11529461 7500891931 (sr:b.subtilis dna) (db:genpept-bct1) (de:b.subtilis spoiid operon encoding spoiid sporulation gene, completecds.) (nt:spoiid) (le:292) (re:1323) (di:direct) BACSPO2DA M15736 g143619 Bacillus subtilis 1423 -11529461 304080 spoiid unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:3449) (re:4480) (di:direct) BSATPC Z81356 g1648852 Bacillus subtilis 1423 -11529461 219027 spoiid (fn:required for complete dissolution of the) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: spoiic) (le:178687) (re:179718) (di:complement) BSUB0019 Z99122 g2636200 Bacillus subtilis 1423 -11529461 7000686628 spoiid stage ii sporulation protein spoiid (cl:stage ii sporulation protein d) (db:pir) (mp:316 (degrees)) SZBS2D A69711 Bacillus subtilis 1423 -11529461 216869 spoiid unknown (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:3449) (re:4480) (di:direct) BSATPC Z81356 g1648852 Bacillus subtilis 1423 -11529461 5000688965 (de:(spoiid) (pn:stage ii sporulation protein d:stage ii sporulation protein d) (gn:spoiic) (gtcfc:12.15) (ec:) (sp2d_bacsu) (keggfc:11.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis)) spoIID spoIID Bacillus subtilis 1423 10040983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755666	1855	24011	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755668	1856	24012	582	194

Description

6500725604 ipc-27d:csfx:spoiir hypothetical protein:stage ii sporulation protein r (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIR spoIIR Bacillus subtilis 1423 -11529462 7500891936 spoiir:ipc-27d (de:stage ii sporulation protein r) (db:swissprot) SP2R_BACSU P39151 BACILLUS SUBTILIS 1423 -11529462 7000686633 spoiir pro-sigma-e processing factor spoiir (db:pir2.dat) I40474 I40474 Bacillus subtilis 1423 -11529462 5000688975 spoiir unknown (db:genpept-bct1) (de:b.subtilis spoii-r, glyc and upp genes.) (le:586) (re:1260) (di:direct) BSSPORUPP Z38002 g556879 Bacillus subtilis 1423 -11529462 219660 spoiir (fn:required for processing of pro-sigma-e) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ipc-27d, csfx) (le:196641) (re:197315) (di:complement) BSUB0019 Z99122 g2636222 Bacillus subtilis 1423 -11529462 99132 spoiir:ipc-27d (de:stage ii sporulation protein r) (db:swissprot) SP2R_BACSU P39151 BACILLUS SUBTILIS 1423 -11529462 170562 spoiir pro-sigma-e processing factor spoiir (db:pir) I40474 I40474 Bacillus subtilis 1423 -11529462

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755690	1857	24013	237	78

Description

6500725605 ipa-73d:spsk hypothetical protein:spore coat polysaccharide biosynthesis protein spsk (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsK spsK Bacillus subtilis 1423 -11529463 7500892012 spsk:ipa-73d (de:spore coat polysaccharide biosynthesis protein spsk) (db:swissprot) SPSK_BACSU P39631 BACILLUS SUBTILIS 1423 -11529463 7000686669 spsk spore coat polysaccharide synthesis spsk (db:pir2.dat) S39728 S39728 Bacillus subtilis 1423 -11529463 5000689008 ipa-73d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:73285) (re:74583) (di:direct) BSGENR X73124 g580881 Bacillus subtilis 1423 -11529463 219310 spsk (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-73d) (le:83378) (re:84676) (di:complement) BSUB0020 Z99123 g2636317 Bacillus subtilis 1423 -11529463 99338 spsk:ipa-73d (de:spore coat polysaccharide biosynthesis protein spsk) (db:swissprot) SPSK_BACSU P39631 BACILLUS SUBTILIS 1423 -11529463 170152 spsk spore coat polysaccharide synthesis spsk (db:pir) S39728 S39728 Bacillus subtilis 1423 -11529463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755692	1858	24014	219	73

Description

6500725606 ipa-72d:spsj hypothetical protein:spore coat polysaccharide biosynthesis protein spsj (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsJ spsJ Bacillus subtilis 1423 -11529464 7500892011 spsj:ipa-72d (de:spore coat polysaccharide biosynthesis protein spsj) (db:swissprot) SPSJ_BACSU P39630 BACILLUS SUBTILIS 1423 -11529464 7000686668 spsj dtdpglucose 4:6-dehydratase:spsj:spore coat polysaccharide synthesis spsj (cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology) (ec:4.2.1.46) (db:pir2.dat) S39727 S39727 Bacillus subtilis 1423 -11529464 5000689007 ipa-72d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:72324) (re:73271) (di:direct) BSGENR X73124 g413996 Bacillus subtilis 1423 -11529464 219309 spsj (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-72d) (le:84690) (re:85637) (di:complement) BSUB0020 Z99123 g2636318 Bacillus subtilis 1423 -11529464 99337 spsj:ipa-72d (de:spore coat polysaccharide biosynthesis protein spsj) (db:swissprot) SPSJ_BACSU P39630 BACILLUS SUBTILIS 1423 -11529464 170151 spsj dtdpglucose 4:6-dehydratase:spsj:spore coat polysaccharide synthesis spsj (cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology) (ec:4.2.1.46) (db:pir) S39727 S39727 Bacillus subtilis 1423 -11529464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755693	1859	24015	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755699	1860	24016	609	202

Description

6500725607 ipa-71d:spsi hypothetical protein:spore coat polysaccharide biosynthesis protein spsi (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsI spsI Bacillus subtilis 1423 -11529465 7500892010 spsi:ipa-71d (de:spore coat polysaccharide biosynthesis protein spsi) (db:swissprot) SPSI_BACSU P39629 BACILLUS SUBTILIS 1423 -11529465 7000686667 spsi spore coat polysaccharide synthesis spsi (cl:glucose-1-phosphate thymidylytransferase) (db:pir2.dat) S39726 S39726 Bacillus subtilis 1423 -11529465 5000689006 ipa-71d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:71584) (re:72324) (di:direct) BSGENR X73124 g580880 Bacillus subtilis 1423 -11529465 219308 spsi (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-71d) (le:85637) (re:86377) (di:complement) BSUB0020 Z99123 g2636319 Bacillus subtilis 1423 -11529465 99336 spsi:ipa-71d (de:spore coat polysaccharide biosynthesis protein spsi) (db:swissprot) SPSI_BACSU P39629 BACILLUS SUBTILIS 1423 -11529465 170150 spsi spore coat polysaccharide synthesis spsi (db:pir) S39726 S39726 Bacillus subtilis 1423 -11529465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755700	1861	24017	711	236

Description

6500725608 ipa-69d:spsh:spsg hypothetical protein:spore coat polysaccharide synthesis (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsG spsG Bacillus subtilis 1423 -11529466 7000694604 spsg spore coat polysaccharide synthesis protein spsg:protein ipa-69d:protein ipa-70d (db:pir2.dat) E69717 E69717 Bacillus subtilis 1423 -11529466 7500965201 spsg (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-69d, spsh) (le:86402) (re:87421) (di:complement) BSUB0020 Z99123 g2636320 Bacillus subtilis 1423 -11529466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755707	1862	24018	669	223

Description

6500725609 ipa-68d:spsf hypothetical protein:spore coat polysaccharide biosynthesis protein spsf (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsF spsF Bacillus subtilis 1423 -11529467 7500892009 spsf:ipa-68d (de:spore coat polysaccharide biosynthesis protein spsf) (db:swissprot) SPSF_BACSU P39626 BACILLUS SUBTILIS 1423 -11529467 7000686666 spsf spore coat polysaccharide synthesis protein spsf:protein ipa-68d (db:pir2.dat) S39723 S39723 Bacillus subtilis 1423 -11529467 5000689003 ipa-68d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:69815) (re:70534) (di:direct) BSGENR X73124 g413992 Bacillus subtilis 1423 -11529467 219305 spsf (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-68d) (le:87428) (re:88147) (di:complement) BSUB0020 Z99123 g2636321 Bacillus subtilis 1423 -11529467 99333 spsf:ipa-68d (de:spore coat polysaccharide biosynthesis protein spsf) (db:swissprot) SPSF_BACSU P39626 BACILLUS SUBTILIS 1423 -11529467 170147 spsf spore coat polysaccharide synthesis spsf (db:pir) S39723 S39723 Bacillus subtilis 1423 -11529467

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755712	1863	24019	891	296

Description

6500725610 ipa-67d:spse hypothetical protein:spore coat polysaccharide biosynthesis protein spse (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsE spsE Bacillus subtilis 1423 -11529468 7500892008 spse:ipa-67d (de:spore coat polysaccharide biosynthesis protein spse) (db:swissprot) SPSE_BACSU P39625 BACILLUS SUBTILIS 1423 -11529468 7000686665 spse spore coat polysaccharide synthesis protein spse:protein ipa-66d (db:pir2.dat) S39722 S39722 Bacillus subtilis 1423 -11529468 5000689002 ipa-67d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:68701) (re:69822) (di:direct) BSGENR X73124 g413991 Bacillus subtilis 1423 -11529468 219304 spse (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-67d) (le:88140) (re:89261) (di:complement) BSUB0020 Z99123 g2636322 Bacillus subtilis 1423 -11529468 99332 spse:ipa-67d (de:spore coat polysaccharide biosynthesis protein spse) (db:swissprot) SPSE_BACSU P39625 BACILLUS SUBTILIS 1423 -11529468 170146 spse spore coat polysaccharide synthesis spse (db:pir) S39722 S39722 Bacillus subtilis 1423 -11529468

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755725	1864	24020	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755735	1865	24021	840	279

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755759	1866	24022	276	91

Description

6500725611 ipa-66d:spsd hypothetical protein:spore coat polysaccharide biosynthesis protein spsd (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsD spsD Bacillus subtilis 1423 -11529469 7500892007 spsd:ipa-66d (de:spore coat polysaccharide biosynthesis protein spsd) (db:swissprot) SPSD_BACSU P39624 BACILLUS SUBTILIS 1423 -11529469 7000686664 spsd spore coat polysaccharide synthesis spsd (db:pir2.dat) S39721 S39721 Bacillus subtilis 1423 -11529469 5000689001 ipa-66d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:67832) (re:68701) (di:direct) BSGENR X73124 g580879 Bacillus subtilis 1423 -11529469 219303 spsd (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-66d) (le:89261) (re:90130) (di:complement) BSUB0020 Z99123 g2636323 Bacillus subtilis 1423 -11529469 99331 spsd:ipa-66d (de:spore coat polysaccharide biosynthesis protein spsd) (db:swissprot) SPSD_BACSU P39624 BACILLUS SUBTILIS 1423 -11529469 170145 spsd spore coat polysaccharide synthesis spsd (db:pir) S39721 S39721 Bacillus subtilis 1423 -11529469

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755761	1867	24023	393	130

Description

6500725612 ipa-65d:spsc hypothetical protein:spore coat polysaccharide biosynthesis protein spsc (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsC spsC Bacillus subtilis 1423 -11529470 7500892006 spsc:ipa-65d (de:spore coat polysaccharide biosynthesis protein spsc) (db:swissprot) SPSC_BACSU P39623 BACILLUS SUBTILIS 1423 -11529470 7000686663 spsc spore coat polysaccharide synthesis protein spsc:protein ipa-65d (cl:erythromycin resistance protein) (db:pir2.dat) S39720 S39720 Bacillus subtilis 1423 -11529470 5000689000 ipa-65d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:66662) (re:67831) (di:direct) BSGENR X73124 g413989 Bacillus subtilis 1423 -11529470 219302 spsc (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-65d) (le:90131) (re:91300) (di:complement) BSUB0020 Z99123 g2636324 Bacillus subtilis 1423 -11529470 99330 spsc:ipa-65d (de:spore coat polysaccharide biosynthesis protein spsc) (db:swissprot) SPSC_BACSU P39623 BACILLUS SUBTILIS 1423 -11529470 170144 spsc spore coat polysaccharide synthesis spsc (cl:erythromycin resistance protein) (db:pir) S39720 S39720 Bacillus subtilis 1423 -11529470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755767	1868	24024	528	175

Description

6500725613 ipa-64d:spsb hypothetical protein:spore coat polysaccharide biosynthesis protein spsb (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsB spsB Bacillus subtilis 1423 -11529471 7500892005 spsb:ipa-64d (de:spore coat polysaccharide biosynthesis protein spsb) (db:swissprot) SPSB_BACSU P39622 BACILLUS SUBTILIS 1423 -11529471 7000686662 spsb spore coat polysaccharide synthesis spsb (db:pir2.dat) S39719 S39719 Bacillus subtilis 1423 -11529471 5000688999 ipa-64d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:65223) (re:66641) (di:direct) BSGENR X73124 g580878 Bacillus subtilis 1423 -11529471 219301 spsb (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-64d) (le:91321) (re:92739) (di:complement) BSUB0020 Z99123 g2636325 Bacillus subtilis 1423 -11529471 99329 spsb:ipa-64d (de:spore coat polysaccharide biosynthesis protein spsb) (db:swissprot) SPSB_BACSU P39622 BACILLUS SUBTILIS 1423 -11529471 170143 spsb spore coat polysaccharide synthesis spsb (db:pir) S39719 S39719 Bacillus subtilis 1423 -11529471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755768	1869	24025	378	125

Description

GTC ORF with score 157 to: (sr:fission yeast strain=bap1) (db:genpept-pln2) (de:schizosaccharomyces pombe brefeldin a resistance protein (hba1) andunknown orf genes, complete cds.) (nt:contains ran binding protein similarity domain) (le:1001) (re:2200)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755769	1870	24026	453	150

Description

GTC ORF with score 122 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid t04a8, complete sequence.) (nt:glutamate/lysine rich second exon shows similarity) (le:29672:30250:31465:32568) (re:29764:30790:31736:32790) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755912	1871	24027	219	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755922	1872	24028	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755928	1873	24029	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755930	1874	24030	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755948	1875	24031	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755953	1876	24032	438	145

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755971	1877	24033	591	196

Description

6500725614 ipa-63d:spsa hypothetical protein:spore coat polysaccharide biosynthesis protein spsa (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spsA spsA Bacillus subtilis 1423 -11529472 7500892004 spsa:ipa-63d (de:spore coat polysaccharide biosynthesis protein spsa) (db:swissprot) SPSA_BACSU P39621 BACILLUS SUBTILIS 1423 -11529472 7000686661 spsa spore coat polysaccharide synthesis spsa (db:pir2.dat) S39718 S39718 Bacillus subtilis 1423 -11529472 5000688998 ipa-63d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:64448) (re:65218) (di:direct) BSGENR X73124 g580877 Bacillus subtilis 1423 -11529472 219300 spsa (fn:spore coat polysaccharide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-63d) (le:92744) (re:93514) (di:complement) BSUB0020 Z99123 g2636326 Bacillus subtilis 1423 -11529472 99328 spsa:ipa-63d (de:spore coat polysaccharide biosynthesis protein spsa) (db:swissprot) SPSA_BACSU P39621 BACILLUS SUBTILIS 1423 -11529472 170142 spsa spore coat polysaccharide synthesis spsa (db:pir) S39718 S39718 Bacillus subtilis 1423 -11529472

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755982	1878	24034	435	144

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501755994	1879	24035	645	214

Description

5000688945 spore coat protein:spore coat protein f (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotF cotF Bacillus subtilis 1423 -11529473 65520 cotf (de:spore coat protein f) (db:swissprot) COTF_BACSU P23261 BACILLUS SUBTILIS 1423 -11529473 7000684876 cotf spore coat protein cotf (db:pir2.dat) S65978 S65978 Bacillus subtilis 1423 -11529473 7500879154 cotf spore coat protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:15106) (re:15588) (di:direct) BAC180K D26185 g467338 Bacillus subtilis 1423 -11529473 214938 cotf spore coat protein (sr:b.subtilis 168 (strain p417) dna) (db:genpept-bct1) (de:b.subtilis spore coat protein (cotf) gene, complete cds.) (le:130) (re:612) (di:direct) BACSPRCT M58592 g143664 Bacillus subtilis 1423 -11529473 216902 cotf spore coat protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:167038) (re:167520) (di:direct) BSUB0021 Z99124 g2636600 Bacillus subtilis 1423 -11529473 206283 cotf spore coat protein cotf (db:pir) S65978 S65978 Bacillus subtilis 1423 -11529473 6500725615 spore coat protein:spore coat protein f (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) cotF cotF Bacillus subtilis 1423 -11529473

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756001	1880	24036	516	171

Description

5000688961 antagonist of soj:stage 0 sporulation protein j (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spo0J spo0J Bacillus subtilis 1423 -11529474 214980 spo0j (de:stage 0 sporulation protein j) (db:swissprot) SP0J_BACSU P26497 BACILLUS SUBTILIS 1423 -11529474 170558 spo0j:spo0j93 soj antagonist / chromosome positioning and transport protein spo0j:spo0j93 protein:stage 0 sporulation protein j93 (cl:bacillus subtilis transport protein spo0j) (db:pir2.dat) A38536 I40445 Bacillus subtilis 1423 -11529474 7500891895 spo0j stage 0 sporultion (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:53552) (re:54400) (di:complement) BAC180K D26185 g467380 Bacillus subtilis 1423 -11529474 219467 spooj93 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (le:9000) (re:9848) (di:direct) BSORIGS X62539 g40031 Bacillus subtilis 1423 -11529474 6500725616 spo0j antagonist of soj (fn:involved in positionning part of the chromosome) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:205484) (re:206332) (di:complement) BSUB0021 Z99124 g2636643 Bacillus subtilis 1423 -11529474 99083 spo0j (de:stage 0 sporulation protein j) (db:swissprot) SP0J_BACSU P26497 BACILLUS SUBTILIS 1423 -11529474 7000686625 spo0j:spo0j93 soj antagonist / chromosome positioning and transport protein spo0j:spo0j93 protein:stage 0 sporulation protein j93 (db:pir) A38536 A38536 Bacillus subtilis 1423 -11529474

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756004	1881	24037	528	175

Description

5000688954 hypothetical protein:soj protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) soj soj Bacillus subtilis 1423 -11529475 214981 soj (de:soj protein) (db:swissprot) SOJ_BACSU P37522 BACILLUS SUBTILIS 1423 -11529475 7000686618 soj spo0a activation inhibitor soj:forespore chromosome partitioning centromere-like function protein soj:hypothetical protein 4 replication origin region:probable spo0j regulation protein soj (cl:regulatory protein spo0j) (db:pir2.dat) I40444 I40444 Bacillus subtilis 1423 -11529475 7500891850 regulation of spo0j and orf283 probable (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:54393) (re:55154) (di:complement) BAC180K D26185 g467381 Bacillus subtilis 1423 -11529475 219466 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:unnamed protein product) (le:8246) (re:9007) (di:direct) BSORIGS X62539 g580906 Bacillus subtilis 1423 -11529475 7502851615 soj (fn:centromere-like function with spo0j involved in) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:206325) (re:207086) (di:complement) BSUB0021 Z99124 g2636644 Bacillus subtilis 1423 -11529475 98949 soj (de:soj protein) (db:swissprot) SOJ_BACSU P37522 BACILLUS SUBTILIS 1423 -11529475 170463 soj spo0a activation inhibitor soj:forespore chromosome partitioning centromere-like function protein soj:hypothetical protein 4 replication origin region:probable spo0j regulation protein soj (cl:regulatory protein spo0j) (db:pir) I40444 I40444 Bacillus subtilis 1423 -11529475 6500725617 hypothetical protein:soj protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) soj soj Bacillus subtilis 1423 -11529475

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756169	1882	24038	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756170	1883	24039	576	191

Description

5000689465 spoiiij-associated protein:jag protein:spoiiij associated protein (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) jag jag Bacillus subtilis 1423 -11529476 219460 jag (de:jag protein (spoiiij associated protein)) (db:swissprot) JAG_BACSU Q01620 BACILLUS SUBTILIS 1423 -11529476 7000685656 jag spoiiij-associated protein jag:hypothetical protein 2 replication origin region (db:pir2.dat) I40438 I40438 Bacillus subtilis 1423 -11529476 7500884378 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:61196) (re:61822) (di:complement) BAC180K D26185 g467387 Bacillus subtilis 1423 -11529476 214987 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:unnamed protein product) (le:1578) (re:2204) (di:direct) BSORIGS X62539 g580905 Bacillus subtilis 1423 -11529476 219595 jag jag (fn:unknown. spoiiij associated gene) (db:genpept-bct1) (de:b.subtilis genes rnpa encoding rnase p, spoiiij, jag.) (le:1180) (re:1806) (di:direct) BSRNPASPO Z14225 g580919 Bacillus subtilis 1423 -11529476 6500725618 jag spoiiij-associated protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:213128) (re:213754) (di:complement) BSUB0021 Z99124 g2636650 Bacillus subtilis 1423 -11529476 80153 jag (de:jag protein (spoiiij associated protein)) (db:swissprot) JAG_BACSU Q01620 BACILLUS SUBTILIS 1423 -11529476 170303 jag spoiiij-associated protein jag:hypothetical protein 2 replication origin region (db:pir) I40438 I40438 Bacillus subtilis 1423 -11529476

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756174	1884	24040	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756194	1885	24041	294	98

Description

6500725619 spo0j87:spoiiij hypothetical protein:stage iii sporulation protein j precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.1) (db:gtc-bacillus subtilis) spoIIIJ spoIIIJ Bacillus subtilis 1423 -11529477 7000692971 spoiiij stage iii sporulation protein spoiiij:hypothetical protein 1 replication origin region (cl:stage iii sporulation protein:stage iii sporulation protein homology) (db:pir2.dat) I40437 I40437 Bacillus subtilis 1423 -11529477 7500955387 spoiiij stage iii sporulation (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:61819) (re:62604) (di:complement) BAC180K D26185 g467388 Bacillus subtilis 1423 -11529477 214988 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:unnamed protein product) (le:796) (re:1581) (di:direct) BSORIGS X62539 g40023 Bacillus subtilis 1423 -11529477 219459 spoiiij (fn:essential for sigma-g activity at stage iii) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: spo0j87) (le:213751) (re:214536) (di:complement) BSUB0021 Z99124 g2636651 Bacillus subtilis 1423 -11529477 170561 spoiiij stage iii sporulation protein spoiiij:hypothetical protein 1 replication origin region (cl:stage iii sporulation protein:stage iii sporulation protein homology) (db:pir) I40437 I40437 Bacillus subtilis 1423 -11529477

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756196	1886	24042	297	99

Description

5000689023 hypothetical protein:spore germination protein gerd precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerD gerD Bacillus subtilis 1423 -11529478 73555 gerd (de:spore germination protein gerd precursor) (db:swissprot) GERD_BACSU P16450 BACILLUS SUBTILIS 1423 -11529478 7000685381 gerd germination response protein gerd precursor (db:pir2.dat) A37207 A37207 Bacillus subtilis 1423 -11529478 7500882311 (sr:b.subtilis (strain 168) dna, clone lambda-embl-3-2h) (db:genpept-bct1) (de:b.subtilis gerd gene, complete cds.) (nt:gerd protein) (le:381) (re:938) (di:direct) BACGERD M27259 g142965 Bacillus subtilis 1423 -11529478 215655 gerd (fn:germination response to l-alanine and to the) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:158514) (re:159071) (di:complement) BSUB0001 Z99104 g2632422 Bacillus subtilis 1423 -11529478 222744 gerd gerd protein (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:8075) (re:8632) (di:complement) D64126 D64126 g1644214 Bacillus subtilis 1423 -11529478 170009 gerd germination response protein gerd precursor (db:pir) A37207 A37207 Bacillus subtilis 1423 -11529478 6500725620 hypothetical protein:spore germination protein gerd precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerD gerD Bacillus subtilis 1423 -11529478

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756200	1887	24043	237	78

Description

6500725621 gerc58:gerc3:gercc heptaprenyl diphosphate synthase component ii:probable heptaprenyl diphosphate synthase component ii:heppp synthase:spore germination protein c3 (gtcfc:12.15) (ec:2.5.1.30) (keggfc:14.1) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerCC gerCC Bacillus subtilis 1423 -11529479 74468 gercc:gerc3 (ec:2.5.1.30) (de:(heppp synthase) (spore germination protein c3)) (db:swissprot) GRC3_BACSU P31114 BACILLUS SUBTILIS 1423 -11529479 7000685451 gercc heptaprenyl diphosphate synthase component ii gercc (cl:prenyl transferase a) (db:pir2.dat) E69630 E69630 Bacillus subtilis 1423 -11529479 217029 gerc3 gerc3 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:2785) (re:3831) (di:direct) BACVARGNS M80245 g143803 Bacillus subtilis 1423 -11529479 7500882719 gercc heptaprenyl diphosphate synthase component ii (fn:menaquinone biosynthesis (germination)) (db:genpept-bct1) (ec:2.5.1.30) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: gerc58) (le:185617) (re:186663) (di:complement) BSUB0012 Z99115 g2634692 Bacillus subtilis 1423 -11529479 5000689022 (de:(gercc) (pn:probable heptaprenyl diphosphate synthase component ii:heppp synthase:spore germination protein c3:spore germination protein c3) (gn:gerc3) (gtcfc:12.15) (ec:2.5.1.30) (grc3_bacsu) (keggfc:11.1) (bsorffc:6.2.2) () gerCC gerCC Bacillus subtilis 1423 10016984

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756208	1888	24044	261	86

Description

6500725622 gerc2:gercb methyltransferase:probable menaquinone biosynthesis methlytransferase:spore germination protein c2 (gtcfc:9.12:12.15) (ec:2.1.1.-) (keggfc:14.1) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerCB gerCB Bacillus subtilis 1423 -11529480 74466 gercb:gerc2 (ec:2.1.1.-) (de:(spore germination protein c2)) (db:swissprot) GRC2_BACSU P31113 BACILLUS SUBTILIS 1423 -11529480 7000685450 gercb menaquinone biosynthesis methyltransferase gercb (cl:spore germination protein c2:bioc homology) (db:pir2.dat) D69630 D69630 Bacillus subtilis 1423 -11529480 217028 gerc2 gerc2 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:2142) (re:2843) (di:direct) BACVARGNS M80245 g143802 Bacillus subtilis 1423 -11529480 7500882718 gercb methyltransferase (fn:menaquinone biosynthesis (germination)) (db:genpept-bct1) (ec:2.1.1.-) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:186605) (re:187306) (di:complement) BSUB0012 Z99115 g2634693 Bacillus subtilis 1423 -11529480 5000688430 (de:(gercb) (pn:probable menaquinone biosynthesis methlytransferase:spore germination protein c2) (gn:gerc2) (gtcfc:5.13:5.14:9.12) (ec:2.1.1.-) (grc2_bacsu) (keggfc:3.7:5.13:5.14:9.13) (bsorffc:6.2.2) (db:gtc-bacillus subtilis)) gerCB gerCB Bacillus subtilis 1423 10016982

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756209	1889	24045	591	197

Description

6500725623 gerc1:gerca heptaprenyl diphosphate synthase component i:probable heptaprenyl diphosphate synthase component i:heppp synthase:spore germination protein c1 (gtcfc:12.15) (ec:2.5.1.30) (keggfc:14.1) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerCA gerCA Bacillus subtilis 1423 -11529481 74465 gerca:gerc1 (ec:2.5.1.30) (de:(heppp synthase) (spore germination protein c1)) (db:swissprot) GRC1_BACSU P31112 BACILLUS SUBTILIS 1423 -11529481 7000685449 gerca heptaprenyl diphosphate synthase component i gerca (db:pir2.dat) C69630 C69630 Bacillus subtilis 1423 -11529481 217027 gerc1 gerc1 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:1380) (re:2135) (di:direct) BACVARGNS M80245 g143801 Bacillus subtilis 1423 -11529481 7500882717 gerca heptaprenyl diphosphate synthase component i (fn:menaquinone biosynthesis (germination)) (db:genpept-bct1) (ec:2.5.1.30) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:187313) (re:188068) (di:complement) BSUB0012 Z99115 g2634694 Bacillus subtilis 1423 -11529481 5000689021 (de:(gerca) (pn:probable heptaprenyl diphosphate synthase component i:heppp synthase:spore germination protein c1:spore germination protein c1) (gn:gerc1) (gtcfc:12.15) (ec:2.5.1.30) (grc1_bacsu) (keggfc:11.1) (bsorffc:6.2.2) (d)) gerCA gerCA Bacillus subtilis 1423 10016981

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756241	1890	24046	900	299

Description

6500725624 hypothetical protein:germination protein germ (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerM gerM Bacillus subtilis 1423 -11529482 73557 germ (de:germination protein germ) (db:swissprot) GERM_BACSU P39072 BACILLUS SUBTILIS 1423 -11529482 7000685382 germ germination cortex hydrolysis and sporulation stage ii:multiple polar septa protein germ (db:pir2.dat) C69631 C69631 Bacillus subtilis 1423 -11529482 220334 germ (fn:germination (cortex hydrolysis) and sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:105972) (re:107072) (di:complement) BSUB0015 Z99118 g2635303 Bacillus subtilis 1423 -11529482 304207 germ 366 residue protein required for sporulation and (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:defective germination (cortex hydrolase) and) (le:62835) (re:63935) (di:direct) BSZ75208 Z75208 g1770058 Bacillus subtilis 1423 -11529482

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756250	1891	24047	801	267

Description

5000689024 transcriptional regulator:germination protein gere (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerE gerE Bacillus subtilis 1423 -11529483 73556 gere (de:germination protein gere) (db:swissprot) GERE_BACSU P11470 BACILLUS SUBTILIS 1423 -11529483 130895 gere transcription regulator gere (cl:transcription regulator gere) (db:pir1.dat) C27893 C27893 Bacillus subtilis 1423 -11529483 215658 (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis succinate dehydrogenase (sdhc) gene, partial cds, andgermination protein (gere) gene, complete cds.) (nt:germination protein (ttg start codon)) (le:1049) (re:1273) (di:direct) BACGERE M17642 g142969 Bacillus subtilis 1423 -11529483 220330 gere transcriptional regulator (fn:required for the expression of late spore coat) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:108698) (re:108922) (di:complement) BSUB0015 Z99118 g2635306 Bacillus subtilis 1423 -11529483 304203 gere transcriptional regulator of spore coat genes (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:germination defective; defective germination in a) (le:60985) (re:61209) (di:direct) BSZ75208 Z75208 g1770055 Bacillus subtilis 1423 -11529483 6500725625 transcriptional regulator:germination protein gere (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerE gerE Bacillus subtilis 1423 -11529483

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756251	1892	24048	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756270	1893	24049	480	159

Description

6500725626 gera1:geraa hypothetical protein:spore germination protein a1 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerAA gerAA Bacillus subtilis 1423 -11529484 7000693021 geraa:gera spore germination protein i gera (cl:spore germination protein gerba) (db:pir2.dat) E69629 E69629 Bacillus subtilis 1423 -11529484 7000693022 geraa (fn:germination response to l-alanine and related) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:192841) (re:194289) (di:direct) BSUB0017 Z99120 g2635802 Bacillus subtilis 1423 -11529484 7500964006 geraa geraa protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:35998) (re:37446) (di:complement) BS43KBDNA AJ223978 g2832824 Bacillus subtilis 1423 -11529484

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756278	1894	24050	1107	368

Description

6500725627 gera2:gerab hypothetical protein:spore germination protein a2 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerAB gerAB Bacillus subtilis 1423 -11529485 74429 gerab:gera2 (de:spore germination protein a2) (db:swissprot) GRA2_BACSU P07869 BACILLUS SUBTILIS 1423 -11529485 7000685444 gerab spore germination protein ii:germination response to l-alanine gerab (cl:spore germination protein) (db:pir2.dat) F69629 F69629 Bacillus subtilis 1423 -11529485 215649 gerab (sr:b.subtilis 168 dna) (db:genpept-bct1) (de:b.subtilis (168) spore germination operon, geraa, gerab and geracgenes, complete cds.) (nt:formerly called gene ii) (le:23) (re:1120) (di:direct) BACGERA2 M16189 g1236178 Bacillus subtilis 1423 -11529485 7000685445 gerab (fn:germination response to l-alanine and related) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:194258) (re:195355) (di:direct) BSUB0017 Z99120 g2635803 Bacillus subtilis 1423 -11529485 7500882706 gerab gerab protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:34932) (re:36029) (di:complement) BS43KBDNA AJ223978 g2832823 Bacillus subtilis 1423 -11529485 5000689016 (de:(gerab) (pn:spore germination protein a2) (gn:gera2) (gtcfc:12.15) (ec:) (gra2_bacsu) (keggfc:11.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis)) gerAB gerAB Bacillus subtilis 1423 10016946

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756286	1895	24051	192	64

Description

6500725628 gera3:gerac hypothetical protein:spore germination protein a3 precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerAC gerAC Bacillus subtilis 1423 -11529486 7000693023 gerac germination response to l-alanine gerac (cl:spore germination protein iii) (db:pir2.dat) G69629 G69629 Bacillus subtilis 1423 -11529486 7000693024 gerac (fn:germination response to l-alanine and related) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:195352) (re:196473) (di:direct) BSUB0017 Z99120 g2635804 Bacillus subtilis 1423 -11529486 7500955383 gerac gerac protein (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:33814) (re:34935) (di:complement) BS43KBDNA AJ223978 g2832822 Bacillus subtilis 1423 -11529486

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756333	1896	24052	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756359	1897	24053	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756368	1898	24054	486	161

Description

GTC ORF with score 131 to: (or:Rattus norvegicus) (sr:rattus norvegicus (strain sprague-dawley) (library: lambda-gt11) (db:genpept-rod) (ec:3.7.1.2) (de:r.norvegicus fumarylacetoacetate hydrolase (fah) mrna, completecds.) (le:23) (re:1282) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756372	1899	24055	423	141

Description

GTC ORF with score 218 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f12f1 sequence, completesequence.) (nt:similar to fumarylacetoacetate hydrolase, gb|l41670) (le:38769:38966:39186) (re:38831:39091:39260) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756547	1900	24056	1029	343

Description

5000689018 hypothetical protein:spore germination protein b1 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerBA gerBA Bacillus subtilis 1423 -11529487 74456 gerba (de:spore germination protein b1) (db:swissprot) GRB1_BACSU P39569 BACILLUS SUBTILIS 1423 -11529487 7000685446 gerba:gerb-1 spore germination apparatus protein gerba (cl:spore germination protein gerba) (db:pir2.dat) (mp:314 deg.) I39855 I39855 Bacillus subtilis 1423 -11529487 7500882712 gerb (fn:possible spore germination apparatus protein) (sr:bacillus subtilis (strain w168) (library: embl4) dna) (db:genpept-bct1) (de:bacillus subtilis spore germination apparatus proteins (gerba,gerbb, gerbc) gerb gene, complete cds.) (le:96) (re:1544) (d... BACGERBABC L16960 g289275 Bacillus subtilis 1423 -11529487 215651 gerba (fn:germination response to the combination of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:90782) (re:92230) (di:direct) BSUB0019 Z99122 g2636106 Bacillus subtilis 1423 -11529487 170577 gerba:gerb-1 spore germination apparatus protein gerba (db:pir) (mp:314 deg.) I39855 I39855 Bacillus subtilis 1423 -11529487 6500725629 hypothetical protein:spore germination protein b1 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerBA gerBA Bacillus subtilis 1423 -11529487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756559	1901	24057	684	227

Description

5000689019 hypothetical protein:spore germination protein b2 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerBB gerBB Bacillus subtilis 1423 -11529488 74457 gerbb (de:spore germination protein b2) (db:swissprot) GRB2_BACSU P39570 BACILLUS SUBTILIS 1423 -11529488 7000685447 gerbb:gerb-2 spore germination apparatus protein gerbb (cl:spore germination protein) (db:pir2.dat) (mp:314 deg.) I39856 I39856 Bacillus subtilis 1423 -11529488 7500882713 gerb (fn:possible spore germination apparatus protein) (sr:bacillus subtilis (strain w168) (library: embl4) dna) (db:genpept-bct1) (de:bacillus subtilis spore germination apparatus proteins (gerba,gerbb, gerbc) gerb gene, complete cds.) (le:1550) (re:2656) ... BACGERBABC L16960 g289276 Bacillus subtilis 1423 -11529488 215652 gerbb (fn:germination response to the combination of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:92236) (re:93342) (di:direct) BSUB0019 Z99122 g2636107 Bacillus subtilis 1423 -11529488 170578 gerbb:gerb-2 spore germination apparatus protein gerbb (cl:spore germination protein) (db:pir) (mp:314 deg.) I39856 I39856 Bacillus subtilis 1423 -11529488 6500725630 hypothetical protein:spore germination protein b2 (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerBB gerBB Bacillus subtilis 1423 -11529488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756560	1902	24058	270	89

Description

5000689020 hypothetical protein:spore germination protein b3 precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerBC gerBC Bacillus subtilis 1423 -11529489 74461 gerbc (de:spore germination protein b3 precursor) (db:swissprot) GRB3_BACSU P39571 BACILLUS SUBTILIS 1423 -11529489 7000685448 gerbc:gerb-3 spore germination apparatus protein gerbc (cl:spore germination protein iii) (db:pir2.dat) (mp:314 deg.) I39857 I39857 Bacillus subtilis 1423 -11529489 7500882716 gerb (fn:possible spore germination apparatus protein) (sr:bacillus subtilis (strain w168) (library: embl4) dna) (db:genpept-bct1) (de:bacillus subtilis spore germination apparatus proteins (gerba,gerbb, gerbc) gerb gene, complete cds.) (le:2653) (re:3777) ... BACGERBABC L16960 g289277 Bacillus subtilis 1423 -11529489 215653 gerbc (fn:germination response to the combination of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:93339) (re:94463) (di:direct) BSUB0019 Z99122 g2636108 Bacillus subtilis 1423 -11529489 170579 gerbc:gerb-3 spore germination apparatus protein gerbc (cl:spore germination protein iii) (db:pir) (mp:314 deg.) I39857 I39857 Bacillus subtilis 1423 -11529489 6500725631 hypothetical protein:spore germination protein b3 precursor (gtcfc:12.15) (keggfc:14.2) (bsorffc:6.2.2) (db:gtc-bacillus subtilis) gerBC gerBC Bacillus subtilis 1423 -11529489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756562	1903	24059	627	209

Description

GTC ORF with score 119 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae hypothetical protein) (le:32916) (re:35417) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756563	1904	24060	369	122

Description

GTC ORF with score 173 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f24j7 (essaiiproject).) (nt:similarity to cyclin c homolog 1,) (le:64662:65940:67037:67466) (re:64752:66168:67229:67641) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756581	1905	24061	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756590	1906	24062	861	286

Description

6500725632 ybee:glpt glycerol-3-phosphate permease:glycerol-3-phosphate transporter:g-3-p transporter:g-3-p permease (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) glpT glpT Bacillus subtilis 1423 -11529490 7500882520 glpt (de:permease)) (db:swissprot) GLPT_BACSU P37948 BACILLUS SUBTILIS 1423 -11529490 7000685420 glpt glycerol-3-phosphate transport protein glpt:glycerol-3-phosphate permease glpt (cl:hexose phosphate transport protein uhpt) (db:pir2.dat) I40417 I40417 Bacillus subtilis 1423 -11529490 5000688745 glpt glycerol 3-phosphate permease (fn:uptake of glycerol 3-phosphate) (db:genpept-bct1) (de:b.subtilis glpt and glpq genes for glycerol 3-phosphate permeaseand glycerophosphoryl diester phosphodiesterase.) (le:315) (re:1649) (di:direct) BSGLPTQ Z26522 g403372 Bacillus subtilis 1423 -11529490 219337 glpt glycerol-3-phosphate permease (fn:uptake of glycerol-3-phosphate) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ybee) (le:39333) (re:40667) (di:complement) BSUB0002 Z99105 g2632500 Bacillus subtilis 1423 -11529490 7500882521 ybee (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:36984) (re:38318) (di:complement) AB006424 AB006424 g3599636 Bacillus subtilis 1423 -11529490 74054 glpt (de:permease)) (db:swissprot) GLPT_BACSU P37948 BACILLUS SUBTILIS 1423 -11529490 153209 glpt glycerol-3-phosphate transport protein glpt:glycerol-3-phosphate permease glpt (cl:hexose phosphate transport protein uhpt) (db:pir) I40417 I40417 Bacillus subtilis 1423 -11529490

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756596	1907	24063	291	96

Description

6500725633 ycgc:lctp l-lactate permease (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) lctP lctP Bacillus subtilis 1423 -11529491 7000694152 lctp l-lactate permease lctp (cl:l-lactate permease) (db:pir2.dat) F69649 F69649 Bacillus subtilis 1423 -11529491 7500964885 lctp l-lactate permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ycgc) (le:135677) (re:137302) (di:direct) BSUB0002 Z99105 g2632592 Bacillus subtilis 1423 -11529491

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756599	1908	24064	195	64

Description

6500725634 yflo:citm secondary transporter of the mg2+/citrate complex:mg2+/citrate complex secondary transporter (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) citM citM Bacillus subtilis 1423 -11529492 64705 citm (de:mg2+/citrate complex secondary transporter) (db:swissprot) CITM_BACSU P55069 BACILLUS SUBTILIS 1423 -11529492 7000684830 citm secondary transporter of the mg2+/citrate complex citm (db:pir2.dat) C69600 C69600 Bacillus subtilis 1423 -11529492 220151 citm secondary transporter of the mg2+/citrate (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yflo) (le:31071) (re:32372) (di:direct) BSUB0005 Z99108 g2633085 Bacillus subtilis 1423 -11529492 7500878780 citm (fn:secondary transporter of the mg2+/citrate) (db:genpept-bct2) (de:bacillus subtilis citm gene, complete cds.) (le:281) (re:1582) (di:direct) BSU62003 U62003 g1470088 Bacillus subtilis 1423 -11529492 5000689069 (de:(citm) (pn:mg2) (gtcfc:13.07) (ec:) (citm_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) citM citM Bacillus subtilis 1423 10007367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756602	1909	24065	405	134

Description

5000688744 glycerol uptake facilitator:glycerol uptake facilitator protein (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) glpF glpF Bacillus subtilis 1423 -11529493 74027 glpf (de:glycerol uptake facilitator protein) (db:swissprot) GLPF_BACSU P18156 BACILLUS SUBTILIS 1423 -11529493 7000685416 glpf glycerol uptake facilitator glpf (cl:glycerol facilitator protein) (db:pir2.dat) (mp:75 (degrees)) C47700 C47700 Bacillus subtilis 1423 -11529493 7500882496 glpf glycerol uptake facilitator (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis antiterminator regulatory protein (glpp),glycerol uptake facilitator (glpf) genes, complete cds, glycerolkinase (glpk) gene, 5' end.) (nt:putative) (le:1085) (re:1909) (di:direct) BACGLPPFK M99611 g142997 Bacillus subtilis 1423 -11529493 215687 glpf glycerol uptake facilitator (fn:glycerol utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:199186) (re:200010) (di:direct) BSUB0005 Z99108 g2633251 Bacillus subtilis 1423 -11529493 4000707099 glpf glycerol uptake facilitator (fn:glycerol utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:2506) (re:3330) (di:direct) BSUB0006 Z99109 g2633263 Bacillus subtilis 1423 -11529493 6000684759 glpf putative glycerol uptake facilitator (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:see embl m99611 and swiss prot p18156.) (le:2154) (re:2978) (di:direct) BSY14079 Y14079 g2226136 Bacillus subtilis 1423 -11529493 154810 glpf glycerol uptake facilitator glpf (cl:glycerol facilitator protein) (db:pir) (mp:75 (degrees)) C47700 C47700 Bacillus subtilis 1423 -11529493 6500725635 glycerol uptake facilitator:glycerol uptake facilitator protein (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) glpF glpF Bacillus subtilis 1423 -11529493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756605	1910	24066	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756606	1911	24067	510	170

Description

6500725636 phosphotransferase system:pts enzyme i (gtcfc:12.2) (ec:2.7.3.9) (keggfc:14.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) ptsI ptsI Bacillus subtilis 1423 -11529494 216531 ptsi phosphotransferase system pts enzyme i (fn:general energy coupling protein of the pts;) (db:genpept-bct1) (ec:2.7.3.9) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:64327) (re:65979) (di:direct) BSUB0008 Z99111 g2633762 Bacillus subtilis 1423 -11529494 7000694466 ptsi pts enzyme i ptsi (cl:phosphotransferase system enzyme i:phosphotransferase system enzyme i homology) (db:pir) G69683 G69683 Bacillus subtilis 1423 -11529494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756607	1912	24068	408	135

Description

6500725637 acpp:acpa acyl carrier protein:acp (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) acpA acpA Bacillus subtilis 1423 -11529495 58268 acpa:acpp (de:acyl carrier protein (acp)) (db:swissprot) ACP_BACSU P80643 BACILLUS SUBTILIS 1423 -11529495 7000684504 acpa:srb acyl carrier protein:8.5k protein (cl:acyl carrier protein:acyl carrier protein homology) (db:pir2.dat) JC4822 JC4822 Bacillus subtilis 1423 -11529495 7500876357 acpa acyl carrier protein (fn:fatty acid biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: acpp) (le:66316) (re:66549) (di:direct) BSUB0009 Z99112 g2633964 Bacillus subtilis 1423 -11529495 222723 orf2 orf2 (sr:bacillus subtilis dna) (db:genpept-bct2) (de:bacillus subtilis genes for orf1, orf2, orf3, orf4 and srb, partialand complete cds.) (le:140) (re:373) (di:direct) D64116 D64116 g1237013 Bacillus subtilis 1423 -11529495 170050 acpa:srb acyl carrier protein acpa:8.5k protein (cl:acyl carrier protein:acyl carrier protein homology) (db:pir) JC4822 JC4822 Bacillus subtilis 1423 -11529495 5000689067 (de:(acpa) (pn:acyl carrier protein:acp) (gn:acpp) (gtcfc:13.07) (ec:) (acp_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) acpA acpA Bacillus subtilis 1423 10001048

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756609	1913	24069	672	223

Description

6500725638 sacl:levg phosphotransferase system:pts fructose-specific enzyme iid component:pts system:fructose-specific iid component:eiid-fru:fructose-permease iid component:phosphotransferase enzyme ii:d component:p30 (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) levG levG Bacillus subtilis 1423 -11529496 219374 levg (de:(p30)) (db:swissprot) PTFD_BACSU P26382 BACILLUS SUBTILIS 1423 -11529496 7000686216 levg pts fructose-specific enzyme iid component levg (cl:phosphotransferase system mannose-specific enzyme ii, factor ii-m) (db:pir2.dat) S11401 S11401 Bacillus subtilis 1423 -11529496 7500888944 levg fructose-specific iid component (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:7253) (re:8080) (di:direct) BS233DEG X92868 g2108265 Bacillus subtilis 1423 -11529496 5000688750 levg p30 (db:genpept-bct1) (de:b.subtilis levanase operon levd, leve, levf, levg and sacc(partial) genes for fructose phosphotransferase system polypeptidesp16,18,28,30 and levanase.) (le:1854) (re:2681) (di:direct) BSLEVANOP X56098 g39981 Bacillus subtilis 1423 -11529496 1500685442 levg phosphotransferase system pts (fn:levanase operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: sacl) (le:160051) (re:160878) (di:complement) BSUB0014 Z99117 g2635150 Bacillus subtilis 1423 -11529496 92159 levg (de:(p30)) (db:swissprot) PTFD_BACSU P26382 BACILLUS SUBTILIS 1423 -11529496 138886 levg pts fructose-specific enzyme iid component levg (cl:phosphotransferase system mannose-specific enzyme ii, factor ii-m) (db:pir) S11401 S11401 Bacillus subtilis 1423 -11529496

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756612	1914	24070	465	154

Description

GTC ORF with score 104 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana dna chromosome 4, bac clone f8b4 (essaiiproject).) (nt:similarity to cdc28/cdc2-like kinase associating) (le:47842:48271:48426) (re:48154:48339:49698) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756621	1915	24071	1014	337

Description

6500725639 sacl:levf phosphotransferase system:pts fructose-specific enzyme iic component:pts system:fructose-specific iic component:eiic-fru:fructose-permease iic component:phosphotransferase enzyme ii:c component:p28 (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) levF levF Bacillus subtilis 1423 -11529497 219373 levf (de:(p28)) (db:swissprot) PTFC_BACSU P26381 BACILLUS SUBTILIS 1423 -11529497 7000686215 levf pts fructose-specific enzyme iic component levf (cl:phosphotransferase system mannose-specific enzyme ii, factor ii-p) (db:pir2.dat) S11400 S11400 Bacillus subtilis 1423 -11529497 7500888943 levf fructose-specific iic component (db:genpept-bct1) (de:b.subtilis 23.9kb fragment from map position 233 degrees on thechromosome.) (le:6423) (re:7232) (di:direct) BS233DEG X92868 g2108264 Bacillus subtilis 1423 -11529497 5000688749 levf p28 (db:genpept-bct1) (de:b.subtilis levanase operon levd, leve, levf, levg and sacc(partial) genes for fructose phosphotransferase system polypeptidesp16,18,28,30 and levanase.) (le:1024) (re:1833) (di:direct) BSLEVANOP X56098 g39980 Bacillus subtilis 1423 -11529497 1500685441 levf phosphotransferase system pts (fn:levanase operon) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: sacl) (le:160899) (re:161708) (di:complement) BSUB0014 Z99117 g2635151 Bacillus subtilis 1423 -11529497 92158 levf (de:(p28)) (db:swissprot) PTFC_BACSU P26381 BACILLUS SUBTILIS 1423 -11529497 138888 levf pts fructose-specific enzyme iic component levf (cl:phosphotransferase system mannose-specific enzyme ii, factor ii-p) (db:pir) S11400 S11400 Bacillus subtilis 1423 -11529497

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756629	1916	24072	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756640	1917	24073	684	227

Description

GTC ORF with score 118 to: (or:Homo sapiens) (sr:human) (db:genpept-pri2) (de:homo sapiens melanoma-associated antigen (mage-c1) gene, completecds.) (nt:mage melanoma-associated antigens family member) (le:2122:2458) (re:2125:5882) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756661	1918	24074	285	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756675	1919	24075	966	321

Description

6500725640 ysec:aran sugar-binding protein (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) araN araN Bacillus subtilis 1423 -11529498 7000694146 aran l-arabinose transport sugar-binding protein aran (db:pir2.dat) A69588 A69588 Bacillus subtilis 1423 -11529498 220295 aran sugar-binding protein (fn:l-arabinose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: ysec) (le:145646) (re:146947) (di:complement) BSUB0015 Z99118 g2635340 Bacillus subtilis 1423 -11529498 304168 ysec hypothetical protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to lace of agrobacterium) (le:22960) (re:24261) (di:direct) BSZ75208 Z75208 g1770019 Bacillus subtilis 1423 -11529498

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756678	1920	24076	234	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756853	1921	24077	495	164

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756863	1922	24078	453	150

Description

6500725641 pullulanase (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) amyX amyX Bacillus subtilis 1423 -11529499 7000694471 amyx pullulanase amyx (db:pir2.dat) G69585 G69585 Bacillus subtilis 1423 -11529499 4000714201 amyx (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (nt:similarity to pullulanase precursor from k.) (le:115307) (re:117463) (di:direct) AF008220 AF008220 g2293205 Bacillus subtilis 1423 -11529499 7500965119 amyx pullulanase (fn:starch-degrading enzyme) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:62963) (re:65119) (di:complement) BSUB0016 Z99119 g2635477 Bacillus subtilis 1423 -11529499

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756864	1923	24079	804	267

Description

6500725642 multiple sugar-binding protein (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) msmE msmE Bacillus subtilis 1423 -11529500 7000694264 msme multiple sugar-binding protein msme (db:pir2.dat) H69660 H69660 Bacillus subtilis 1423 -11529500 4000714175 msme sugar-binding protein (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:79986) (re:81266) (di:complement) AF008220 AF008220 g2293308 Bacillus subtilis 1423 -11529500 7500964982 msme multiple sugar-binding protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:99161) (re:100441) (di:direct) BSUB0016 Z99119 g2635511 Bacillus subtilis 1423 -11529500

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756870	1924	24080	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756877	1925	24081	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756882	1926	24082	252	84

Description

6500725643 hypothetical protein:sugar transport (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) amyD amyD Bacillus subtilis 1423 -11529501 7000694648 amyd sugar transport amyd (cl:inner membrane protein ugpa) (db:pir2.dat) E69585 E69585 Bacillus subtilis 1423 -11529501 4000714174 amyd sugar transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:79082) (re:79993) (di:complement) AF008220 AF008220 g2293307 Bacillus subtilis 1423 -11529501 7500965232 amyd (fn:sugar transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:100434) (re:101345) (di:direct) BSUB0016 Z99119 g2635512 Bacillus subtilis 1423 -11529501

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756892	1927	24083	540	179

Description

6500725644 maltose transport protein (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) amyC amyC Bacillus subtilis 1423 -11529502 7000694192 amyc maltose transport protein amyc (cl:maltose transport protein malg) (db:pir2.dat) D69585 D69585 Bacillus subtilis 1423 -11529502 4000714173 amyc sugar transporter (db:genpept-bct1) (de:bacillus subtilis rrnb-dnab genomic region.) (le:78255) (re:79085) (di:complement) AF008220 AF008220 g2293306 Bacillus subtilis 1423 -11529502 7500964919 amyc maltose transport protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:101342) (re:102172) (di:direct) BSUB0016 Z99119 g2635513 Bacillus subtilis 1423 -11529502

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756899	1928	24084	204	67

Description

6500725645 yvbr:arae permease (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) araE araE Bacillus subtilis 1423 -11529503 7000694145 arae l-arabinose transport permease arae (cl:glucose transport protein) (db:pir2.dat) F69587 F69587 Bacillus subtilis 1423 -11529503 7500964881 arae permease (fn:l-arabinose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (nt:alternate gene name: yvbr) (le:83585) (re:84979) (di:complement) BSUB0018 Z99121 g2635909 Bacillus subtilis 1423 -11529503

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756902	1929	24085	537	178

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756903	1930	24086	690	229

Description

5000688768 ribose abc transporter:membrane protein:high affinity ribose transport protein rbsd (gtcfc:12.2:12.6) (keggfc:11.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) rbsD rbsD Bacillus subtilis 1423 -11529504 307932 rbsd (de:high affinity ribose transport protein rbsd) (db:swissprot) RBSD_BACSU P36946 BACILLUS SUBTILIS 1423 -11529504 7000686282 rbsd ribose abc transporter membrane protein rbsd (cl:fucose operon u protein) (db:pir2.dat) I40464 I40464 Bacillus subtilis 1423 -11529504 7500889474 rbsd membrane ribose binding protein (db:genpept-bct1) (de:b.subtilis rbsr, rbsk, rbsd, rbsa, rbsc and rbsb (partial) genes.) (le:2150) (re:2545) (di:direct) BSRIBOSOP Z25798 g397496 Bacillus subtilis 1423 -11529504 219586 rbsd ribose abc transporter membrane protein (fn:ribose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:105238) (re:105633) (di:direct) BSUB0019 Z99122 g2636118 Bacillus subtilis 1423 -11529504 7502851616 rbsd membrane transport protein (db:genpept-bct1) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (nt:part of the ribose transport operon) (le:4385) (re:4780) (di:complement) BSZ92953 Z92953 g1894760 Bacillus subtilis 1423 -11529504 93575 rbsd (de:high affinity ribose transport protein rbsd) (db:swissprot) RBSD_BACSU P36946 BACILLUS SUBTILIS 1423 -11529504 170338 rbsd ribose abc transporter membrane protein rbsd (db:pir) I40464 I40464 Bacillus subtilis 1423 -11529504 307908 rbsd membrane transport protein (db:genpept-bct2) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (nt:part of the ribose transport operon) (le:4385) (re:4780) (di:complement) BSZ92953 Z92953 g1894760 Bacillus subtilis 1423 -11529504 6500725646 ribose abc transporter:membrane protein:high affinity ribose transport protein rbsd (gtcfc:12.2:12.6) (keggfc:11.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) rbsD rbsD Bacillus subtilis 1423 -11529504

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756911	1931	24087	357	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756913	1932	24088	360	119

Description

6500725647 ribose abc transporter:atp-binding protein (gtcfc:12.2:12.6) (keggfc:11.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) rbsA rbsA Bacillus subtilis 1423 -11529505 7000694520 rbsa ribose abc transporter atp-binding protein rbsa (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) H69689 H69689 Bacillus subtilis 1423 -11529505 307931 rbsa ribose abc transporter atp-binding protein (fn:ribose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:105649) (re:107130) (di:direct) BSUB0019 Z99122 g2636119 Bacillus subtilis 1423 -11529505 7500955275 rbsa atp-binding transport protein (db:genpept-bct1) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (nt:part of the ribose transport operon) (le:2888) (re:4369) (di:complement) BSZ92953 Z92953 g1894759 Bacillus subtilis 1423 -11529505

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756924	1933	24089	552	183

Description

6500725648 ribose abc transporter:permease:ribose transport system permease protein rbsc (gtcfc:12.2:12.6) (keggfc:11.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) rbsC rbsC Bacillus subtilis 1423 -11529506 7000694521 rbsc ribose abc transporter permease rbsc (cl:l-arabinose transport system permease arah) (db:pir2.dat) B69690 B69690 Bacillus subtilis 1423 -11529506 307930 rbsc ribose abc transporter permease (fn:ribose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:107132) (re:108100) (di:direct) BSUB0019 Z99122 g2636120 Bacillus subtilis 1423 -11529506 7500965152 rbsc membrane transport protein (db:genpept-bct1) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (nt:part of the ribose transport operon) (le:1918) (re:2886) (di:complement) BSZ92953 Z92953 g1894758 Bacillus subtilis 1423 -11529506

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756931	1934	24090	279	92

Description

6500725649 ribose abc transporter:ribose-binding protein (gtcfc:12.2:12.6) (keggfc:11.1) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) rbsB rbsB Bacillus subtilis 1423 -11529507 7000694522 rbsb ribose abc transporter ribose-binding protein rbsb:periplasmic ribose-binding protein rbsb (cl:lac repressor) (db:pir2.dat) A69690 A69690 Bacillus subtilis 1423 -11529507 307929 rbsb ribose abc transporter ribose-binding protein (fn:ribose transport) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:108112) (re:109029) (di:direct) BSUB0019 Z99122 g2636121 Bacillus subtilis 1423 -11529507 7500955298 rbsb periplasmic substrate-binding protein (db:genpept-bct1) (de:b.subtilis yws(a,b,c) genes and rbs(a,c,d,k,r) genes.) (nt:part of the ribose transport operon) (le:989) (re:1906) (di:complement) BSZ92953 Z92953 g1894757 Bacillus subtilis 1423 -11529507

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756932	1935	24091	336	111

Description

5000688733 celb:licc phosphotransferase system:pts lichenan-specific enzyme iic component:pts system:cellobiose-specific iic component:eiic-cel:cellobiose-permease iic component:phosphotransferase enzyme ii:c component (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) licC licC Bacillus subtilis 1423 -11529508 7500888932 celb:licc (de:permease iic component) (phosphotransferase enzyme ii, c component)) (db:swissprot) PTCC_BACSU P46317 BACILLUS SUBTILIS 1423 -11529508 7000686211 licc pts lichenan-specific enzyme iic component licc:probable cellobiose phosphotransferase enzyme ii (cl:phosphotransferase system enzyme ii factor ii, phosphoenolpyruvate-dependent) (db:pir2.dat) F69651 F69651 Bacillus subtilis 1423 -11529508 301560 celb putative cellobiose phosphotransferase enzyme (db:genpept-bct1) (de:b.subtilis cela, celb, celc, celd and ywaa genes.) (nt:gtg start codon) (le:2564) (re:3922) (di:direct) BSCELABCD Z49992 g895749 Bacillus subtilis 1423 -11529508 219050 licc phosphotransferase system pts (fn:lichenan degradation products utilization) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: celb) (le:160586) (re:161944) (di:complement) BSUB0020 Z99123 g2636393 Bacillus subtilis 1423 -11529508 7502851617 celb cellobiose phosphotransferase enzyme ii (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:62521) (re:63879) (di:direct) D83026 D83026 g1783267 Bacillus subtilis 1423 -11529508 92141 celb:licc (de:permease iic component) (phosphotransferase enzyme ii, c component)) (db:swissprot) PTCC_BACSU P46317 BACILLUS SUBTILIS 1423 -11529508 170452 licc pts lichenan-specific enzyme iic component licc:probable cellobiose phosphotransferase enzyme ii (db:pir) F69651 F69651 Bacillus subtilis 1423 -11529508 222893 celb cellobiose phosphotransferase enzyme ii (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:putative) (le:62521) (re:63879) (di:direct) D83026 D83026 g1783267 Bacillus subtilis 1423 -11529508 6500725650 celb phosphotransferase system:pts lichenan-specific enzyme iic component:pts system:cellobiose-specific iic component:eiic-cel:cellobiose-permease iic component:phosphotransferase enzyme ii:c component (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) licC licC Bacillus subtilis 1423 -11529508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756933	1936	24092	207	68

Description

6500725651 yxkg:msmx multiple sugar-binding transport atp-binding protein (gtcfc:12.2) (keggfc:14.2) (bsorffc:1.1.2) (db:gtc-bacillus subtilis) msmX msmX Bacillus subtilis 1423 -11529509 7500885965 msmx (de:probable multiple sugar-binding transport atp-binding protein msmx) (db:swissprot) MSMX_BACSU P94360 BACILLUS SUBTILIS 1423 -11529509 7000694265 msmx multiple sugar-binding transport atp-binding protein msmx (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B69661 B69661 Bacillus subtilis 1423 -11529509 301539 msmx multiple sugar-binding transport atp-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxkg) (le:184525) (re:185622) (di:complement) BSUB0020 Z99123 g2636416 Bacillus subtilis 1423 -11529509 222872 msmx (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:highly homologous to many atp-binding transport) (le:38843) (re:39940) (di:direct) D83026 D83026 g1783246 Bacillus subtilis 1423 -11529509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756936	1937	24093	636	211

Description

5000688763 uracil permease:uracil transporter (gtcfc:12.3) (keggfc:14.2) (bsorffc:1.1.3) (db:gtc-bacillus subtilis) pyrP pyrP Bacillus subtilis 1423 -11529510 92654 pyrp (de:uracil permease (uracil transporter)) (db:swissprot) PYRP_BACSU P39766 BACILLUS SUBTILIS 1423 -11529510 170341 pyrp membrane-bound uracil permease pyrp (cl:uracil transport protein uraa) (db:pir2.dat) A57986 A38984 Bacillus subtilis 1423 -11529510 7500889193 pyrp putative membrane-bound uracil permease (sr:bacillus subtilis (strains jh861 and 1a610) dna) (db:genpept-bct1) (de:bacillus subtilis pyrimidine biosynthetic (pyr) gene cluster (pyrr,pyrp,pyrb, pyrc, pyraa, pyrab, pyrd, pyrf and pyre) genes,complete cds.) (nt:orf1b) (le:1409) (re:2713) (di:di... BACPYROP M59757 g387578 Bacillus subtilis 1423 -11529510 216558 pyrp uracil permease (fn:pyrimidine biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:20005) (re:21309) (di:direct) BSUB0009 Z99112 g2633921 Bacillus subtilis 1423 -11529510 7000686254 pyrp membrane-bound uracil permease pyrp (db:pir) A57986 A39845 Bacillus subtilis 1423 -11529510 6500725652 uracil permease:uracil transporter (gtcfc:12.3) (keggfc:14.2) (bsorffc:1.1.3) (db:gtc-bacillus subtilis) pyrP pyrP Bacillus subtilis 1423 -11529510

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756940	1938	24094	306	101

Description

6500725653 ypaq:pbux xanthine permease (gtcfc:12.3) (keggfc:14.2) (bsorffc:1.1.3) (db:gtc-bacillus subtilis) pbuX pbuX Bacillus subtilis 1423 -11529511 220237 pbux (de:xanthine permease) (db:swissprot) PBUX_BACSU P42086 BACILLUS SUBTILIS 1423 -11529511 7000686099 pbux xanthine permease pbux (cl:xanthine permease pbux) (db:pir2.dat) S51310 S51310 Bacillus subtilis 1423 -11529511 7500887711 ypaq transport protein (fn:pyrimidine salvage) (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:26% of identity to the bacillus caldolyticus uracil) (le:2007) (re:3323) (di:direct) BACYACA L77246 g1256618 Bacillus subtilis 1423 -11529511 217075 pbux xanthine permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: ypaq) (le:121829) (re:123145) (di:complement) BSUB0012 Z99115 g2634625 Bacillus subtilis 1423 -11529511 5000688761 pbux xanthine permease (db:genpept-bct1) (de:b.subtilis xpt and pbux genes.) (le:938) (re:2254) (di:direct) BSXPTPBUX X83878 g633170 Bacillus subtilis 1423 -11529511 88768 pbux (de:xanthine permease) (db:swissprot) PBUX_BACSU P42086 BACILLUS SUBTILIS 1423 -11529511 170665 pbux xanthine permease pbux (db:pir) S51310 S51310 Bacillus subtilis 1423 -11529511

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756948	1939	24095	1149	383

Description

6500725654 pyrimidine-nucleoside transport protein:pyrimidine nucleoside transport protein (gtcfc:12.3) (keggfc:14.2) (bsorffc:1.1.3) (db:gtc-bacillus subtilis) nupC nupC Bacillus subtilis 1423 -11529512 7500965121 nupc pyrimidine-nucleoside transport protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:49852) (re:51033) (di:complement) BSUB0021 Z99124 g2636487 Bacillus subtilis 1423 -11529512 7000694478 nupc pyrimidine-nucleoside transport protein nupc (db:pir) A69668 A69668 Bacillus subtilis 1423 -11529512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501756967	1940	24096	318	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757137	1941	24097	639	213

Description

5000688751 na+ abc transporter:atp-binding protein:atp-binding transport protein nata (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) natA natA Bacillus subtilis 1423 -11529513 85273 nata (de:atp-binding transport protein nata (na+ abc transporter)) (db:swissprot) NATA_BACSU P46903 BACILLUS SUBTILIS 1423 -11529513 7000685938 nata na+ abc transporter extrusion atp-binding protein nata (cl:atp-binding cassette homology) (db:pir2.dat) A69666 A69666 Bacillus subtilis 1423 -11529513 219920 nata nata (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of atp-binding transport protein) (le:9522) (re:10262) (di:direct) AB000617 AB000617 g2415726 Bacillus subtilis 1423 -11529513 5500684632 nata nata (db:genpept-bct1) (de:bacillus subtilis nata (nata) and natb (natb) genes, complete cds.) (le:2252) (re:2992) (di:direct) BSU30873 U30873 g973330 Bacillus subtilis 1423 -11529513 7500886320 nata na+ abc transporter atp-binding protein (fn:catalyses atp-dependent electrogenic na+) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:101333) (re:102073) (di:direct) BSUB0002 Z99105 g2632561 Bacillus subtilis 1423 -11529513 6500725655 na+ abc transporter:atp-binding protein:atp-binding transport protein nata (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) natA natA Bacillus subtilis 1423 -11529513

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757145	1942	24098	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757149	1943	24099	372	123

Description

5000689468 na+ abc transporter:membrane protein:protein natb (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) natB natB Bacillus subtilis 1423 -11529514 85274 natb (de:protein natb) (db:swissprot) NATB_BACSU P46904 BACILLUS SUBTILIS 1423 -11529514 7000685939 natb na+ abc transporter extrusion membrane protein natb (db:pir2.dat) B69666 B69666 Bacillus subtilis 1423 -11529514 219921 natb natb (db:genpept-bct1) (de:bacillus subtilis nata (nata) and natb (natb) genes, complete cds.) (le:2993) (re:4153) (di:direct) BSU30873 U30873 g1663528 Bacillus subtilis 1423 -11529514 7500886321 natb na+ abc transporter membrane protein (fn:catalyses atp-dependent electrogenic na+) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:102074) (re:103234) (di:direct) BSUB0002 Z99105 g2632562 Bacillus subtilis 1423 -11529514 6500725656 na+ abc transporter:membrane protein:protein natb (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) natB natB Bacillus subtilis 1423 -11529514

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757150	1944	24100	456	151

Description

GTC ORF with score 192 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c27f2.) (nt:nearly identical to c. elegans predicted protein) (le:3229:3485:3716) (re:3421:3673:3822) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757161	1945	24101	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757170	1946	24102	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757173	1947	24103	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757185	1948	24104	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757188	1949	24105	459	152

Description

6500725657 hypothetical protein:probable amino-acid abc transporter atp-binding protein (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckI yckI Bacillus subtilis 1423 -11529515 7500921889 ycki (de:probable amino-acid abc transporter atp-binding protein ycki) (db:swissprot) YCKI_BACSU P39456 BACILLUS SUBTILIS 1423 -11529515 7000693051 ycki abc-type transport protein ycki (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) C69761 C69761 Bacillus subtilis 1423 -11529515 6000690109 ycki (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glutamine abc transporter (atp-binding) (le:214139) (re:214882) (di:complement) BSUB0002 Z99105 g2632645 Bacillus subtilis 1423 -11529515 7500921891 ycki (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to glutamine abc transporter (atp-binding) (le:6039) (re:6782) (di:complement) BSUB0003 Z99106 g2632660 Bacillus subtilis 1423 -11529515 222624 ycki homologue of glutamine transport atp-binding (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:88442) (re:89185) (di:complement) D50453 D50453 g1805430 Bacillus subtilis 1423 -11529515

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757189	1950	24106	429	142

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757200	1951	24107	1083	361

Description

5000688775 hypothetical protein:probable amino-acid abc transporter permease protein (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckJ yckJ Bacillus subtilis 1423 -11529516 7500921893 yckj (de:probable amino-acid abc transporter permease protein) (db:swissprot) YCKJ_BACSU P42200 BACILLUS SUBTILIS 1423 -11529516 7000687486 yckj glutamine abc transporter permease homolog yckj:abc-type transport system probable membrane spanning protein (cl:histidine permease protein m) (db:pir2.dat) I40451 I40451 Bacillus subtilis 1423 -11529516 6000685420 orf2 putative membrane spanning subunit (db:genpept-bct1) (de:b.subtilis putative amino acid transporter gene.) (nt:potential abc-transport system) (le:909) (re:1613) (di:direct) BSPAAT X77636 g666982 Bacillus subtilis 1423 -11529516 219473 yckj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glutamine abc transporter (permease)) (le:214896) (re:215600) (di:complement) BSUB0002 Z99105 g2632646 Bacillus subtilis 1423 -11529516 222625 yckj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to glutamine abc transporter (permease)) (le:6796) (re:7500) (di:complement) BSUB0003 Z99106 g2632661 Bacillus subtilis 1423 -11529516 7502851618 yckj homologue of glutamine transport system (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:89199) (re:89903) (di:complement) D50453 D50453 g1805431 Bacillus subtilis 1423 -11529516 110845 yckj (de:probable amino-acid abc transporter permease protein) (db:swissprot) YCKJ_BACSU P42200 BACILLUS SUBTILIS 1423 -11529516 169840 yckj glutamine abc transporter permease homolog yckj:abc-type transport system probable membrane spanning protein (db:pir) I40451 I40451 Bacillus subtilis 1423 -11529516 6500725658 hypothetical protein:probable amino-acid abc transporter permease protein (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckJ yckJ Bacillus subtilis 1423 -11529516

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757224	1952	24108	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757229	1953	24109	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757230	1954	24110	585	195

Description

6500725659 hypothetical protein:probable amino-acid abc transporter binding protein precursor (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckK yckK Bacillus subtilis 1423 -11529517 7000693053 yckk probable glutamine abc transporter (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) E69761 E69761 Bacillus subtilis 1423 -11529517 222626 yckk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glutamine abc transporter) (le:215587) (re:216393) (di:complement) BSUB0002 Z99105 g2632647 Bacillus subtilis 1423 -11529517 6000690111 yckk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to glutamine abc transporter) (le:7487) (re:8293) (di:complement) BSUB0003 Z99106 g2632662 Bacillus subtilis 1423 -11529517 7500964029 yckk homologue of glutamine-binding periplasmic (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:89890) (re:90696) (di:complement) D50453 D50453 g1805432 Bacillus subtilis 1423 -11529517

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757231	1955	24111	198	65

Description

6500725660 hypothetical protein:similar to ferrichrome abc transporter:permease (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclN yclN Bacillus subtilis 1423 -11529518 7000692983 ycln ferrichrome abc transporter permease homolog ycln (cl:vitamin b12 transport protein btuc) (db:pir2.dat) B69763 B69763 Bacillus subtilis 1423 -11529518 222644 ycln (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to ferrichrome abc transporter (permease)) (le:29202) (re:30152) (di:direct) BSUB0003 Z99106 g2632681 Bacillus subtilis 1423 -11529518 7500955188 ycln homologue of ferric anguibactin transport system (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:111605) (re:112555) (di:direct) D50453 D50453 g1805450 Bacillus subtilis 1423 -11529518

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757240	1956	24112	243	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757241	1957	24113	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757253	1958	24114	681	226

Description

6500725661 hypothetical protein:similar to ferrichrome abc transporter:permease (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclO yclO Bacillus subtilis 1423 -11529519 7000692984 yclo ferrichrome abc transporter permease homolog yclo (cl:ferrichrome abc transporter) (db:pir2.dat) C69763 C69763 Bacillus subtilis 1423 -11529519 222645 yclo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to ferrichrome abc transporter (permease)) (le:30145) (re:31092) (di:direct) BSUB0003 Z99106 g2632682 Bacillus subtilis 1423 -11529519 7500955189 yclo homologue of ferric anguibactin transport system (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:112548) (re:113495) (di:direct) D50453 D50453 g1805451 Bacillus subtilis 1423 -11529519

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757257	1959	24115	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757280	1960	24116	981	326

Description

6500725662 hypothetical protein:similar to ferrichrome abc transporter:atp-binding protein (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclP yclP Bacillus subtilis 1423 -11529520 7000692979 yclp ferrichrome abc transporter atp-binding p homolog yclp (cl:atp-binding cassette homology) (db:pir2.dat) D69763 D69763 Bacillus subtilis 1423 -11529520 222646 yclp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to ferrichrome abc transporter (atp-binding) (le:31086) (re:31844) (di:direct) BSUB0003 Z99106 g2632683 Bacillus subtilis 1423 -11529520 7500963979 yclp homologue of iron dicitrate transport (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:113489) (re:114247) (di:direct) D50453 D50453 g1805452 Bacillus subtilis 1423 -11529520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757431	1961	24117	480	160

Description

6500725663 hypothetical protein:similar to ferrichrome abc transporter:binding protein (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclQ yclQ Bacillus subtilis 1423 -11529521 7000692981 yclq probable ferrichrome abc transporter yclq (cl:iron(iii) dicitrate transport protein) (db:pir2.dat) E69763 E69763 Bacillus subtilis 1423 -11529521 222647 yclq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to ferrichrome abc transporter (binding) (le:31866) (re:32819) (di:direct) BSUB0003 Z99106 g2632684 Bacillus subtilis 1423 -11529521 7500963980 yclq ferric anguibactin-binding protein precusor fatb (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:114269) (re:115222) (di:direct) D50453 D50453 g1805453 Bacillus subtilis 1423 -11529521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757435	1962	24118	240	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757444	1963	24119	201	66

Description

6500725664 hypothetical protein:similar to ferrichrome abc transporter:atp-binding protein (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmF yfmF Bacillus subtilis 1423 -11529522 7000692980 yfmf ferrichrome abc transporter atp-binding p homolog yfmf (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) E69812 E69812 Bacillus subtilis 1423 -11529522 5500687919 yfmf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to ferrichrome abc transporter (atp-binding) (le:19591) (re:20391) (di:complement) BSUB0005 Z99108 g2633073 Bacillus subtilis 1423 -11529522 7500955192 yfmf (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:28130) (re:28930) (di:direct) D86417 D86417 g2443249 Bacillus subtilis 1423 -11529522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757445	1964	24120	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757449	1965	24121	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757450	1966	24122	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757451	1967	24123	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757453	1968	24124	477	158

Description

6500725665 hypothetical protein:similar to ferrichrome abc transporter:permease (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmE yfmE Bacillus subtilis 1423 -11529523 7000692986 yfme ferrichrome abc transporter permease homolog yfme (cl:vitamin b12 transport protein btuc) (db:pir2.dat) D69812 D69812 Bacillus subtilis 1423 -11529523 5500687918 yfme (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to ferrichrome abc transporter (permease)) (le:20404) (re:21405) (di:complement) BSUB0005 Z99108 g2633074 Bacillus subtilis 1423 -11529523 7500955187 yfme (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:27116) (re:28117) (di:direct) D86417 D86417 g2443248 Bacillus subtilis 1423 -11529523

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757458	1969	24125	648	215

Description

6500725666 hypothetical protein:similar to ferrichrome abc transporter:permease (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmD yfmD Bacillus subtilis 1423 -11529524 7000692985 yfmd ferrichrome abc transporter permease homolog yfmd (cl:ferrichrome abc transporter) (db:pir2.dat) C69812 C69812 Bacillus subtilis 1423 -11529524 5500687917 yfmd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to ferrichrome abc transporter (permease)) (le:21402) (re:22403) (di:complement) BSUB0005 Z99108 g2633075 Bacillus subtilis 1423 -11529524 7500955190 yfmd (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:26118) (re:27119) (di:direct) D86417 D86417 g2443247 Bacillus subtilis 1423 -11529524

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757460	1970	24126	396	132

Description

6500725667 hypothetical protein:similar to ferrichrome abc transporter:binding protein (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmC yfmC Bacillus subtilis 1423 -11529525 7000692982 yfmc ferrichrome abc transporter binding prote homolog yfmc (cl:iron(iii) dicitrate transport protein) (db:pir2.dat) B69812 B69812 Bacillus subtilis 1423 -11529525 5500687916 yfmc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to ferrichrome abc transporter (binding) (le:22475) (re:23422) (di:complement) BSUB0005 Z99108 g2633076 Bacillus subtilis 1423 -11529525 7500955815 yfmc (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:25099) (re:26046) (di:direct) D86417 D86417 g2443246 Bacillus subtilis 1423 -11529525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757461	1971	24127	876	291

Description

5000689353 hypothetical protein:probable amino-acid abc transporter atp-binding protein in bmru-ansr intergenic region (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiZ yqiZ Bacillus subtilis 1423 -11529526 115968 yqiz (de:intergenic region) (db:swissprot) YQIZ_BACSU P54537 BACILLUS SUBTILIS 1423 -11529526 7000688451 yqiz abc-type transport protein yqiz (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) H69962 H69962 Bacillus subtilis 1423 -11529526 216195 yqiz (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:228354) (re:229076) (di:direct) BACJH642 D84432 g1303951 Bacillus subtilis 1423 -11529526 7500952517 yqiz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to amino acid abc transporter (atp-binding) (le:94543) (re:95265) (di:complement) BSUB0013 Z99116 g2634830 Bacillus subtilis 1423 -11529526 6500725668 hypothetical protein:probable amino-acid abc transporter atp-binding protein in bmru-ansr intergenic region (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiZ yqiZ Bacillus subtilis 1423 -11529526

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757462	1972	24128	918	305

Description

5000689352 hypothetical protein:probable amino-acid abc transporter permease protein in bmru-ansr intergenic region (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiY yqiY Bacillus subtilis 1423 -11529527 115967 yqiy (de:intergenic region) (db:swissprot) YQIY_BACSU P54536 BACILLUS SUBTILIS 1423 -11529527 7000688450 yqiy amino acid abc transporter permease homolog yqiy (cl:histidine permease protein m) (db:pir2.dat) G69962 G69962 Bacillus subtilis 1423 -11529527 216194 yqiy (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:227702) (re:228361) (di:direct) BACJH642 D84432 g1303950 Bacillus subtilis 1423 -11529527 7500952516 yqiy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to amino acid abc transporter (permease)) (le:95258) (re:95917) (di:complement) BSUB0013 Z99116 g2634831 Bacillus subtilis 1423 -11529527 6500725669 hypothetical protein:probable amino-acid abc transporter permease protein in bmru-ansr intergenic region (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiY yqiY Bacillus subtilis 1423 -11529527

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757473	1973	24129	543	180

Description

5000689351 hypothetical protein:probable amino-acid abc transporter binding protein in bmru-ansr intergenic region precursor (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiX yqiX Bacillus subtilis 1423 -11529528 115966 yqix (de:intergenic region precursor) (db:swissprot) YQIX_BACSU P54535 BACILLUS SUBTILIS 1423 -11529528 7000688449 yqix amino acid abc transporter binding protei homolog yqix (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) F69962 F69962 Bacillus subtilis 1423 -11529528 216193 yqix (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:226854) (re:227621) (di:direct) BACJH642 D84432 g1303949 Bacillus subtilis 1423 -11529528 7500952515 yqix (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to amino acid abc transporter (binding) (le:95998) (re:96765) (di:complement) BSUB0013 Z99116 g2634832 Bacillus subtilis 1423 -11529528 6500725670 hypothetical protein:probable amino-acid abc transporter binding protein in bmru-ansr intergenic region precursor (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiX yqiX Bacillus subtilis 1423 -11529528

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757479	1974	24130	498	165

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757482	1975	24131	363	120

Description

GTC ORF with score 92 to: (fn:catalyzes the phosphorylation of aps to) (sr:hollow green seaweed) (db:genpept-pln2) (ec:2.7.1.25) (de:enteromorpha intestinalis 5'-adenylylsulfate kinase mrna, completecds.) (nt:eapk1) (le:25) (re:840) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757491	1976	24132	435	145

Description

6500725671 yzmf:yqgk hypothetical protein:hypothetical abc transporter atp-binding protein in soda-comga intergenic region:orf75 (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgK yqgK Bacillus subtilis 1423 -11529529 115907 yqgk (de:intergenic region (orf75)) (db:swissprot) YQGK_BACSU P46342 BACILLUS SUBTILIS 1423 -11529529 7000688402 yqgk phosphate abc transporter atp-binding pro homolog yqgk (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) E69956 E69956 Bacillus subtilis 1423 -11529529 216102 yqgk (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:141613) (re:142395) (di:direct) BACJH642 D84432 g1303858 Bacillus subtilis 1423 -11529529 216527 orf75 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for homologues of the e. coli pst geneproducts.) (nt:similality to phosphate transport protein (pstb) of) (le:3782) (re:4564) (di:direct) BACPST D58414 g903307 Bacillus subtilis 1423 -11529529 7500952450 yqgk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yzmf; similar to phosphate abc) (le:181226) (re:182008) (di:complement) BSUB0013 Z99116 g2634928 Bacillus subtilis 1423 -11529529 5000689310 (de:(yqgk) (pn:hypothetical abc transporter atp-binding protein in soda-comga intergenic region:orf75) (gtcfc:13.07) (ec:) (yqgk_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqgK yqgK Bacillus subtilis 1423 10057633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757495	1977	24133	603	201

Description

6500725672 yzme:yqgj hypothetical protein:hypothetical abc transporter atp-binding protein in soda-comga intergenic region:orf74 (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgJ yqgJ Bacillus subtilis 1423 -11529530 115906 yqgj (de:intergenic region (orf74)) (db:swissprot) YQGJ_BACSU P46341 BACILLUS SUBTILIS 1423 -11529530 7000688401 yqgj phosphate abc transporter atp-binding pro homolog yqgj (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) D69956 D69956 Bacillus subtilis 1423 -11529530 216101 yqgj (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:140793) (re:141602) (di:direct) BACJH642 D84432 g1303857 Bacillus subtilis 1423 -11529530 216526 orf74 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for homologues of the e. coli pst geneproducts.) (nt:similality to phosphate transport protein (pstb) of) (le:2962) (re:3771) (di:direct) BACPST D58414 g903306 Bacillus subtilis 1423 -11529530 7500952449 yqgj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yzme; similar to phosphate abc) (le:182019) (re:182828) (di:complement) BSUB0013 Z99116 g2634929 Bacillus subtilis 1423 -11529530 5000689309 (de:(yqgj) (pn:hypothetical abc transporter atp-binding protein in soda-comga intergenic region:orf74) (gtcfc:13.07) (ec:) (yqgj_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqgJ yqgJ Bacillus subtilis 1423 10057632

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757500	1978	24134	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757510	1979	24135	249	82

Description

6500725673 yzmd:yqgi hypothetical protein:probable abc transporter permease protein in soda-comga intergenic region:orf73 (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgI yqgI Bacillus subtilis 1423 -11529531 115905 yqgi (de:region (orf73)) (db:swissprot) YQGI_BACSU P46340 BACILLUS SUBTILIS 1423 -11529531 7000688400 yqgi phosphate abc transporter permease homolog yqgi (db:pir2.dat) C69956 C69956 Bacillus subtilis 1423 -11529531 216100 yqgi (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:139888) (re:140772) (di:direct) BACJH642 D84432 g1303856 Bacillus subtilis 1423 -11529531 216525 orf73 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for homologues of the e. coli pst geneproducts.) (nt:similality to phosphate transport protein (psta) of) (le:2057) (re:2941) (di:direct) BACPST D58414 g903305 Bacillus subtilis 1423 -11529531 7500952448 yqgi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yzmd; similar to phosphate abc) (le:182849) (re:183733) (di:complement) BSUB0013 Z99116 g2634930 Bacillus subtilis 1423 -11529531 5000689308 (de:(yqgi) (pn:probable abc transporter permease protein in soda-comga intergenic region:orf73) (gtcfc:13.07) (ec:) (yqgi_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqgI yqgI Bacillus subtilis 1423 10057631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757512	1980	24136	366	121

Description

6500725674 yzmc:yqgh hypothetical protein:probable abc transporter permease protein in soda-comga intergenic region:orf72 (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgH yqgH Bacillus subtilis 1423 -11529532 115904 yqgh (de:region (orf72)) (db:swissprot) YQGH_BACSU P46339 BACILLUS SUBTILIS 1423 -11529532 7000688399 yqgh phosphate abc transporter permease homolog yqgh (db:pir2.dat) B69956 B69956 Bacillus subtilis 1423 -11529532 216099 yqgh (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:138959) (re:139888) (di:direct) BACJH642 D84432 g1303855 Bacillus subtilis 1423 -11529532 216524 orf72 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for homologues of the e. coli pst geneproducts.) (nt:similality to phosphate transport protein (pstc) of) (le:1128) (re:2057) (di:direct) BACPST D58414 g903304 Bacillus subtilis 1423 -11529532 7500952447 yqgh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yzmc; similar to phosphate abc) (le:183733) (re:184662) (di:complement) BSUB0013 Z99116 g2634931 Bacillus subtilis 1423 -11529532 5000689307 (de:(yqgh) (pn:probable abc transporter permease protein in soda-comga intergenic region:orf72) (gtcfc:13.07) (ec:) (yqgh_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqgH yqgH Bacillus subtilis 1423 10057630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757523	1981	24137	831	276

Description

6500725675 yzmb:yqgg hypothetical protein:probable abc transporter binding protein in soda-comga intergenic region precursor:orf108 (gtcfc:12.6:14.1) (keggfc:11.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgG yqgG Bacillus subtilis 1423 -11529533 115903 yqgg (de:region precursor (orf108)) (db:swissprot) YQGG_BACSU P46338 BACILLUS SUBTILIS 1423 -11529533 7000688398 yqgg phosphate abc transporter binding protein homolog yqgg (cl:methanobacterium phosphate-binding protein psts) (db:pir2.dat) A69956 A69956 Bacillus subtilis 1423 -11529533 216098 yqgg (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:137988) (re:138890) (di:direct) BACJH642 D84432 g1303854 Bacillus subtilis 1423 -11529533 216523 orf108 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna for homologues of the e. coli pst geneproducts.) (nt:similality to phosphate-binding protein (psts) of) (le:157) (re:1059) (di:direct) BACPST D58414 g903303 Bacillus subtilis 1423 -11529533 7500952446 yqgg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yzmb; similar to phosphate abc) (le:184731) (re:185633) (di:complement) BSUB0013 Z99116 g2634932 Bacillus subtilis 1423 -11529533 5000689306 (de:(yqgg) (pn:probable abc transporter binding protein in soda-comga intergenic region precursor:orf108) (gtcfc:13.07) (ec:) (yqgg_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqgG yqgG Bacillus subtilis 1423 10057629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757708	1982	24138	384	127

Description

5000689080 ferrichrome abc transporter:atp-binding protein:ferrichrome transport atp-binding protein fhuc (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuC fhuC Bacillus subtilis 1423 -11529534 219194 fhuc (de:ferrichrome transport atp-binding protein fhuc) (db:swissprot) FHUC_BACSU P49938 BACILLUS SUBTILIS 1423 -11529534 7000685237 fhuc ferrichrome abc transporter atp-binding protein fhuc (cl:atp-binding cassette homology) (db:pir2.dat) B69622 B69622 Bacillus subtilis 1423 -11529534 7000685238 fhuc (fn:ferrichrome transport system) (db:genpept-bct1) (de:b.subtilis fhudbgc genes.) (nt:protein-dependent) (le:3514) (re:4323) (di:direct) BSFHUDBGC X93092 g1070015 Bacillus subtilis 1423 -11529534 7502851619 fhuc ferrichrome abc transporter atp-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:14899) (re:15708) (di:complement) BSUB0018 Z99121 g2635843 Bacillus subtilis 1423 -11529534 7500881441 fhuc ferrichrome transport protein:fhuc (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:12029) (re:12838) (di:direct) BS43KBDNA AJ223978 g2832798 Bacillus subtilis 1423 -11529534 71556 fhuc (de:ferrichrome transport atp-binding protein fhuc) (db:swissprot) FHUC_BACSU P49938 BACILLUS SUBTILIS 1423 -11529534 6500725676 ferrichrome abc transporter:atp-binding protein:ferrichrome transport atp-binding protein fhuc (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuC fhuC Bacillus subtilis 1423 -11529534

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757710	1983	24139	429	143

Description

5000689081 ferrichrome abc transporter:permease:ferrichrome transport permease protein fhug (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuG fhuG Bacillus subtilis 1423 -11529535 219193 fhug (de:ferrichrome transport permease protein fhug) (db:swissprot) FHUG_BACSU P49937 BACILLUS SUBTILIS 1423 -11529535 7000685244 fhug ferrichrome abc transporter permease fhug (db:pir2.dat) D69622 D69622 Bacillus subtilis 1423 -11529535 7000685245 fhug (fn:ferrichrome transport system) (db:genpept-bct1) (de:b.subtilis fhudbgc genes.) (nt:protein-dependent) (le:2488) (re:3498) (di:direct) BSFHUDBGC X93092 g1070014 Bacillus subtilis 1423 -11529535 7502851620 fhug ferrichrome abc transporter permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:15724) (re:16734) (di:complement) BSUB0018 Z99121 g2635844 Bacillus subtilis 1423 -11529535 7500881447 fhug ferrichrome transport protein:fhug (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:11003) (re:12013) (di:direct) BS43KBDNA AJ223978 g2832797 Bacillus subtilis 1423 -11529535 71561 fhug (de:ferrichrome transport permease protein fhug) (db:swissprot) FHUG_BACSU P49937 BACILLUS SUBTILIS 1423 -11529535 6500725677 ferrichrome abc transporter:permease:ferrichrome transport permease protein fhug (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuG fhuG Bacillus subtilis 1423 -11529535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757711	1984	24140	678	226

Description

5000689079 ferrichrome abc transporter:permease:ferrichrome transport permease protein fhub (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuB fhuB Bacillus subtilis 1423 -11529536 219192 fhub (de:ferrichrome transport permease protein fhub) (db:swissprot) FHUB_BACSU P49936 BACILLUS SUBTILIS 1423 -11529536 7000685234 fhub ferrichrome abc transporter permease fhub (db:pir2.dat) A69622 A69622 Bacillus subtilis 1423 -11529536 7000685235 fhub (fn:ferrichrome transport system) (db:genpept-bct1) (de:b.subtilis fhudbgc genes.) (nt:protein-dependent) (le:1334) (re:2488) (di:direct) BSFHUDBGC X93092 g1070013 Bacillus subtilis 1423 -11529536 7502851621 fhub ferrichrome abc transporter permease (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:16734) (re:17888) (di:complement) BSUB0018 Z99121 g2635845 Bacillus subtilis 1423 -11529536 7500881439 fhub ferrichrome transport protein:fhub (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:9849) (re:11003) (di:direct) BS43KBDNA AJ223978 g2832796 Bacillus subtilis 1423 -11529536 71554 fhub (de:ferrichrome transport permease protein fhub) (db:swissprot) FHUB_BACSU P49936 BACILLUS SUBTILIS 1423 -11529536 6500725678 ferrichrome abc transporter:permease:ferrichrome transport permease protein fhub (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuB fhuB Bacillus subtilis 1423 -11529536

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757722	1985	24141	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757740	1986	24142	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757742	1987	24143	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757745	1988	24144	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757748	1989	24145	414	137

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757749	1990	24146	348	115

Description

5000688742 ferrichrome abc transporter:ferrichrome-binding protein:ferrichrome-binding protein precursor (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuD fhuD Bacillus subtilis 1423 -11529537 215591 fhud (de:ferrichrome-binding protein precursor) (db:swissprot) FHUD_BACSU P37580 BACILLUS SUBTILIS 1423 -11529537 7000685240 fhud ferrichrome abc transporter fhud precursor:ferrichrome-binding protein fhud (cl:bacillus subtilis ferrichrome abc transporter fhud) (db:pir2.dat) S32930 S32930 Bacillus subtilis 1423 -11529537 7500881443 fhud ferrichrome-binding protein (sr:bacillus subtilis (strain marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis (marburg 168) ferrichrome-binding protein (fhud)gene, complete cds.) (le:214) (re:1161) (di:direct) BACFHUD M87283 g289272 Bacillus subtilis 1423 -11529537 219191 fhud (fn:ferrichrome transport system) (db:genpept-bct1) (de:b.subtilis fhudbgc genes.) (nt:protein-dependent) (le:289) (re:1236) (di:complement) BSFHUDBGC X93092 g1070012 Bacillus subtilis 1423 -11529537 7502851622 fhud ferrichrome abc transporter ferrichrome-binding (db:genpept-bct1) (de:bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.) (le:17986) (re:18933) (di:direct) BSUB0018 Z99121 g2635846 Bacillus subtilis 1423 -11529537 7000685241 fhud ferrichrome binding protein:fhud (db:genpept-bct2) (de:bacillus subtilis 42.7kb dna fragment from yvsa to yvqa.) (le:8804) (re:9751) (di:complement) BS43KBDNA AJ223978 g2832795 Bacillus subtilis 1423 -11529537 71558 fhud (de:ferrichrome-binding protein precursor) (db:swissprot) FHUD_BACSU P37580 BACILLUS SUBTILIS 1423 -11529537 169983 fhud ferrichrome abc transporter fhud precursor:ferrichrome-binding protein fhud (db:pir) S32930 S32930 Bacillus subtilis 1423 -11529537 6500725679 ferrichrome abc transporter:ferrichrome-binding protein:ferrichrome-binding protein precursor (gtcfc:12.6) (keggfc:11.1) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) fhuD fhuD Bacillus subtilis 1423 -11529537

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757761	1991	24147	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757762	1992	24148	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757772	1993	24149	279	93

Description

5000688741 integral membrane protein:iron-uptake system protein feuc (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) feuC feuC Bacillus subtilis 1423 -11529538 71482 feuc (de:iron-uptake system protein feuc) (db:swissprot) FEUC_BACSU P40411 BACILLUS SUBTILIS 1423 -11529538 7000685231 feuc iron-uptake system integral membrane protein feuc (db:pir2.dat) G69621 G69621 Bacillus subtilis 1423 -11529538 216961 feuc feuc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome, trni-feuabc region.) (le:14283) (re:15467) (di:complement) BACTHRTRNA D84213 g1256154 Bacillus subtilis 1423 -11529538 7500881425 feuc integral membrane protein (fn:component of iron-uptake system) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:180168) (re:181352) (di:complement) BSUB0001 Z99104 g2632428 Bacillus subtilis 1423 -11529538 6500725680 integral membrane protein:iron-uptake system protein feuc (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) feuC feuC Bacillus subtilis 1423 -11529538

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757773	1994	24150	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757777	1995	24151	438	145

Description

GTC ORF with score 255 to: (sr:synechococcus pcc 7942) (db:genpept-bct1) (ec:4.3.99.1) (de:synechococcus pcc 7942 cyanate lyase (cyns) gene, complete cds.) (nt:cyanase; putative; bicarbonate-dependent) (le:22) (re:462) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757784	1996	24152	243	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757798	1997	24153	393	130

Description

GTC ORF with score 184 to: (db:genpept-pln2) (de:emericella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj),(stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757801	1998	24154	267	88

Description

GTC ORF with score 144 to: (db:genpept-pln2) (de:emericella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj),(stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757808	1999	24155	1068	355

Description

5000688740 integral membrane protein:iron-uptake system protein feub (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) feuB feuB Bacillus subtilis 1423 -11529539 71481 feub (de:iron-uptake system protein feub) (db:swissprot) FEUB_BACSU P40410 BACILLUS SUBTILIS 1423 -11529539 7000685230 feub iron-uptake system integral membrane protein feub (db:pir2.dat) I39843 I39843 Bacillus subtilis 1423 -11529539 7500881424 feub (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:1) (re:1005) (di:complement) AB002150 AB002150 g1944002 Bacillus subtilis 1423 -11529539 215589 feub (fn:component of iron-uptake system) (sr:bacillus subtilis (individual_isolate ms94, strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis feua, b, and c genes, 3 orfs, 2 complete cds'sand 5'end.) (nt:homologous to e. coli hydrophobic fe-uptake) (l... BACFEUABC L19954 g438459 Bacillus subtilis 1423 -11529539 1500685222 feub integral membrane protein (fn:component of iron-uptake system) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:181345) (re:182349) (di:complement) BSUB0001 Z99104 g2632429 Bacillus subtilis 1423 -11529539 170300 feub iron-uptake system integral membrane protein feub (db:pir) I39843 I39843 Bacillus subtilis 1423 -11529539 6500725681 integral membrane protein:iron-uptake system protein feub (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) feuB feuB Bacillus subtilis 1423 -11529539

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757814	2000	24156	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757971	2001	24157	927	308

Description

GTC ORF with score 268 to: (db:genpept) (de:caenorhabditis elegans cosmid t06d8, complete sequence.) (nt:cdna est embl:d74028 comes from this gene; cdna est) (le:27283:27595:27720:28002) (re:27303:27670:27949:28390) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757973	2002	24158	423	140

Description

5000688739 iron-binding protein:iron-uptake system binding protein precursor (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) feuA feuA Bacillus subtilis 1423 -11529540 71480 feua (de:iron-uptake system binding protein precursor) (db:swissprot) FEUA_BACSU P40409 BACILLUS SUBTILIS 1423 -11529540 7000685229 feua iron-uptake system binding protein feua (db:pir2.dat) I39842 I39842 Bacillus subtilis 1423 -11529540 7500881423 feua (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:1024) (re:1977) (di:complement) AB002150 AB002150 g1944003 Bacillus subtilis 1423 -11529540 215588 feua (fn:component of iron-uptake system) (sr:bacillus subtilis (individual_isolate ms94, strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis feua, b, and c genes, 3 orfs, 2 complete cds'sand 5'end.) (nt:likely n-terminal signal sequence; mature prote... BACFEUABC L19954 g438458 Bacillus subtilis 1423 -11529540 1500685221 feua iron-binding protein (fn:component of iron-uptake system) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:182368) (re:183321) (di:complement) BSUB0001 Z99104 g2632430 Bacillus subtilis 1423 -11529540 170299 feua iron-uptake system binding protein feua (db:pir) I39842 I39842 Bacillus subtilis 1423 -11529540 6500725682 iron-binding protein:iron-uptake system binding protein precursor (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) feuA feuA Bacillus subtilis 1423 -11529540

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757989	2003	24159	450	149

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757992	2004	24160	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501757998	2005	24161	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758006	2006	24162	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758013	2007	24163	432	143

Description

6500725683 ycca:lmrb drug-export protein (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) lmrB lmrB Bacillus subtilis 1423 -11529541 7000694163 lmrb lincomycin-resistance protein lmrb (db:pir2.dat) E69652 E69652 Bacillus subtilis 1423 -11529541 5500687007 ycca lmrb (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:lincomycin-resistance protein, similar to) (le:1746) (re:3185) (di:complement) AB000617 AB000617 g2415718 Bacillus subtilis 1423 -11529541 7500964895 lmrb drug-export protein (fn:lincomycin-resistance) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ycca) (le:93557) (re:94996) (di:complement) BSUB0002 Z99105 g2632553 Bacillus subtilis 1423 -11529541

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758014	2008	24164	1038	345

Description

6500725684 ycgd:bmr3:mdr multidrug-efflux transporter (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) mdr mdr Bacillus subtilis 1423 -11529542 7000694249 mdr multidrug-efflux transporter puromycin:nerfloxacin:tosufloxa mdr (cl:multidrug-efflux transporter) (db:pir2.dat) B69656 B69656 Bacillus subtilis 1423 -11529542 7500955414 mdr multidrug-efflux transporter (fn:resistance to puromycin, nerfloxacin,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ycgd, bmr3) (le:137610) (re:138890) (di:complement) BSUB0002 Z99105 g2632593 Bacillus subtilis 1423 -11529542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758031	2009	24165	1065	354

Description

GTC ORF with score 523 to: (sr:information) (db:genpept) (de:homo sapiens pac clone dj0659j06 from 7q33-q35, complete sequence.) (nt:similar to several hypothetical proteins: u70849) (le:<57403:59472:60232:62272) (re:57562:59613:60418:62434) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758044	2010	24166	591	197

Description

6500725685 atp-binding transport protein:nucleotide binding protein expz (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) expZ expZ Bacillus subtilis 1423 -11529543 70862 expz (de:nucleotide binding protein expz) (db:swissprot) EXPZ_BACSU P39115 BACILLUS SUBTILIS 1423 -11529543 7000685211 expz atp-binding transport protein expz (cl:atp-binding cassette homology) (db:pir2.dat) G69620 G69620 Bacillus subtilis 1423 -11529543 302812 expz probable atp-binding transport protein (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:137954) (re:139597) (di:complement) AB001488 AB001488 g1881367 Bacillus subtilis 1423 -11529543 6000686382 expz atp-binding transport protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:201700) (re:203343) (di:complement) BSUB0003 Z99106 g2632861 Bacillus subtilis 1423 -11529543 7500881243 expz atp-binding transport protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:3750) (re:5393) (di:complement) BSUB0004 Z99107 g2632874 Bacillus subtilis 1423 -11529543

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758046	2011	24167	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758065	2012	24168	246	81

Description

6500725686 prst:ecs-26:yhad:ecsa abc transporter:atp-binding protein:abc-type transporter atp-binding protein ecsa (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) ecsA ecsA Bacillus subtilis 1423 -11529544 69714 ecsa:prst (de:abc-type transporter atp-binding protein ecsa) (db:swissprot) ECSA_BACSU P55339 BACILLUS SUBTILIS 1423 -11529544 7000685135 ecsa abc transporter atp-binding protein ecsa (cl:atp-binding cassette homology) (db:pir2.dat) F69619 F69619 Bacillus subtilis 1423 -11529544 219181 ecsa putative atp-binding protein of abc-type (db:genpept-bct1) (de:b.subtilis ecsa, ecsb, and ecsc genes.) (le:248) (re:991) (di:direct) BSECSABCG X87807 g1177253 Bacillus subtilis 1423 -11529544 304128 ecsa abc transporter atp-binding protein (fn:regulates both components of the protein) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: prst, ecs-26, yhad) (le:77413) (re:78156) (di:direct) BSUB0006 Z99109 g2633340 Bacillus subtilis 1423 -11529544 4000707048 yhad hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:identified as ecsa. similar to many atp binding abc) (le:2757) (re:3500) (di:complement) BSY14077 Y14077 g2226115 Bacillus subtilis 1423 -11529544 5000689075 (de:(ecsa) (pn:abc-type transporter atp-binding protein ecsa) (gn:prst) (gtcfc:13.07) (ec:) (ecsa_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) ecsA ecsA Bacillus subtilis 1423 10012294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758257	2013	24169	489	163

Description

6500725687 prst:yhac:ecsb abc transporter:membrane protein:protein ecsb (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) ecsB ecsB Bacillus subtilis 1423 -11529545 69715 ecsb:prst (de:protein ecsb) (db:swissprot) ECSB_BACSU P55340 BACILLUS SUBTILIS 1423 -11529545 7000685136 ecsb abc transporter membrane protein ecsb (db:pir2.dat) G69619 G69619 Bacillus subtilis 1423 -11529545 219182 ecsb hypothetical ecsb protein (db:genpept-bct1) (de:b.subtilis ecsa, ecsb, and ecsc genes.) (le:984) (re:2210) (di:direct) BSECSABCG X87807 g1177254 Bacillus subtilis 1423 -11529545 304129 ecsb abc transporter membrane protein (fn:regulates both components of the protein) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: prst, yhac) (le:78149) (re:79375) (di:direct) BSUB0006 Z99109 g2633341 Bacillus subtilis 1423 -11529545 4000707049 yhac hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:identified as ecsb. hypothetical integral membrane) (le:1538) (re:2764) (di:complement) BSY14077 Y14077 g2226114 Bacillus subtilis 1423 -11529545 5000689076 (de:(ecsb) (pn:protein ecsb) (gn:prst) (gtcfc:13.07) (ec:) (ecsb_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) ecsB ecsB Bacillus subtilis 1423 10012295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758279	2014	24170	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758282	2015	24171	795	264

Description

6500725688 prst:yhab:ecsc hypothetical protein:protein ecsc (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) ecsC ecsC Bacillus subtilis 1423 -11529546 69716 ecsc:prst (de:protein ecsc) (db:swissprot) ECSC_BACSU P55341 BACILLUS SUBTILIS 1423 -11529546 7000685137 ecsc hypothetical protein ecsc (db:pir2.dat) H69619 H69619 Bacillus subtilis 1423 -11529546 219183 ecsc hypothetical ecsc protein (db:genpept-bct1) (de:b.subtilis ecsa, ecsb, and ecsc genes.) (le:2230) (re:2940) (di:direct) BSECSABCG X87807 g1177255 Bacillus subtilis 1423 -11529546 304130 ecsc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: prst, yhab) (le:79395) (re:80105) (di:direct) BSUB0006 Z99109 g2633342 Bacillus subtilis 1423 -11529546 4000707050 yhab hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:identified as ecsc.) (le:808) (re:1518) (di:complement) BSY14077 Y14077 g2226113 Bacillus subtilis 1423 -11529546 5000689077 (de:(ecsc) (pn:protein ecsc) (gn:prst) (gtcfc:13.07) (ec:) (ecsc_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) ecsC ecsC Bacillus subtilis 1423 10012296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758292	2016	24172	297	98

Description

6500725689 yolh:sunt sublancin 168 lantibiotic transporter (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) sunT sunT Bacillus subtilis 1423 -11529547 7000694636 sunt sublancin 168 lantibiotic transporter sunt (cl:atp-binding cassette homology) (db:pir2.dat) A69720 A69720 Bacillus subtilis 1423 -11529547 7000694637 sunt sublancin 168 lantibiotic transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: yolh) (le:71047) (re:73164) (di:complement) BSUB0012 Z99115 g2634567 Bacillus subtilis 1423 -11529547 7500965226 yolh abc transporter (fn:probable bacteriocin exporter) (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:16986) (re:19103) (di:direct) AF020713 AF020713 g3025498 Bacteriophage SPBc2 66797 -11529547

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758296	2017	24173	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758297	2018	24174	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758305	2019	24175	1179	392

Description

6500725690 yolg:suna sublancin 168 lantibiotic antimicrobial precursor peptide (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) sunA sunA Bacillus subtilis 1423 -11529548 7000694634 suna sublancin 168 precursor (cl:unassigned lanthionine-containing peptides) (db:pir2.dat) H69719 H69719 Bacillus subtilis 1423 -11529548 5500687317 suna sublancin 168 lantibiotic antimicrobial (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: yolg) (le:73222) (re:73392) (di:complement) BSUB0012 Z99115 g2634568 Bacillus subtilis 1423 -11529548 7000694635 suna sublancin 168 precursor peptide (db:genpept-bct2) (de:bacillus subtilis uvr repair protein (uvrx), sublancin 168precursor peptide (suna), and sublancin transporter protein (sunt)genes, complete cds.) (nt:lantibiotic antimicrobial peptide; suna) (le:2822) (re:2992) (di:direct) AF014938 AF014938 g2343278 Bacillus subtilis 1423 -11529548 7500954593 yolg putative lipoprotein (fn:putative bacteriocin) (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:16758) (re:16928) (di:direct) AF020713 AF020713 g3025497 Bacteriophage SPBc2 66797 -11529548

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758313	2020	24176	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758317	2021	24177	330	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758321	2022	24178	579	193

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758331	2023	24179	777	258

Description

5000688732 multidrug resistance protein:bmru protein (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) bmrU bmrU Bacillus subtilis 1423 -11529549 61899 bmru (de:bmru protein) (db:swissprot) BMRU_BACSU P39074 BACILLUS SUBTILIS 1423 -11529549 7000684726 bmru multidrug resistance protein cotranscribed with bmr bmru (db:pir2.dat) F69595 F69595 Bacillus subtilis 1423 -11529549 215290 bmru (fn:unknown, but cotranscribed with bmr) (db:genpept-bct1) (de:bacillus subtilis bmru, multidrug efflux transporter (bmr) and itsregulator (bmrr) genes, complete cds, and branched-chain 2-oxo aciddehydrogenase (bfmb) gene, 3' end.) (le:227) (re:1120) (... BACBMRURBE L25604 g409286 Bacillus subtilis 1423 -11529549 216191 bmru (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:225092) (re:225985) (di:complement) BACJH642 D84432 g1303947 Bacillus subtilis 1423 -11529549 7500877876 bmru multidrug resistance protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:97634) (re:98527) (di:direct) BSUB0013 Z99116 g2634834 Bacillus subtilis 1423 -11529549 6500725691 multidrug resistance protein:bmru protein (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) bmrU bmrU Bacillus subtilis 1423 -11529549

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758334	2024	24180	792	263

Description

GTC ORF with score 1095 to: (sr:aspergillus aculeatus (isolate:no.f-50) cdna to mrna, clone:pagb7) (db:genpept-pln1) (ec:3.2.1.21) (de:aspergillus aculeatus mrna for beta-glucosidase, complete cds.) (le:111) (re:2693) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758335	2025	24181	414	137

Description

6500725692 bmr1:bmr multidrug-efflux transporter:multidrug resistance protein 1:multidrug-efflux transporter 1 (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) bmr bmr Bacillus subtilis 1423 -11529550 61895 bmr:bmr1 (de:multidrug resistance protein 1 (multidrug-efflux transporter 1)) (db:swissprot) BMR1_BACSU P33449 BACILLUS SUBTILIS 1423 -11529550 7000684724 bmr multidrug-efflux transporter bmr:multidrug resistance protein bmr (cl:tetracycline resistance protein) (db:pir2.dat) A39705 A39705 Bacillus subtilis 1423 -11529550 7500877870 bmr multidrug-efflux transporter (db:genpept-bct1) (de:bacillus subtilis bmru, multidrug efflux transporter (bmr) and itsregulator (bmrr) genes, complete cds, and branched-chain 2-oxo aciddehydrogenase (bfmb) gene, 3' end.) (le:1221) (re:2390) (di:direct) BACBMRURBE L25604 g409287 Bacillus subtilis 1423 -11529550 215291 (sr:b.subtilis dna) (db:genpept-bct1) (de:b.subtilis multidrug-resistant protein (bmr) gene, complete cds.) (nt:multidrug-resistance protein (bmr)) (le:195) (re:1364) (di:direct) BACBMRX M33768 g142606 Bacillus subtilis 1423 -11529550 215294 bmr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:223822) (re:224991) (di:complement) BACJH642 D84432 g1303946 Bacillus subtilis 1423 -11529550 216190 bmr multidrug-efflux transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: bmr1) (le:98628) (re:99797) (di:direct) BSUB0013 Z99116 g2634835 Bacillus subtilis 1423 -11529550 154109 bmr multidrug-efflux transporter bmr:multidrug resistance protein bmr (cl:tetracycline resistance protein) (db:pir) A39705 A39705 Bacillus subtilis 1423 -11529550 5000688731 (de:(bmr) (pn:multidrug resistance protein 1:multidrug-efflux transporter 1) (gn:bmr1) (gtcfc:12.01:12.02:12.03) (ec:) (bmr1_bacsu) (keggfc:11.2) (bsorffc:1.0.0) (db:gtc-bacillus subtilis)) bmr bmr Bacillus subtilis 1423 10004599

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758336	2026	24182	375	124

Description

GTC ORF with score 569 to: (or:Aspergillus aculeatus) (sr:aspergillus aculeatus (isolate:no.f-50) cdna to mrna, clone:pagb7) (db:genpept-pln1) (ec:3.2.1.21) (de:aspergillus aculeatus mrna for beta-glucosidase, complete cds.) (le:111) (re:2693) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758347	2027	24183	207	68

Description

6500725693 acfa:bmr2:bmt:blt multidrug-efflux transporter:multidrug resistance protein 2:multidrug-efflux transporter 2 (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) blt blt Bacillus subtilis 1423 -11529551 61896 blt:bmt:bmr2 (de:multidrug resistance protein 2 (multidrug-efflux transporter 2)) (db:swissprot) BMR2_BACSU P39843 BACILLUS SUBTILIS 1423 -11529551 7000684725 blt multidrug-efflux transporter blt (cl:tetracycline resistance protein) (db:pir2.dat) I39792 I39792 Bacillus subtilis 1423 -11529551 7500877871 blt (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:1438) (re:2640) (di:complement) BACJH642 D84432 g1303699 Bacillus subtilis 1423 -11529551 215288 blt multidrug-efflux transporter (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: acfa, bmr2, bmt) (le:116792) (re:117994) (di:direct) BSUB0014 Z99117 g2635104 Bacillus subtilis 1423 -11529551 215943 blt (fn:multidrug efflux transporter) (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct2) (de:bacillus subtilis multidrug efflux transporter (blt) gene;transcription regulator (bltr) gene; transacetylase (bltd) gene.) (le:1237) (re:2439) (di:direct) BACBLTRD L32599 g483941 Bacillus subtilis 1423 -11529551 170357 blt multidrug-efflux transporter blt (cl:tetracycline resistance protein) (db:pir) I39792 I39792 Bacillus subtilis 1423 -11529551 5000688730 (de:(blt) (pn:multidrug resistance protein 2:multidrug-efflux transporter 2) (gn:bmt:bmr2) (gtcfc:12.01:12.02:12.03) (ec:) (bmr2_bacsu) (keggfc:11.2) (bsorffc:1.0.0) (db:gtc-bacillus subtilis)) blt blt Bacillus subtilis 1423 10004600

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758359	2028	24184	258	86

Description

6500725694 yxkn:cydd abc membrane transporter:atp-binding protein:transport atp-binding protein cydd (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) cydD cydD Bacillus subtilis 1423 -11529552 5500685061 cydd (de:transport atp-binding protein cydd) (db:swissprot) CYDD_BACSU P94367 BACILLUS SUBTILIS 1423 -11529552 7000684959 cydd abc transporter required for expression of cytochrome bd atp- cydd (cl:atp-binding cassette homology) (db:pir2.dat) D69611 D69611 Bacillus subtilis 1423 -11529552 222879 cydd abc membrane transporter atp-binding protein (fn:required for expression of cytochrome bd) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxkn) (le:173756) (re:175483) (di:complement) BSUB0020 Z99123 g2636408 Bacillus subtilis 1423 -11529552 301546 cydd (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to many atp-binding transport proteins;) (le:48982) (re:50709) (di:direct) D83026 D83026 g1783253 Bacillus subtilis 1423 -11529552

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758363	2029	24185	438	145

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758375	2030	24186	387	128

Description

6500725695 yxkm:cydc abc membrane transporter:atp-binding protein:transport atp-binding protein cydc (gtcfc:12.6) (keggfc:14.2) (bsorffc:1.1.6) (db:gtc-bacillus subtilis) cydC cydC Bacillus subtilis 1423 -11529553 5500685060 cydc (de:transport atp-binding protein cydc) (db:swissprot) CYDC_BACSU P94366 BACILLUS SUBTILIS 1423 -11529553 7000684958 cydc abc transporter required for expression of cytochrome bd atp- cydc (cl:atp-binding cassette homology) (db:pir2.dat) C69611 C69611 Bacillus subtilis 1423 -11529553 222878 cydc abc membrane transporter atp-binding protein (fn:required for expression of cytochrome bd) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: yxkm) (le:175480) (re:177183) (di:complement) BSUB0020 Z99123 g2636409 Bacillus subtilis 1423 -11529553 301545 cydc (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence covering lic-cel region.) (nt:homologous to many atp-binding transport proteins) (le:47282) (re:48985) (di:direct) D83026 D83026 g1783252 Bacillus subtilis 1423 -11529553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758380	2031	24187	729	242

Description

6500725696 class i heat-shock protein:molecular chaperonin (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) groES groES Bacillus subtilis 1423 -11529554 1500693360 groes class i heat-shock protein molecular (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:48877) (re:49203) (di:direct) BSUB0004 Z99107 g2632915 Bacillus subtilis 1423 -11529554 7500955474 groes (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (le:35879) (re:36205) (di:direct) D88802 D88802 g1945118 Bacillus subtilis 1423 -11529554 7000692377 groes class i heat-shock protein chaperonin groes (cl:chaperonin groes) (db:pir) E69637 E69637 Bacillus subtilis 1423 -11529554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758387	2032	24188	969	322

Description

6500725697 class i heat-shock protein:molecular chaperonin:60 kd chaperonin:protein cpn60:groel protein (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) groEL groEL Bacillus subtilis 1423 -11529555 7000689426 groel 58k heat shock protein groel:class i heat-shock protein chaperonin groel (cl:chaperonin groel) (db:pir2.dat) B41884 B41884 Bacillus subtilis 1423 -11529555 7500955475 groel chaperonin (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:60 kd chaperonin (protein cpn60) (groel protein)) (le:322) (re:1956) (di:direct) AB007637 AB007637 g2521994 Bacillus subtilis 1423 -11529555 215803 groel heat shock protein (fn:molecular chaperone) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis heat shock protein (groel and groes) genes,complete cds.) (le:685) (re:2319) (di:direct) BACGROESL M81132 g143027 Bacillus subtilis 1423 -11529555 215851 groel heat shock protein (sr:bacillus subtilis (strain mb11) dna) (db:genpept-bct1) (de:b.subtilis groes and groel genes, complete cds's.) (le:499) (re:2133) (di:direct) BACHSPA M84965 g143063 Bacillus subtilis 1423 -11529555 5500686805 groel class i heat-shock protein molecular (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:49250) (re:50884) (di:direct) BSUB0004 Z99107 g2632916 Bacillus subtilis 1423 -11529555 154568 groel 58k heat shock protein groel:class i heat-shock protein chaperonin groel (cl:chaperonin groel) (db:pir) B41884 B41884 Bacillus subtilis 1423 -11529555

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758391	2033	24189	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758408	2034	24190	474	157

Description

5000688841 molecular chaperonin:protein export protein prsa precursor (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) prsA prsA Bacillus subtilis 1423 -11529556 7500888597 prsa (de:protein export protein prsa precursor) (db:swissprot) PRSA_BACSU P24327 BACILLUS SUBTILIS 1423 -11529556 7000686190 prsa post-translocation molecular chaperone prsa:33k lipoprotein prsa (db:pir2.dat) S15269 S15269 Bacillus subtilis 1423 -11529556 4000707266 prsa 33kda lipoprotein (db:genpept-bct1) (de:b.subtilis prsa gene for a 33kda lipoprotein.) (le:63) (re:941) (di:direct) BS33KDA X57271 g39782 Bacillus subtilis 1423 -11529556 218960 prsa molecular chaperonin (fn:essential for the stability of secreted) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:70340) (re:71218) (di:complement) BSUB0006 Z99109 g2633331 Bacillus subtilis 1423 -11529556 7502851623 prsa 33kda lipoprotein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:see swiss prot p24327) (le:9695) (re:10573) (di:direct) BSY14077 Y14077 g2226124 Bacillus subtilis 1423 -11529556 91289 prsa (de:protein export protein prsa precursor) (db:swissprot) PRSA_BACSU P24327 BACILLUS SUBTILIS 1423 -11529556 169834 prsa post-translocation molecular chaperone prsa:33k lipoprotein prsa (db:pir) S15269 S15269 Bacillus subtilis 1423 -11529556 6500725698 molecular chaperonin:protein export protein prsa precursor (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) prsA prsA Bacillus subtilis 1423 -11529556

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758574	2035	24191	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758577	2036	24192	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758590	2037	24193	774	257

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758596	2038	24194	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758600	2039	24195	339	112

Description

GTC ORF with score 162 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:f286; 100 pct identical amino acid sequence and) (le:5736) (re:6596) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758603	2040	24196	669	222

Description

6500725699 molecular chaperonin (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) csaA csaA Bacillus subtilis 1423 -11529557 7500879434 csaa (de:csaa protein) (db:swissprot) CSAA_BACSU P37584 BACILLUS SUBTILIS 1423 -11529557 7000692359 csaa chaperonin involved in protein secretion csaa (db:pir2.dat) E69607 E69607 Bacillus subtilis 1423 -11529557 5500687856 csaa csaa (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis methionyl trna synthase (664) (le:59208) (re:59540) (di:complement) AF027868 AF027868 g2619042 Bacillus subtilis 1423 -11529557 7500879436 csaa molecular chaperonin (fn:involved in protein secretion) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:78299) (re:78631) (di:complement) BSUB0011 Z99114 g2634297 Bacillus subtilis 1423 -11529557 4000714731 csaa csa (db:genpept-bct1) (de:b.subtilis csaa gene.) (le:28) (re:360) (di:direct) CSCSAAG X58387 g2285914 Bacillus subtilis 1423 -11529557

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758605	2041	24197	804	267

Description

GTC ORF with score 111 to: (db:genpept-bct2) (de:streptomyces hygroscopicus putative pteridine-dependentdioxygenase, pks modules 1,2,3 and 4, and putative regulatoryprotein genes, complete cds and putative hydroxylase gene, partialcds.) (nt:orf8) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758623	2042	24198	414	137

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758625	2043	24199	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758653	2044	24200	489	162

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758667	2045	24201	813	270

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758671	2046	24202	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758674	2047	24203	276	91

Description

5000688782 heat-shock protein:dnaj protein (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) dnaJ dnaJ Bacillus subtilis 1423 -11529558 68865 dnaj (de:dnaj protein) (db:swissprot) DNAJ_BACSU P17631 BACILLUS SUBTILIS 1423 -11529558 7000685075 dnaj heat shock protein dnaj (cl:heat shock protein dnaj:dnaj amino-terminal homology) (db:pir2.dat) B41874 B41874 Bacillus subtilis 1423 -11529558 7500880415 dnaj heat shock protein (sr:bacillus subtilis (strain mb11) dna) (db:genpept-bct1) (de:b.subtilis orf39, grpe, dnak, and dnaj genes, complete cds's.) (le:3967) (re:5085) (di:direct) BACHSP M84964 g143060 Bacillus subtilis 1423 -11529558 215849 dnaj (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:93702) (re:94820) (di:direct) BACJH642 D84432 g1303809 Bacillus subtilis 1423 -11529558 216053 dnaj heat-shock protein (fn:activation of dnak) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:24610) (re:25728) (di:complement) BSUB0014 Z99117 g2634992 Bacillus subtilis 1423 -11529558 152144 dnaj heat shock protein dnaj (cl:heat shock protein dnaj:dnaj amino-terminal homology) (db:pir) B41874 B41874 Bacillus subtilis 1423 -11529558 6500725700 heat-shock protein:dnaj protein (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) dnaJ dnaJ Bacillus subtilis 1423 -11529558

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758676	2048	24204	645	214

Description

6500725701 class i heat-shock protein:chaperonin:dnak protein:heat shock protein 70:hsp70 (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) dnaK dnaK Bacillus subtilis 1423 -11529559 7000689347 dnak dnak-type molecular chaperone dnak:heat shock protein (cl:heat shock protein 70) (db:pir2.dat) S09500 S09500 Bacillus subtilis 1423 -11529559 7500955103 dnak heat shock protein (sr:bacillus subtilis (strain mb11) dna) (db:genpept-bct1) (de:b.subtilis orf39, grpe, dnak, and dnaj genes, complete cds's.) (le:1932) (re:3767) (di:direct) BACHSP M84964 g143059 Bacillus subtilis 1423 -11529559 215848 dnak (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:91667) (re:93502) (di:direct) BACJH642 D84432 g1303808 Bacillus subtilis 1423 -11529559 216052 (db:genpept-bct1) (de:b.subtilis dnak and dnaj (partial) genes for heat shock protein anddnaj product.) (nt:heat shock protein (aa 1-611)) (le:33) (re:1868) (di:direct) BSDNAKJ X52064 g580854 Bacillus subtilis 1423 -11529559 219168 dnak class i heat-shock protein chaperonin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:25928) (re:27763) (di:complement) BSUB0014 Z99117 g2634993 Bacillus subtilis 1423 -11529559 151971 dnak dnak-type molecular chaperone dnak:heat shock protein (cl:heat shock protein 70) (db:pir) S09500 S09500 Bacillus subtilis 1423 -11529559

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758702	2049	24205	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758703	2050	24206	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758916	2051	24207	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758917	2052	24208	351	116

Description

6500725702 heat-shock protein:grpe protein (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) grpE grpE Bacillus subtilis 1423 -11529560 7000693083 grpe heat shock protein grpe:dnak activator grpe (cl:heat shock protein grpe) (db:pir2.dat) S08418 S08418 Bacillus subtilis 1423 -11529560 7500964047 grpe heat shock protein (sr:bacillus subtilis (strain mb11) dna) (db:genpept-bct1) (de:b.subtilis orf39, grpe, dnak, and dnaj genes, complete cds's.) (le:1345) (re:1908) (di:direct) BACHSP M84964 g143058 Bacillus subtilis 1423 -11529560 215847 grpe (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:91080) (re:91643) (di:direct) BACJH642 D84432 g1303807 Bacillus subtilis 1423 -11529560 216051 (db:genpept-bct1) (de:bacillus subtilis dna for grpe gene and dnak gene (partial).) (nt:grpe gene (aa 1-187)) (le:275) (re:838) (di:direct) BSGRPE X51477 g39928 Bacillus subtilis 1423 -11529560 219346 grpe heat-shock protein (fn:activation of dnak) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:27787) (re:28350) (di:complement) BSUB0014 Z99117 g2634994 Bacillus subtilis 1423 -11529560 170033 grpe heat shock protein grpe:dnak activator grpe (db:pir) S08418 S08418 Bacillus subtilis 1423 -11529560

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758924	2053	24209	678	226

Description

6500725703 yxbb:ss92a:htpg class iii heat-shock protein:chaperonin:heat shock protein htpg:high temperature protein g (gtcfc:12.7) (keggfc:14.2) (bsorffc:6.5.1) (db:gtc-bacillus subtilis) htpG htpG Bacillus subtilis 1423 -11529561 78019 htpg:ss92a (de:heat shock protein htpg (high temperature protein g)) (db:swissprot) HTPG_BACSU P46208 BACILLUS SUBTILIS 1423 -11529561 7000685567 htpg class iii heat-shock protein chaperonin htpg (cl:heat shock protein 90) (db:pir2.dat) H69642 H69642 Bacillus subtilis 1423 -11529561 215752 htpg probable htpg protein (sr:bacillus subtilis (strain:bgsc 1a1) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 36 kb region between gnt and ioloperons.) (nt:conserved universally, induced by heat shock) (le:27770) (re:29650) (di:direct) AB005554 AB005554 g904201 Bacillus subtilis 1423 -11529561 7500883598 htpg class iii heat-shock protein chaperonin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yxbb) (le:88943) (re:90823) (di:complement) BSUB0021 Z99124 g2636528 Bacillus subtilis 1423 -11529561 5000689038 (de:(htpg) (pn:heat shock protein htpg:high temperature protein g:heat shock protein htpg homolog) (gn:ss92a) (gtcfc:13.02) (ec:) (htpg_bacsu) (keggfc:11.2) (bsorffc:7.1.0) (db:gtc-bacillus subtilis)) htpG htpG Bacillus subtilis 1423 10020358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758925	2054	24210	639	213

Description

5000688799 hypothetical protein:xpac protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) xpaC xpaC Bacillus subtilis 1423 -11529562 108142 xpac (de:xpac protein) (db:swissprot) XPAC_BACSU P37467 BACILLUS SUBTILIS 1423 -11529562 7000687048 xpac 5-bromo-4-chloroindolyl phosphate hydrolysis protein xpac:xpac protein (db:pir2.dat) S27526 S27526 Bacillus subtilis 1423 -11529562 7500894476 xpac hydrolysis of 5-bromo-4-chloroindolyl phosphate (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:99445) (re:100059) (di:direct) BAC180K D26185 g467415 Bacillus subtilis 1423 -11529562 215015 xpac (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orf1 and xpac gene, complete cds's; ssrrna gene,3' end; orf3c 5' end.) (le:532) (re:1146) (di:direct) BACXPAC M96156 g143830 Bacillus subtilis 1423 -11529562 217059 xpac (fn:hydrolysis of 5-bromo 4-chloroindolyl phosphate) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:35843) (re:36457) (di:direct) BSUB0001 Z99104 g2632292 Bacillus subtilis 1423 -11529562 170669 xpac 5-bromo-4-chloroindolyl phosphate hydrolysis protein xpac:xpac protein (db:pir) S27526 S27526 Bacillus subtilis 1423 -11529562 6500725704 hypothetical protein:xpac protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) xpaC xpaC Bacillus subtilis 1423 -11529562

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758933	2055	24211	501	166

Description

6500725705 diva:divic cell-division initiation protein:cell division protein divic (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) divIC divIC Bacillus subtilis 1423 -11529563 68719 divic:diva (de:cell division protein divic) (db:swissprot) DIVC_BACSU P37471 BACILLUS SUBTILIS 1423 -11529563 7000685058 divic cell division initiation protein septum formation divic (db:pir2.dat) B53380 B53380 Bacillus subtilis 1423 -11529563 7500880341 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:132768) (re:133145) (di:direct) BAC180K D26185 g467451 Bacillus subtilis 1423 -11529563 215051 divic cell division protein (db:genpept-bct1) (de:bacillus subtilis cell division protein (divic) gene, complete cds,transfer rna genes, complete sequence and sporulation protein(spoiie) gene, 5' end of cds.) (le:456) (re:833) (di:direct) BACDIVIC L23497 g385177 Bacillus subtilis 1423 -11529563 215537 divic cell-division initiation protein (fn:required for both vegetative and sporulation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:69166) (re:69543) (di:direct) BSUB0001 Z99104 g2632329 Bacillus subtilis 1423 -11529563 169899 divic cell division initiation protein septum formation divic (db:pir) B53380 B53380 Bacillus subtilis 1423 -11529563 5000688788 (de:(divic) (pn:cell division protein divic) (gn:diva) (gtcfc:12.08) (ec:) (divc_bacsu) (keggfc:11.2) (bsorffc:5.3.0) (db:gtc-bacillus subtilis)) divIC divIC Bacillus subtilis 1423 10011304

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758945	2056	24212	1497	499

Description

6500725706 cell-division protein and general stress protein:class iii heat-shock:cell division protein ftsh homolog (gtcfc:12.8) (ec:3.4.24.-) (keggfc:14.1) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) ftsH ftsH Bacillus subtilis 1423 -11529564 72446 ftsh (ec:3.4.24.-) (de:cell division protein ftsh homolog,) (db:swissprot) FTSH_BACSU P37476 BACILLUS SUBTILIS 1423 -11529564 7000685323 ftsh cell-division protein / general stress protein ftsh:class iii heat shock protein ftsh (cl:cell division protein ftsh:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir2.dat) E69627 E69627 Bacillus subtilis 1423 -11529564 7500881818 ftsh cell division protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:140584) (re:142497) (di:direct) BAC180K D26185 g467458 Bacillus subtilis 1423 -11529564 215058 ftsh cell-division protein and general stress protein (fn:involved in major cellular processes such as) (db:genpept-bct1) (ec:3.4.24.-) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:76982) (re:78895) (di:direct) BSUB0001 Z99104 g2632336 Bacillus subtilis 1423 -11529564 206160 ftsh cell-division protein / general stress protein ftsh:class iii heat shock protein ftsh (cl:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir) E69627 E69627 Bacillus subtilis 1423 -11529564 5000688790 (de:(ftsh) (pn:cell division protein ftsh homolog) (gtcfc:12.08) (ec:3.4.24.-) (ftsh_bacsu) (keggfc:11.1) (bsorffc:5.3.0) (db:gtc-bacillus subtilis)) ftsH ftsH Bacillus subtilis 1423 10014997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758963	2057	24213	264	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758967	2058	24214	690	230

Description

6500725707 ylxb:ftsl cell-division protein:cell division protein ftsl homolog (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) ftsL ftsL Bacillus subtilis 1423 -11529565 72458 ftsl (de:cell division protein ftsl homolog) (db:swissprot) FTSL_BACSU Q07867 BACILLUS SUBTILIS 1423 -11529565 7000685326 ftsl cell-division protein septum formation ftsl (db:pir2.dat) B53292 B53292 Bacillus subtilis 1423 -11529565 7500881840 ftsl cell-division protein (fn:septum formation (early stage)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ylxb) (le:186209) (re:186562) (di:direct) BSUB0008 Z99111 g2633886 Bacillus subtilis 1423 -11529565 216439 ftsl (fn:potential role in cell division; similar to the) (db:genpept-bct1) (de:b.subtilis ylla, yllb, yllc, ftsl, pbpb and spovd genes.) (nt:required for cell division) (le:3230) (re:3583) (di:direct) BSYLLSPO Z68230 g1122761 Bacillus subtilis 1423 -11529565 220247 membrane protein (fn:potential role in cell division) (sr:bacillus subtilis (strain 168trpc2) dna) (db:genpept-bct2) (de:bacillus subtilis penicillin-binding protein (pbpb and spovd)genes, complete and partial cds respectively.) (nt:the derived product of this orf has ... BACPBPSPOV L09703 g304164 Bacillus subtilis 1423 -11529565 170415 ftsl cell-division protein septum formation ftsl (db:pir) B53292 B53292 Bacillus subtilis 1423 -11529565 5000688791 (de:(ftsl) (pn:cell division protein ftsl homolog) (gtcfc:12.08) (ec:) (ftsl_bacsu) (keggfc:11.2) (bsorffc:5.3.0) (db:gtc-bacillus subtilis)) ftsL ftsL Bacillus subtilis 1423 10015009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758972	2059	24215	426	141

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758984	2060	24216	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758989	2061	24217	297	98

Description

GTC ORF with score 165 to: (sr:human) (db:genpept-pri3) (de:homo sapiens lysosomal pepstatin insensitive protease (cln2) gene,complete cds.) (nt:deficient in late-infantile neuronal ceroid) (le:1329:1462:1814:2938) (re:1345:1533:1953:3088) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758990	2062	24218	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758992	2063	24219	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501758997	2064	24220	783	260

Description

GTC ORF with score 285 to: (or:Arabidopsis thaliana) (sr:thale cress) (db:genpept-pln1) (de:genomic sequence for arabidopsis thaliana bac f21j9, completesequence.) (nt:dehydrogenase isolog) (le:62282:62655:63327) (re:62521:62724:63612) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759008	2065	24221	879	293

Description

6500725708 dds:tms-12:divib cell-division initiation protein:division initiation protein:cell division and sporulation protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) divIB divIB Bacillus subtilis 1423 -11529566 68718 divib:dds (de:division initiation protein (cell division and sporulation protein)) (db:swissprot) DIVB_BACSU P16655 BACILLUS SUBTILIS 1423 -11529566 7000685057 divib:dds cell division initiation protein septum formation divib:cell division protein dds:sporulation protein dds (db:pir2.dat) B43727 B43727 Bacillus subtilis 1423 -11529566 7500880340 dds cell division and sporulation protein (sr:bacillus subtilis (clone: lambda-bs1) dna) (db:genpept-bct1) (de:bacillus subtilis (clone lambda-bs1) cell division and sporulationprotein (dds) gene, complete cds.) (le:1521) (re:2312) (di:direct) BACDDSA M31827 g142834 Bacillus subtilis 1423 -11529566 215485 (sr:b.subtilis (strain 168; prototroph sb19) dna) (db:genpept-bct1) (de:b.subtilis division initiation protein (divib) gene, 5' end.) (nt:division initiation protein) (le:295) (re:1086) (di:direct) BACDIV M31800 g142850 Bacillus subtilis 1423 -11529566 215534 divib cell-division initiation protein (fn:probably involved in stabilizing or promoting) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: dds, tms-12) (le:198310) (re:199101) (di:direct) BSUB0008 Z99111 g2633895 Bacillus subtilis 1423 -11529566 169965 divib:dds cell division initiation protein septum formation divib:cell division protein dds:sporulation protein dds (db:pir) B43727 B43727 Bacillus subtilis 1423 -11529566 5000688787 (de:(divib) (pn:division initiation protein:cell division and sporulation protein) (gn:dds) (gtcfc:12.08) (ec:) (divb_bacsu) (keggfc:11.2) (bsorffc:5.3.0) (db:gtc-bacillus subtilis)) divIB divIB Bacillus subtilis 1423 10011303

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759011	2066	24222	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759014	2067	24223	456	152

Description

6500725709 spoiin:ftsa cell-division protein:cell division protein ftsa (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) ftsA ftsA Bacillus subtilis 1423 -11529567 72440 ftsa (de:cell division protein ftsa) (db:swissprot) FTSA_BACSU P28264 BACILLUS SUBTILIS 1423 -11529567 7000685322 ftsa cell-division protein septum formation ftsa (cl:cell division protein ftsa) (db:pir2.dat) I39847 I39847 Bacillus subtilis 1423 -11529567 7500881795 ftsa (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis ftsza genes, complete cds.) (le:581) (re:1903) (di:direct) BACFTSZA M22630 g142940 Bacillus subtilis 1423 -11529567 215632 ftsa cell-division protein (fn:required for septum formation during) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: spoiin) (le:201080) (re:202402) (di:direct) BSUB0008 Z99111 g2633899 Bacillus subtilis 1423 -11529567 170005 ftsa cell-division protein septum formation ftsa (db:pir) I39847 I39847 Bacillus subtilis 1423 -11529567 5000688789 (de:(ftsa) (pn:cell division protein ftsa) (gtcfc:12.08) (ec:) (ftsa_bacsu) (keggfc:11.2) (bsorffc:5.3.0) (db:gtc-bacillus subtilis)) ftsA ftsA Bacillus subtilis 1423 10014991

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759016	2068	24224	984	328

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759027	2069	24225	411	136

Description

6500725710 ts-1:ftsz cell-division initiation protein:cell division protein ftsz (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) ftsZ ftsZ Bacillus subtilis 1423 -11529568 72477 ftsz (de:cell division protein ftsz) (db:swissprot) FTSZ_BACSU P17865 BACILLUS SUBTILIS 1423 -11529568 131343 ftsz cell division initiation protein septum formation ftsz (cl:cell division protein ftsz) (db:pir1.dat) I39848 I39848 Bacillus subtilis 1423 -11529568 215633 ftsz (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis ftsza genes, complete cds.) (le:1939) (re:3087) (di:direct) BACFTSZA M22630 g142941 Bacillus subtilis 1423 -11529568 7500881869 ftsz cell-division initiation protein (fn:required for septum formation during) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ts-1) (le:202438) (re:203586) (di:direct) BSUB0008 Z99111 g2633900 Bacillus subtilis 1423 -11529568 5000688792 (de:(ftsz) (pn:cell division protein ftsz:cell division ftsz protein) (gtcfc:12.08) (ec:) (ftsz_bacsu) (keggfc:11.2) (bsorffc:5.3.0) (db:gtc-bacillus subtilis)) ftsZ ftsZ Bacillus subtilis 1423 10015028

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759029	2070	24226	195	65

Description

GTC ORF with score 103 to: (db:genpept-bct1) (de:methanobacterium thermoautotrophicum from bases 161632 to 172569(section 15 of 148) of the complete genome.) (nt:function code:5.01 - l-amino acid metabolism,) (le:5667) (re:6947) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759040	2071	24227	486	161

Description

6500725711 ylmj:diviva cell-division initiation protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) divIVA divIVA Bacillus subtilis 1423 -11529569 7000692345 diviva cell-division initiation protein septum placement diviva (db:pir2.dat) B69616 B69616 Bacillus subtilis 1423 -11529569 220149 diviva diviva (db:genpept-bct1) (de:b.subtilis partial ylmi gene and diviva gene.) (le:130) (re:624) (di:direct) BSDIVIVA Z86114 g1881418 Bacillus subtilis 1423 -11529569 297579 diviva minicell-associated protein diviva (db:genpept-bct1) (de:bacillus subtilis minicell-associated protein (diviva) gene,complete cds, and isoleucyl-trna-synthetase (iles) gene, partialcds.) (nt:minicell-associated protein) (le:1173) (re:1667) (di:direct) BSU60901 U60901 g1518680 Bacillus subtilis 1423 -11529569 307221 diviva cell-division initiation protein (fn:required for initiation of cell division and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylmj) (le:13502) (re:13996) (di:direct) BSUB0009 Z99112 g2633915 Bacillus subtilis 1423 -11529569

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759042	2072	24228	615	204

Description

6500725712 ylyc:gid glucose-inhibited division protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) gid gid Bacillus subtilis 1423 -11529570 7500882363 gid (de:gid protein) (db:swissprot) GID_BACSU P39815 BACILLUS SUBTILIS 1423 -11529570 7000693041 gid glucose-inhibited division protein gid (db:pir2.dat) A69632 A69632 Bacillus subtilis 1423 -11529570 7500882365 gid glucose-inhibited division protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylyc) (le:86791) (re:88098) (di:direct) BSUB0009 Z99112 g2633985 Bacillus subtilis 1423 -11529570 5500687818 gid gid protein (db:genpept-bct1) (de:bacillus subtilis ylqg to codv gene region.) (le:5959) (re:7266) (di:direct) BSYLQGCOD AJ000975 g2462971 Bacillus subtilis 1423 -11529570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759045	2073	24229	237	78

Description

6500725713 divivb1:divivb:mind atpase activator of minc:septum site-determining protein mind (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) minD minD Bacillus subtilis 1423 -11529571 219391 mind:divivb (de:septum site-determining protein mind) (db:swissprot) MIND_BACSU Q01464 BACILLUS SUBTILIS 1423 -11529571 131332 mind cell division inhibitor septum placement mind:septum placement determinant mind (cl:cell division inhibitor mind) (db:pir1.dat) G45239 S31205 Bacillus subtilis 1423 -11529571 215546 mind mind protein (fn:division inhibitor) (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orfa, orfb, mreb, mrec, mred, minc, and mindgenes, complete coding regions.) (nt:location of the diviv-b1 mutation; mutation resul... BACDIVREG M96343 g142859 Bacillus subtilis 1423 -11529571 216360 mind (fn:septum site determining) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis (mreb) gene complete cds, (mrec) gene completecds, (mred) gene complete cds, (minc) gene complete cds, (mind)gene complete cds.) (nt:putative)... BACMREMIN M95582 g143216 Bacillus subtilis 1423 -11529571 5000688798 mind mind (fn:atpase activator of minc) (db:genpept-bct1) (de:b.subtilis minc, mind, and spoivfa (partial) genes.) (le:906) (re:1712) (di:direct) BSMINCD Z15113 g580893 Bacillus subtilis 1423 -11529571 7500885640 mind atpase activator of minc (fn:cell-division inhibition (septum placement)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:alternate gene name: divivb1) (le:61908) (re:62714) (di:complement) BSUB0015 Z99118 g2635264 Bacillus subtilis 1423 -11529571 83730 mind:divivb (de:septum site-determining protein mind) (db:swissprot) MIND_BACSU Q01464 BACILLUS SUBTILIS 1423 -11529571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759048	2074	24230	687	228

Description

5000688797 hypothetical protein:septum site-determining protein minc (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) minC minC Bacillus subtilis 1423 -11529572 216359 minc (de:septum site-determining protein minc) (db:swissprot) MINC_BACSU Q01463 BACILLUS SUBTILIS 1423 -11529572 170522 minc cell-division inhibitor septum placement minc:septum placement determinant minc (db:pir2.dat) F45239 S31204 Bacillus subtilis 1423 -11529572 7500885638 minc minc protein (fn:division inhibitor) (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orfa, orfb, mreb, mrec, mred, minc, and mindgenes, complete coding regions.) (nt:mutation results in minicell phenotype) (le:4033)... BACDIVREG M96343 g142858 Bacillus subtilis 1423 -11529572 215545 minc (fn:septum site determination) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis (mreb) gene complete cds, (mrec) gene completecds, (mred) gene complete cds, (minc) gene complete cds, (mind)gene complete cds.) (nt:putativ... BACMREMIN M95582 g143215 Bacillus subtilis 1423 -11529572 219390 minc minc (fn:cell division inhibitor) (db:genpept-bct1) (de:b.subtilis minc, mind, and spoivfa (partial) genes.) (le:224) (re:904) (di:direct) BSMINCD Z15113 g580892 Bacillus subtilis 1423 -11529572 7502851624 minc (fn:cell-division inhibition (septum placement)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:62716) (re:63396) (di:complement) BSUB0015 Z99118 g2635265 Bacillus subtilis 1423 -11529572 83728 minc (de:septum site-determining protein minc) (db:swissprot) MINC_BACSU Q01463 BACILLUS SUBTILIS 1423 -11529572 7000685849 minc cell-division inhibitor septum placement minc:septum placement determinant minc (db:pir) F45239 E45240 Bacillus subtilis 1423 -11529572 6500725714 hypothetical protein:septum site-determining protein minc (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) minC minC Bacillus subtilis 1423 -11529572

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759062	2075	24231	591	196

Description

5000688795 hypothetical protein:maf protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) maf maf Bacillus subtilis 1423 -11529573 82854 maf (de:maf protein) (db:swissprot) MAF_BACSU Q02169 BACILLUS SUBTILIS 1423 -11529573 7000685781 maf septum formation maf:hypothetical protein a mreb 5 region:spoiib 3-region hypothetical protein (cl:septum formation protein maf) (db:pir2.dat) (mp:245 deg.) A45239 A45239 Bacillus subtilis 1423 -11529573 7500885263 orfa (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orfa, orfb, mreb, mrec, mred, minc, and mindgenes, complete coding regions.) (nt:homologous to unidentified e. coli protein) (le:156) (re:725) (di:direct) BACDIVREG M96343 g142853 Bacillus subtilis 1423 -11529573 215540 maf (fn:possible septation function) (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis maf gene, complete cds; orfb, complete cds; mrebgene, 5' end.) (le:951) (re:1520) (di:direct) BACMAFMREB L08793 g143161 Bacillus subtilis 1423 -11529573 216304 maf (fn:septum formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:66703) (re:67272) (di:complement) BSUB0015 Z99118 g2635270 Bacillus subtilis 1423 -11529573 170328 maf septum formation maf:hypothetical protein a mreb 5 region:spoiib 3-region hypothetical protein (db:pir) (mp:245 deg.) A45239 A45239 Bacillus subtilis 1423 -11529573 6500725715 hypothetical protein:maf protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) maf maf Bacillus subtilis 1423 -11529573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759065	2076	24232	684	227

Description

GTC ORF with score 122 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t19l18 genomic sequence,complete sequence.) (nt:unknown protein) (le:68891:69319:69692:69866) (re:69224:69602:69793:69937) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759079	2077	24233	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759083	2078	24234	495	164

Description

6500725716 cell-division protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) ftsX ftsX Bacillus subtilis 1423 -11529574 7000692347 ftsx cell-division protein ftsx (db:pir2.dat) G69627 G69627 Bacillus subtilis 1423 -11529574 5500701742 ftsx cell-division protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:25908) (re:26798) (di:complement) BSUB0019 Z99122 g2636051 Bacillus subtilis 1423 -11529574 7500963512 ftsx cell division protein (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:3495) (re:4385) (di:direct) AF017113 AF017113 g2618835 Bacillus subtilis 1423 -11529574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759087	2079	24235	1509	503

Description

6500725717 cell-division atp-binding protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) ftsE ftsE Bacillus subtilis 1423 -11529575 7000692342 ftse cell-division atp-binding protein ftse (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) D69627 D69627 Bacillus subtilis 1423 -11529575 5500701741 ftse cell-division atp-binding protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:26791) (re:27477) (di:complement) BSUB0019 Z99122 g2636052 Bacillus subtilis 1423 -11529575 7500955274 ftse cell division atp-binding protein (db:genpept-bct2) (de:bacillus subtilis 300-304 degree genomic sequence.) (le:2816) (re:3502) (di:direct) AF017113 AF017113 g2618833 Bacillus subtilis 1423 -11529575

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759088	2080	24236	402	133

Description

6500725718 mreb-like protein (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) mbl mbl Bacillus subtilis 1423 -11529576 7500964964 mbl mreb-like protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:149278) (re:150219) (di:complement) BSUB0019 Z99122 g2636166 Bacillus subtilis 1423 -11529576 7000694237 mbl mreb-like protein mbl (db:pir) F69655 F69655 Bacillus subtilis 1423 -11529576

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759261	2081	24237	315	104

Description

6500725719 ipa-42d:ywcf hypothetical protein:hypothetical 43.3 kd protein in qoxd-vpr intergenic region (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) ywcF ywcF Bacillus subtilis 1423 -11529577 7500952895 ywcf:ipa-42d (de:hypothetical 43.3 kd protein in qoxd-vpr intergenic region) (db:swissprot) YWCF_BACSU P39604 BACILLUS SUBTILIS 1423 -11529577 7000688657 ywcf cell-division protein homolog ywcf:protein ipa-42d (db:pir2.dat) S39697 S39697 Bacillus subtilis 1423 -11529577 5000688800 ipa-42d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:44053) (re:45234) (di:direct) BSGENR X73124 g413966 Bacillus subtilis 1423 -11529577 219279 ywcf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-42d; similar to) (le:112728) (re:113909) (di:complement) BSUB0020 Z99123 g2636347 Bacillus subtilis 1423 -11529577 116678 ywcf:ipa-42d (de:hypothetical 43.3 kd protein in qoxd-vpr intergenic region) (db:swissprot) YWCF_BACSU P39604 BACILLUS SUBTILIS 1423 -11529577 170126 ywcf cell-division protein homolog ywcf (db:pir) S39697 S39697 Bacillus subtilis 1423 -11529577

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759267	2082	24238	684	227

Description

GTC ORF with score 292 to: (fn:oxygenation of trichodiene to yield unknown) (db:genpept-pln1) (de:fusarium sporotrichioides trichodiene oxygenase (tri4) gene,complete cds.) (nt:cytochrome p450; cyp58; tri6 (u22150), tri3) (le:383:685:1702:1939) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759277	2083	24239	624	207

Description

5000688794 glucose-inhibited division protein:glucose inhibited division protein b (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) gidB gidB Bacillus subtilis 1423 -11529578 219463 gidb (de:glucose inhibited division protein b) (db:swissprot) GIDB_BACSU P25813 BACILLUS SUBTILIS 1423 -11529578 131320 gidb glucose-inhibited division protein gidb (cl:gidb protein) (db:pir1.dat) BWBSGB I40441 Bacillus subtilis 1423 -11529578 214984 gidb unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:56866) (re:57585) (di:complement) BAC180K D26185 g467384 Bacillus subtilis 1423 -11529578 7500882345 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:homologous to e.coli gidb) (le:5815) (re:6534) (di:direct) BSORIGS X62539 g40027 Bacillus subtilis 1423 -11529578 6500725720 gidb glucose-inhibited division protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:208798) (re:209517) (di:complement) BSUB0021 Z99124 g2636647 Bacillus subtilis 1423 -11529578 73610 gidb (de:glucose inhibited division protein b) (db:swissprot) GIDB_BACSU P25813 BACILLUS SUBTILIS 1423 -11529578

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759280	2084	24240	1107	368

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759286	2085	24241	396	131

Description

GTC ORF with score 95 to: (sr:information) (db:genpept-pri2) (de:homo sapiens pac clone dj1110n13 from 7p21-p22, complete sequence.) (nt:match to est r27226 (nid:g783361) and est r27227) (le:<6781:20213:21562) (re:6975:20316:21694) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759289	2086	24242	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759292	2087	24243	489	163

Description

5000688793 glucose-inhibited division protein:glucose inhibited division protein a (gtcfc:12.8) (keggfc:14.2) (bsorffc:5.3.1) (db:gtc-bacillus subtilis) gidA gidA Bacillus subtilis 1423 -11529579 219462 gida (de:glucose inhibited division protein a) (db:swissprot) GIDA_BACSU P25812 BACILLUS SUBTILIS 1423 -11529579 131317 gida glucose-inhibited division protein gida (cl:gida protein) (db:pir1.dat) BWBSGA I40440 Bacillus subtilis 1423 -11529579 214985 gida unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:57599) (re:59485) (di:complement) BAC180K D26185 g467385 Bacillus subtilis 1423 -11529579 7500882334 (db:genpept-bct1) (de:b.subtilis genes rpmh, rnpa, 50kd, gida and gidb.) (nt:homologous to e.coli gida) (le:3915) (re:5801) (di:direct) BSORIGS X62539 g40026 Bacillus subtilis 1423 -11529579 6500725721 gida glucose-inhibited division protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:209531) (re:211417) (di:complement) BSUB0021 Z99124 g2636648 Bacillus subtilis 1423 -11529579 73604 gida (de:glucose inhibited division protein a) (db:swissprot) GIDA_BACSU P25812 BACILLUS SUBTILIS 1423 -11529579

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759293	2088	24244	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759301	2089	24245	435	144

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759302	2090	24246	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759316	2091	24247	285	94

Description

GTC ORF with score 179 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome i bac f11p17 genomic sequence,complete sequence.) (nt:unknown protein; location of est emb|z25559) (le:58205:58265:58601) (re:58221:58360:58757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759321	2092	24248	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759333	2093	24249	258	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759345	2094	24250	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759367	2095	24251	483	160

Description

6500725722 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein tlpc (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) tlpC tlpC Bacillus subtilis 1423 -11529580 217141 tlpc methyl-accepting chemotaxis protein tlpc (sr:bacillus subtilis (strain:168trpc2) dna, clone_lib:lambda dashi) (db:genpept-bct1) (de:bacillus subtilis dna around 28 degrees region of chromosomecontaining ycka-h genes.) (le:5616) (re:7337) (di:complement) BACYCK D30762 g710635 Bacillus subtilis 1423 -11529580 222610 tlpc methyl-accepting chemotaxis protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:177692) (re:179413) (di:complement) BSUB0002 Z99105 g2632630 Bacillus subtilis 1423 -11529580 7500964941 tlpc methyl-accepting chemotaxis protein of b. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:51996) (re:53717) (di:complement) D50453 D50453 g1805416 Bacillus subtilis 1423 -11529580 7000694216 tlpc methyl-accepting chemotaxis protein tlpc (db:pir) B69724 B69724 Bacillus subtilis 1423 -11529580

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759368	2096	24252	498	165

Description

6500725723 mot:motb motility protein b:cheaxis b protein:ility protein b (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) motB motB Bacillus subtilis 1423 -11529581 84045 motb (de:chemotaxis motb protein (motility protein b)) (db:swissprot) MOTB_BACSU P28612 BACILLUS SUBTILIS 1423 -11529581 7000685863 motb motility protein flagellar motor rotation motb (db:pir2.dat) B42882 B42882 Bacillus subtilis 1423 -11529581 7500885797 motb motility protein b (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis motility protein a (mota) and motility protein b(motb) gene, complete cds.) (le:1624) (re:2409) (di:direct) BACMOTAB M77238 g143208 Bacillus subtilis 1423 -11529581 216354 motb motility protein b (fn:required for flagellar motor rotation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: mot) (le:38352) (re:39137) (di:complement) BSUB0008 Z99111 g2633739 Bacillus subtilis 1423 -11529581 170355 motb motility protein flagellar motor rotation motb (db:pir) B42882 B42882 Bacillus subtilis 1423 -11529581 5000688834 (de:(motb) (pn:motility protein b:chemotaxis motb protein:motility protein b) (gtcfc:12.09) (ec:) (motb_bacsu) (keggfc:11.2) (bsorffc:6.3.0) (db:gtc-bacillus subtilis)) motB motB Bacillus subtilis 1423 10026247

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759370	2097	24253	540	179

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759372	2098	24254	531	176

Description

6500725724 mot:mota motility protein a:cheaxis a protein:ility protein a (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) motA motA Bacillus subtilis 1423 -11529582 84042 mota (de:chemotaxis mota protein (motility protein a)) (db:swissprot) MOTA_BACSU P28611 BACILLUS SUBTILIS 1423 -11529582 7000685862 mota motility protein flagellar motor rotation mota (cl:flagellar motor rotation protein) (db:pir2.dat) A42882 A42882 Bacillus subtilis 1423 -11529582 7500885783 mota motility protein a (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis motility protein a (mota) and motility protein b(motb) gene, complete cds.) (le:840) (re:1652) (di:direct) BACMOTAB M77238 g143207 Bacillus subtilis 1423 -11529582 216353 mota motility protein a (fn:required for flagellar motor rotation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: mot) (le:39109) (re:39921) (di:complement) BSUB0008 Z99111 g2633740 Bacillus subtilis 1423 -11529582 170354 mota motility protein flagellar motor rotation mota (db:pir) A42882 A42882 Bacillus subtilis 1423 -11529582 5000688833 (de:(mota) (pn:motility protein a:chemotaxis mota protein:motility protein a) (gtcfc:12.09) (ec:) (mota_bacsu) (keggfc:11.2) (bsorffc:6.3.0) (db:gtc-bacillus subtilis)) motA motA Bacillus subtilis 1423 10026244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759376	2099	24255	282	93

Description

6500725725 prg71:mcpc methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein mcpc (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) mcpC mcpC Bacillus subtilis 1423 -11529583 83211 mcpc:prg71 (de:methyl-accepting chemotaxis protein mcpc) (db:swissprot) MCPC_BACSU P54576 BACILLUS SUBTILIS 1423 -11529583 7000685804 mcpc methyl-accepting chemotaxis protein mcpc (db:pir2.dat) A69656 A69656 Bacillus subtilis 1423 -11529583 219544 mcpc methyl-accepting chemotaxis protein (db:genpept-bct1) (de:b.subtilis mcpc gene.) (le:906) (re:2870) (di:direct) BSMCPCGEN X97385 g1280446 Bacillus subtilis 1423 -11529583 7500885390 mcpc methyl-accepting chemotaxis protein (fn:chemotaxis deficiency toward cysteine, proline,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: prg71) (le:68244) (re:70208) (di:direct) BSUB0008 Z99111 g2633766 Bacillus subtilis 1423 -11529583 5000689092 (de:(mcpc) (pn:methyl-accepting chemotaxis protein mcpc) (gn:prg71) (gtcfc:13.07) (ec:) (mcpc_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) mcpC mcpC Bacillus subtilis 1423 10025430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759380	2100	24256	630	209

Description

GTC ORF with score 169 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759382	2101	24257	552	184

Description

6500725726 hypothetical protein:chemotaxis chev protein (gtcfc:12.9) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) cheV cheV Bacillus subtilis 1423 -11529584 219060 chev (ec:2.7.3.-) (de:chemotaxis chev protein,) (db:swissprot) CHEV_BACSU P37599 BACILLUS SUBTILIS 1423 -11529584 7000684809 chev chea activity-modulating chemotaxis protein chev (cl:chemotaxis chev protein:response regulator homology) (db:pir2.dat) A55592 A55592 Bacillus subtilis 1423 -11529584 7500878641 chev chev protein (fn:involved in chemotaxis) (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:7958) (re:8869) (di:direct) BS16829KB AJ222587 g2632222 Bacillus subtilis 1423 -11529584 219764 chev (db:genpept-bct1) (de:b.subtilis chev gene.) (le:124) (re:1035) (di:direct) BSCHEVGE Z29584 g580837 Bacillus subtilis 1423 -11529584 5000688802 chev (db:genpept-bct1) (de:bacillus subtilis chev gene, complete cds.) (le:124) (re:1035) (di:direct) BSU05345 U05345 g453378 Bacillus subtilis 1423 -11529584 6000684570 chev (fn:modulation of chea activity in response to) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:78214) (re:79125) (di:direct) BSUB0008 Z99111 g2633772 Bacillus subtilis 1423 -11529584 64238 chev (ec:2.7.3.-) (de:chemotaxis chev protein,) (db:swissprot) CHEV_BACSU P37599 BACILLUS SUBTILIS 1423 -11529584 169916 chev chea activity-modulating chemotaxis protein chev (cl:chemotaxis chev protein:response regulator homology) (db:pir) A55592 A55592 Bacillus subtilis 1423 -11529584

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759614	2102	24258	495	164

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759629	2103	24259	240	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759636	2104	24260	687	228

Description

GTC ORF with score 109 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t05h4.) (nt:similar to the beta transducin family; coded for by) (le:21327:21799:22163) (re:21751:22118:22341) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759643	2105	24261	381	126

Description

5000688804 flagellar basal-body rod protein:flagellar basal-body rod protein flgb (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgB flgB Bacillus subtilis 1423 -11529585 71908 flgb (de:flagellar basal-body rod protein flgb) (db:swissprot) FLGB_BACSU P24500 BACILLUS SUBTILIS 1423 -11529585 7000685259 flgb flagellar basal-body rod protein flgb (db:pir2.dat) JG0019 JG0019 Bacillus subtilis 1423 -11529585 7500881542 flgb (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis flagella-associated protein (flgb, flgc, flie)genes, complete cds.) (le:50) (re:439) (di:direct) BACFLG M54965 g142915 Bacillus subtilis 1423 -11529585 215609 flgb flagellar basal-body rod protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:92257) (re:92646) (di:direct) BSUB0009 Z99112 g2633990 Bacillus subtilis 1423 -11529585 169988 flgb flagellar basal-body rod protein flgb (db:pir) JG0019 JG0019 Bacillus subtilis 1423 -11529585 6500725727 flagellar basal-body rod protein:flagellar basal-body rod protein flgb (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgB flgB Bacillus subtilis 1423 -11529585

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759650	2106	24262	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759656	2107	24263	507	168

Description

5000688805 flagellar basal-body rod protein:flagellar basal-body rod protein flgc (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgC flgC Bacillus subtilis 1423 -11529586 71911 flgc (de:flagellar basal-body rod protein flgc) (db:swissprot) FLGC_BACSU P24501 BACILLUS SUBTILIS 1423 -11529586 7000685260 flgc flagellar basal-body rod protein flgc (cl:bacillus subtilis flagellar basal-body rod protein flgc) (db:pir2.dat) JG0020 JG0020 Bacillus subtilis 1423 -11529586 7500881546 flgc (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis flagella-associated protein (flgb, flgc, flie)genes, complete cds.) (le:439) (re:891) (di:direct) BACFLG M54965 g142916 Bacillus subtilis 1423 -11529586 215610 flgc flagellar basal-body rod protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:92646) (re:93098) (di:direct) BSUB0009 Z99112 g2633991 Bacillus subtilis 1423 -11529586 169989 flgc flagellar basal-body rod protein flgc (db:pir) JG0020 JG0020 Bacillus subtilis 1423 -11529586 6500725728 flagellar basal-body rod protein:flagellar basal-body rod protein flgc (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgC flgC Bacillus subtilis 1423 -11529586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759660	2108	24264	891	296

Description

5000688815 flagellar hook-basal body protein:flagellar hook-basal body complex protein flie (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliE fliE Bacillus subtilis 1423 -11529587 71977 flie (de:flagellar hook-basal body complex protein flie) (db:swissprot) FLIE_BACSU P24502 BACILLUS SUBTILIS 1423 -11529587 7000685283 flie flagellar hook-basal body protein flie (db:pir2.dat) JG0021 JG0021 Bacillus subtilis 1423 -11529587 7500881582 flie (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis flagella-associated protein (flgb, flgc, flie)genes, complete cds.) (le:902) (re:1222) (di:direct) BACFLG M54965 g142917 Bacillus subtilis 1423 -11529587 215611 flie flagellar hook-basal body protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:93109) (re:93429) (di:direct) BSUB0009 Z99112 g2633992 Bacillus subtilis 1423 -11529587 169991 flie flagellar hook-basal body protein flie (db:pir) JG0021 JG0021 Bacillus subtilis 1423 -11529587 6500725729 flagellar hook-basal body protein:flagellar hook-basal body complex protein flie (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliE fliE Bacillus subtilis 1423 -11529587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759661	2109	24265	330	110

Description

5000688816 flagellar basal-body m-ring protein:flagellar m-ring protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliF fliF Bacillus subtilis 1423 -11529588 71981 flif (de:flagellar m-ring protein) (db:swissprot) FLIF_BACSU P23447 BACILLUS SUBTILIS 1423 -11529588 7000685284 flif flagellar basal-body m-ring protein flif (db:pir2.dat) JG0022 JG0022 Bacillus subtilis 1423 -11529588 7500881583 flif flagellar basal-body m-ring protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:93475) (re:95085) (di:direct) BSUB0009 Z99112 g2633993 Bacillus subtilis 1423 -11529588 169992 flif flagellar basal-body m-ring protein flif (db:pir) JG0022 JG0022 Bacillus subtilis 1423 -11529588 6500725730 flagellar basal-body m-ring protein:flagellar m-ring protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliF fliF Bacillus subtilis 1423 -11529588

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759670	2110	24266	393	130

Description

6500725731 flaa15:flig flagellar motor switch protein:flagellar motor switch protein flig (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliG fliG Bacillus subtilis 1423 -11529589 215594 flig (de:flagellar motor switch protein flig) (db:swissprot) FLIG_BACSU P23448 BACILLUS SUBTILIS 1423 -11529589 7000685286 flig flagellar motor switch protein flig (cl:flagellar switch protein flig) (db:pir2.dat) B42365 B42365 Bacillus subtilis 1423 -11529589 7500881586 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 2) (le:564) (re:1580) (di:direct) BACFLAAOA M72718 g142897 Bacillus subtilis 1423 -11529589 5000688817 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 2) (le:564) (re:1580) (di:direct) BSFLAAO X56049 g39905 Bacillus subtilis 1423 -11529589 219195 flig flagellar motor switch protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: flaa15) (le:95098) (re:96114) (di:direct) BSUB0009 Z99112 g2633994 Bacillus subtilis 1423 -11529589 7502851625 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 2) (le:564) (re:1580) (di:direct) BSFLAAO X56049 g39905 Bacillus subtilis 1423 -11529589 71985 flig (de:flagellar motor switch protein flig) (db:swissprot) FLIG_BACSU P23448 BACILLUS SUBTILIS 1423 -11529589 169996 flig flagellar motor switch protein flig (cl:flagellar switch protein flig) (db:pir) B42365 B42365 Bacillus subtilis 1423 -11529589

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759671	2111	24267	588	195

Description

5000688818 flagellar assembly protein:probalbe flagellar assembly protein flih (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliH fliH Bacillus subtilis 1423 -11529590 215595 flih (de:probable flagellar assembly protein flih) (db:swissprot) FLIH_BACSU P23449 BACILLUS SUBTILIS 1423 -11529590 7000685288 flih flagellar assembly protein flih:flih protein homolog (db:pir2.dat) C42365 C42365 Bacillus subtilis 1423 -11529590 7500881590 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 3) (le:1698) (re:2324) (di:direct) BACFLAAOA M72718 g142898 Bacillus subtilis 1423 -11529590 219196 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 3) (le:1698) (re:2324) (di:direct) BSFLAAO X56049 g39906 Bacillus subtilis 1423 -11529590 6500725732 flih flagellar assembly protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:96232) (re:96858) (di:direct) BSUB0009 Z99112 g2633995 Bacillus subtilis 1423 -11529590 7502851626 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 3) (le:1698) (re:2324) (di:direct) BSFLAAO X56049 g39906 Bacillus subtilis 1423 -11529590 71990 flih (de:probable flagellar assembly protein flih) (db:swissprot) FLIH_BACSU P23449 BACILLUS SUBTILIS 1423 -11529590 170204 flih flagellar assembly protein flih:flih protein homolog (db:pir) C42365 C42365 Bacillus subtilis 1423 -11529590

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759675	2112	24268	408	135

Description

6500725733 chef:flij flagellar protein:flagellar flij protein:chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliJ fliJ Bacillus subtilis 1423 -11529591 7000692361 flij flagellar basal body formation protein flij:chemotaxis protein chef:flaa operon hypothetical protein 5 (db:pir2.dat) A42366 A42366 Bacillus subtilis 1423 -11529591 7500963984 chef (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 5) (le:3636) (re:4079) (di:direct) BACFLAAOA M72718 g142901 Bacillus subtilis 1423 -11529591 215598 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 5) (le:3636) (re:4079) (di:direct) BSFLAAO X56049 g580860 Bacillus subtilis 1423 -11529591 219199 flij flagellar protein (fn:required for formation of basal body) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: chef) (le:98170) (re:98613) (di:direct) BSUB0009 Z99112 g2633997 Bacillus subtilis 1423 -11529591 7502851627 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 5) (le:3636) (re:4079) (di:direct) BSFLAAO X56049 g580860 Bacillus subtilis 1423 -11529591 169912 flij flagellar basal body formation protein flij:chemotaxis protein chef:flaa operon hypothetical protein 5 (db:pir) A42366 A42366 Bacillus subtilis 1423 -11529591

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759687	2113	24269	978	326

Description

5000688820 hypothetical protein:probable flagellar hook-length control protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliK fliK Bacillus subtilis 1423 -11529592 215600 flik (de:probable flagellar hook-length control protein) (db:swissprot) FLIK_BACSU P23451 BACILLUS SUBTILIS 1423 -11529592 7000685293 flik flagellar hook-length control protein flik:hypothetical protein 7 flaa operon (db:pir2.dat) G42365 G42365 Bacillus subtilis 1423 -11529592 7500881601 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 7) (le:4893) (re:6182) (di:direct) BACFLAAOA M72718 g142903 Bacillus subtilis 1423 -11529592 219201 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 7) (le:4893) (re:6182) (di:direct) BSFLAAO X56049 g39910 Bacillus subtilis 1423 -11529592 7502851628 flik (fn:flagellar hook-length control) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:99427) (re:100716) (di:direct) BSUB0009 Z99112 g2633999 Bacillus subtilis 1423 -11529592 7502851629 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 7) (le:4893) (re:6182) (di:direct) BSFLAAO X56049 g39910 Bacillus subtilis 1423 -11529592 72001 flik (de:probable flagellar hook-length control protein) (db:swissprot) FLIK_BACSU P23451 BACILLUS SUBTILIS 1423 -11529592 169999 flik flagellar hook-length control protein flik:hypothetical protein 7 flaa operon (db:pir) G42365 G42365 Bacillus subtilis 1423 -11529592 6500725734 hypothetical protein:probable flagellar hook-length control protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliK fliK Bacillus subtilis 1423 -11529592

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759694	2114	24270	480	159

Description

5000688806 flgg:flge flagellar hook protein:flagellar basal-body rod protein:distal rod protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgE flgE Bacillus subtilis 1423 -11529593 219203 flgg (de:flagellar basal-body rod protein flgg (distal rod protein)) (db:swissprot) FLGG_BACSU P23446 BACILLUS SUBTILIS 1423 -11529593 7000685265 flge:flgg flagellar hook protein flge:flagellar hook-basal body protein flgg (cl:rod protein flgf) (db:pir2.dat) G69622 G69622 Bacillus subtilis 1423 -11529593 215602 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 9) (le:6623) (re:7417) (di:direct) BACFLAAOA M72718 g142905 Bacillus subtilis 1423 -11529593 7500881557 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 9) (le:6623) (re:7417) (di:direct) BSFLAAO X56049 g39912 Bacillus subtilis 1423 -11529593 6500725735 flge flagellar hook protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: flgg) (le:101157) (re:101951) (di:direct) BSUB0009 Z99112 g2634001 Bacillus subtilis 1423 -11529593 7502851630 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 9) (le:6623) (re:7417) (di:direct) BSFLAAO X56049 g39912 Bacillus subtilis 1423 -11529593 71920 flgg (de:flagellar basal-body rod protein flgg (distal rod protein)) (db:swissprot) FLGG_BACSU P23446 BACILLUS SUBTILIS 1423 -11529593

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759708	2115	24271	204	67

Description

5000688821 flagellar protein:flagellar flil protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliL fliL Bacillus subtilis 1423 -11529594 215603 flil (de:flagellar flil protein) (db:swissprot) FLIL_BACSU P23452 BACILLUS SUBTILIS 1423 -11529594 7000685295 flil flagellar protein required for flagellar formation flil:flil protein homolog (cl:flagellar formation protein flil) (db:pir2.dat) A38845 A38845 Bacillus subtilis 1423 -11529594 7500881602 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 10) (le:7669) (re:8091) (di:direct) BACFLAAOA M72718 g142906 Bacillus subtilis 1423 -11529594 219204 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 10) (le:7669) (re:8091) (di:direct) BSFLAAO X56049 g39913 Bacillus subtilis 1423 -11529594 6500725736 flil flagellar protein (fn:required for flagellar formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:102203) (re:102625) (di:direct) BSUB0009 Z99112 g2634002 Bacillus subtilis 1423 -11529594 7502851631 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 10) (le:7669) (re:8091) (di:direct) BSFLAAO X56049 g39913 Bacillus subtilis 1423 -11529594 72004 flil (de:flagellar flil protein) (db:swissprot) FLIL_BACSU P23452 BACILLUS SUBTILIS 1423 -11529594 170187 flil flagellar protein required for flagellar formation flil:flil protein homolog (db:pir) A38845 A38845 Bacillus subtilis 1423 -11529594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759710	2116	24272	273	90

Description

5000688822 flagellar motor switch protein:flagellar motor switch protein flim (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliM fliM Bacillus subtilis 1423 -11529595 72008 flim (de:flagellar motor switch protein flim) (db:swissprot) FLIM_BACSU P23453 BACILLUS SUBTILIS 1423 -11529595 7000685296 flim flagellar motor switch protein flim (cl:flagellar motor switch protein flim) (db:pir2.dat) B39136 B39136 Bacillus subtilis 1423 -11529595 7500881603 flim flagellar switch protein (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct1) (de:bacillus subtilis flagellar switch protein (flim) gene, completecds and chemotactic response protein (ched) gene, 5' end.) (le:290) (re:1288) (di:direct) BACFLIM M37691 g142922 Bacillus subtilis 1423 -11529595 215619 flim flagellar motor switch protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:102659) (re:103657) (di:direct) BSUB0009 Z99112 g2634003 Bacillus subtilis 1423 -11529595 169994 flim flagellar motor switch protein flim (cl:flagellar motor switch protein flim) (db:pir) B39136 B39136 Bacillus subtilis 1423 -11529595 6500725737 flagellar motor switch protein:flagellar motor switch protein flim (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliM fliM Bacillus subtilis 1423 -11529595

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759711	2117	24273	291	96

Description

6500725738 ched:fliy flagellar motor switch protein:flagellar motor switch protein fliy (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliY fliY Bacillus subtilis 1423 -11529596 72036 fliy:ched (de:flagellar motor switch protein fliy) (db:swissprot) FLIY_BACSU P24073 BACILLUS SUBTILIS 1423 -11529596 7000685305 fliy:ched flagellar motor switch protein fliy:ched protein (db:pir2.dat) S25279 S25279 Bacillus subtilis 1423 -11529596 7500881634 fliy (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis flim gene, 3' end; fliy gene, complete cds; cheygene, 5' end.) (le:65) (re:1201) (di:direct) BACFLIYM M86738 g142926 Bacillus subtilis 1423 -11529596 215622 fliy flagellar motor switch protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ched) (le:103647) (re:104783) (di:direct) BSUB0009 Z99112 g2634004 Bacillus subtilis 1423 -11529596 170002 fliy:ched flagellar motor switch protein fliy:ched protein (db:pir) S25279 S25279 Bacillus subtilis 1423 -11529596 5000688828 (de:(fliy) (pn:flagellar motor switch protein fliy) (gn:ched) (gtcfc:12.09) (ec:) (fliy_bacsu) (keggfc:11.2) (bsorffc:6.3.0) (db:gtc-bacillus subtilis)) fliY fliY Bacillus subtilis 1423 10014592

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759713	2118	24274	198	65

Description

6500725739 chea:fliz flagellar protein:flagellar biosynthetic protein fliz precursor (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliZ fliZ Bacillus subtilis 1423 -11529597 72038 fliz:chea (de:flagellar biosynthetic protein fliz precursor) (db:swissprot) FLIZ_BACSU P35536 BACILLUS SUBTILIS 1423 -11529597 7000685307 fliz flagellar membrane protein fliz:flagellar formation protein fliz (db:pir2.dat) B41886 B41886 Bacillus subtilis 1423 -11529597 7500881635 fliz flagellar protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis flagellar protein (fliz, flip, and fliq),complete cds, and flagellar protein (flir and chey) genes, 5' and3'ends respectively.) (le:93) (re:752) (di:direct) BACFLIZPQ M87005 g142930 Bacillus subtilis 1423 -11529597 215625 fliz flagellar protein (fn:required for flagellar formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:105186) (re:105845) (di:direct) BSUB0009 Z99112 g2634006 Bacillus subtilis 1423 -11529597 169993 fliz flagellar membrane protein fliz:flagellar formation protein fliz (db:pir) B41886 B41886 Bacillus subtilis 1423 -11529597 5000688829 (de:(fliz) (pn:flagellar biosynthetic protein fliz precursor) (gn:chea) (gtcfc:12.09) (ec:) (fliz_bacsu) (keggfc:11.2) (bsorffc:6.3.0) (db:gtc-bacillus subtilis)) fliZ fliZ Bacillus subtilis 1423 10014594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759715	2119	24275	243	80

Description

6500725740 chec:flip flagellar protein:flagellar biosynthetic protein flip (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliP fliP Bacillus subtilis 1423 -11529598 72017 flip:chec (de:flagellar biosynthetic protein flip) (db:swissprot) FLIP_BACSU P35528 BACILLUS SUBTILIS 1423 -11529598 7000685297 flip flagellar biosynthsis-specific protein flip (cl:flagellar biosynthetic protein flip) (db:pir2.dat) C41886 C41886 Bacillus subtilis 1423 -11529598 7500881607 flip flagellar protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis flagellar protein (fliz, flip, and fliq),complete cds, and flagellar protein (flir and chey) genes, 5' and3'ends respectively.) (le:745) (re:1410) (di:direct) BACFLIZPQ M87005 g142931 Bacillus subtilis 1423 -11529598 215626 flip flagellar protein (fn:required for flagellar formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:105838) (re:106503) (di:direct) BSUB0009 Z99112 g2634007 Bacillus subtilis 1423 -11529598 169987 flip flagellar biosynthsis-specific protein flip (db:pir) C41886 C41886 Bacillus subtilis 1423 -11529598 5000688823 (de:(flip) (pn:flagellar biosynthetic protein flip) (gn:chec) (gtcfc:12.09) (ec:) (flip_bacsu) (keggfc:11.2) (bsorffc:6.3.0) (db:gtc-bacillus subtilis)) fliP fliP Bacillus subtilis 1423 10014573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759717	2120	24276	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759719	2121	24277	426	141

Description

5000688824 flagellar protein:flagellar biosynthetic protein fliq (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliQ fliQ Bacillus subtilis 1423 -11529599 72021 fliq (de:flagellar biosynthetic protein fliq) (db:swissprot) FLIQ_BACSU P35535 BACILLUS SUBTILIS 1423 -11529599 7000685298 fliq flagellar biosynthesis-specific protein fliq precursor (cl:flagellar biosynthesis-specific protein) (db:pir1.dat) D41886 D41886 Bacillus subtilis 1423 -11529599 215627 fliq flagellar protein (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis flagellar protein (fliz, flip, and fliq),complete cds, and flagellar protein (flir and chey) genes, 5' and3'ends respectively.) (le:1425) (re:1694) (di:direct) BACFLIZPQ M87005 g142932 Bacillus subtilis 1423 -11529599 7500881612 fliq flagellar protein (fn:required for flagellar formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:106518) (re:106787) (di:direct) BSUB0009 Z99112 g2634008 Bacillus subtilis 1423 -11529599 6500725741 flagellar protein:flagellar biosynthetic protein fliq (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliQ fliQ Bacillus subtilis 1423 -11529599

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759722	2122	24278	804	267

Description

GTC ORF with score 415 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:identical to s.pombe bem46 protein: swiss_prot acc#) (le:10266:11317)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759730	2123	24279	666	222

Description

5000688825 flagellar protein:flagellar biosynthetic protein flir (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliR fliR Bacillus subtilis 1423 -11529600 7500881624 flir (de:flagellar biosynthetic protein flir) (db:swissprot) FLIR_BACSU P35537 BACILLUS SUBTILIS 1423 -11529600 7000685299 flir flagellar biosynthetic protein flir (db:pir2.dat) I40401 I40401 Bacillus subtilis 1423 -11529600 219214 flir flagellar biosynthetic protein (db:genpept-bct1) (de:b.subtilis flir gene.) (le:69) (re:848) (di:direct) BSFLIR X74122 g395392 Bacillus subtilis 1423 -11529600 6500725742 flir flagellar protein (fn:required for flagellar formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:106795) (re:107574) (di:direct) BSUB0009 Z99112 g2634009 Bacillus subtilis 1423 -11529600 72024 flir (de:flagellar biosynthetic protein flir) (db:swissprot) FLIR_BACSU P35537 BACILLUS SUBTILIS 1423 -11529600 169986 flir flagellar biosynthetic protein flir (db:pir) I40401 I40401 Bacillus subtilis 1423 -11529600

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759731	2124	24280	507	169

Description

GTC ORF with score 104 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, essa i ap2 contig fragmentno. 2.) (nt:similarity to nadh dehydrogenase, chondrus crispus;) (le:135069:135827) (re:135246:135898) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759745	2125	24281	429	142

Description

6500725743 flagella-associated protein:flagellar biosynthetic protein flhb (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flhB flhB Bacillus subtilis 1423 -11529601 7000692989 flhb flagellar biosynthetic protein flhb:flagella-associated protein flhb (cl:flagellar biosynthetic protein flhb) (db:pir2.dat) D69623 D69623 Bacillus subtilis 1423 -11529601 7500963983 flhb flagella-associated protein (fn:required for flagellar formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:107574) (re:108656) (di:direct) BSUB0009 Z99112 g2634010 Bacillus subtilis 1423 -11529601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759756	2126	24282	249	82

Description

5000688809 flagella-associated protein:flagellar biosynthesis protein flha (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flhA flhA Bacillus subtilis 1423 -11529602 7500881565 flha (de:flagellar biosynthesis protein flha) (db:swissprot) FLHA_BACSU P35620 BACILLUS SUBTILIS 1423 -11529602 7000685275 flha flagella-associated protein flha (cl:regulatory protein lcrd) (db:pir2.dat) S33664 S33664 Bacillus subtilis 1423 -11529602 219206 flha (db:genpept-bct1) (de:b.subtilis flha gene.) (le:47) (re:2080) (di:direct) BSFLHA X63698 g39917 Bacillus subtilis 1423 -11529602 6500725744 flha flagella-associated protein (fn:required for flagellar formation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:108689) (re:110722) (di:direct) BSUB0009 Z99112 g2634011 Bacillus subtilis 1423 -11529602 71938 flha (de:flagellar biosynthesis protein flha) (db:swissprot) FLHA_BACSU P35620 BACILLUS SUBTILIS 1423 -11529602 169997 flha flagella-associated protein flha (db:pir) S33664 S33664 Bacillus subtilis 1423 -11529602

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759758	2127	24283	447	149

Description

5000688811 flagella-associated protein:flagellar biosynthesis protein flhf (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flhF flhF Bacillus subtilis 1423 -11529603 7500881574 flhf (de:protein)) (db:swissprot) FLHF_BACSU Q01960 BACILLUS SUBTILIS 1423 -11529603 7000685281 flhf flagella-associated probable gtp-binding protein flhf (db:pir2.dat) S25277 S25277 Bacillus subtilis 1423 -11529603 219208 flhf (db:genpept-bct1) (de:b.subtilis flhf gene.) (le:13) (re:1113) (di:direct) BSFLHF X66445 g39919 Bacillus subtilis 1423 -11529603 6500725745 flhf flagella-associated protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:110722) (re:111822) (di:direct) BSUB0009 Z99112 g2634012 Bacillus subtilis 1423 -11529603 71945 flhf (de:flagellar biosynthesis protein flhf) (db:swissprot) FLHF_BACSU Q01960 BACILLUS SUBTILIS 1423 -11529603 170458 flhf flagella-associated probable gtp-binding protein flhf (db:pir) S25277 S25277 Bacillus subtilis 1423 -11529603

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759768	2128	24284	213	70

Description

5000688803 hypothetical protein:purine-binding chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) cheW cheW Bacillus subtilis 1423 -11529604 64239 chew (de:purine-binding chemotaxis protein) (db:swissprot) CHEW_BACSU P39802 BACILLUS SUBTILIS 1423 -11529604 7000684810 chew chemotaxis protein chew (cl:chemotaxis chew protein) (db:pir2.dat) C69599 C69599 Bacillus subtilis 1423 -11529604 7500878642 chew (fn:modulation of chea activity in response to) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:115827) (re:116297) (di:direct) BSUB0009 Z99112 g2634016 Bacillus subtilis 1423 -11529604 6500725746 hypothetical protein:purine-binding chemotaxis protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) cheW cheW Bacillus subtilis 1423 -11529604

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759769	2129	24285	729	242

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759773	2130	24286	993	331

Description

6500725747 methyl-accepting chemotaxis proteins:mcps methyltransferase:chemotaxis protein methyltransferase (gtcfc:12.9) (ec:2.1.1.80) (keggfc:14.1) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) cheR cheR Bacillus subtilis 1423 -11529605 7000694200 cher:cherb chemotactic methyltransferase cherb (cl:protein-glutamate o-methyltransferase:protein-glutamate o-methyltransferase homology) (ec:2.1.1.-) (db:pir2.dat) A69599 A69599 Bacillus subtilis 1423 -11529605 217031 cher cher (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis dbpa, mtr(a,b), gerc(1-3), ndk, cher, aro(b,e,f,h),trp(a-f), hish, and tyra genes, complete cds.) (le:4633) (re:5409) (di:direct) BACVARGNS M80245 g143805 Bacillus subtilis 1423 -11529605 7500964927 cher methyl-accepting chemotaxis proteins mcps (fn:chemotaxis receptor methylation) (db:genpept-bct1) (ec:2.1.1.80) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:184039) (re:184815) (di:complement) BSUB0012 Z99115 g2634690 Bacillus subtilis 1423 -11529605

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759777	2131	24287	480	159

Description

5000688836 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein tlpb (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) tlpB tlpB Bacillus subtilis 1423 -11529606 101649 tlpb (de:methyl-accepting chemotaxis protein tlpb) (db:swissprot) TLPB_BACSU P39217 BACILLUS SUBTILIS 1423 -11529606 7000686804 tlpb methyl-accepting chemotaxis protein tlpb:chemotaxis transducer homolog tlpb (db:pir2.dat) D54078 D54078 Bacillus subtilis 1423 -11529606 7500893224 tlpb transmembrane receptor (sr:bacillus subtilis (strain oi1085) (library: lambda embl3, phage) (db:genpept-bct1) (de:bacillus subtilis transmembrane receptor mcpb, tlpa, mcpa and tlpbgenes, complete cds.) (nt:putative) (le:6604) (re:8592) (di:direct) BACMCPTLP L29189 g459691 Bacillus subtilis 1423 -11529606 216322 tlpb methyl-accepting chemotaxis protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:205367) (re:207355) (di:complement) BSUB0016 Z99119 g2635607 Bacillus subtilis 1423 -11529606 6000685274 tlpb methyl-accepting chemotaxis protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:6137) (re:8125) (di:complement) BSUB0017 Z99120 g2635619 Bacillus subtilis 1423 -11529606 169915 tlpb methyl-accepting chemotaxis protein tlpb:chemotaxis transducer homolog tlpb (db:pir) D54078 D54078 Bacillus subtilis 1423 -11529606 6500725748 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein tlpb (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) tlpB tlpB Bacillus subtilis 1423 -11529606

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759779	2132	24288	249	82

Description

5000688831 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein mcpa:h1 (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) mcpA mcpA Bacillus subtilis 1423 -11529607 83206 mcpa (de:methyl-accepting chemotaxis protein mcpa (h1)) (db:swissprot) MCPA_BACSU P39214 BACILLUS SUBTILIS 1423 -11529607 7000685802 mcpa methyl-accepting chemotaxis transducer mcpa (db:pir2.dat) B54078 B54078 Bacillus subtilis 1423 -11529607 7500885388 mcpa transmembrane receptor (sr:bacillus subtilis (strain oi1085) (library: lambda embl3, phage) (db:genpept-bct1) (de:bacillus subtilis transmembrane receptor mcpb, tlpa, mcpa and tlpbgenes, complete cds.) (nt:putative) (le:4505) (re:6490) (di:direct) BACMCPTLP L29189 g459690 Bacillus subtilis 1423 -11529607 216321 mcpa methyl-accepting chemotaxis protein (fn:chemotaxis deficiency toward glucose and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:207469) (re:209454) (di:complement) BSUB0016 Z99119 g2635608 Bacillus subtilis 1423 -11529607 6000684884 mcpa methyl-accepting chemotaxis protein (fn:chemotaxis deficiency toward glucose and) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:8239) (re:10224) (di:complement) BSUB0017 Z99120 g2635620 Bacillus subtilis 1423 -11529607 170348 mcpa methyl-accepting chemotaxis transducer mcpa (db:pir) B54078 B54078 Bacillus subtilis 1423 -11529607 6500725749 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein mcpa:h1 (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) mcpA mcpA Bacillus subtilis 1423 -11529607

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759782	2133	24289	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759790	2134	24290	675	224

Description

5000688835 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein tlpa (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) tlpA tlpA Bacillus subtilis 1423 -11529608 101647 tlpa (de:methyl-accepting chemotaxis protein tlpa) (db:swissprot) TLPA_BACSU P39216 BACILLUS SUBTILIS 1423 -11529608 7000686803 tlpa methyl-accepting chemotaxis protein tlpa:chemotaxis transducer homolog tlpa:transducer-like protein tlpa (db:pir2.dat) C54078 C54078 Bacillus subtilis 1423 -11529608 7500893223 tlpa transmembrane receptor (sr:bacillus subtilis (strain oi1085) (library: lambda embl3, phage) (db:genpept-bct1) (de:bacillus subtilis transmembrane receptor mcpb, tlpa, mcpa and tlpbgenes, complete cds.) (nt:putative) (le:2391) (re:4379) (di:direct) BACMCPTLP L29189 g459689 Bacillus subtilis 1423 -11529608 216320 tlpa methyl-accepting chemotaxis protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:209580) (re:211568) (di:complement) BSUB0016 Z99119 g2635609 Bacillus subtilis 1423 -11529608 6000685272 tlpa methyl-accepting chemotaxis protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:10350) (re:12338) (di:complement) BSUB0017 Z99120 g2635621 Bacillus subtilis 1423 -11529608 169914 tlpa methyl-accepting chemotaxis protein tlpa:chemotaxis transducer homolog tlpa:transducer-like protein tlpa (db:pir) C54078 C54078 Bacillus subtilis 1423 -11529608 6500725750 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein tlpa (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) tlpA tlpA Bacillus subtilis 1423 -11529608

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759792	2135	24291	654	218

Description

5000688832 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein mcpb:h3 (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) mcpB mcpB Bacillus subtilis 1423 -11529609 83209 mcpb (de:methyl-accepting chemotaxis protein mcpb (h3)) (db:swissprot) MCPB_BACSU P39215 BACILLUS SUBTILIS 1423 -11529609 216319 mcpb transmembrane receptor (sr:bacillus subtilis (strain oi1085) (library: lambda embl3, phage) (db:genpept-bct1) (de:bacillus subtilis transmembrane receptor mcpb, tlpa, mcpa and tlpbgenes, complete cds.) (nt:putative) (le:226) (re:2214) (di:direct) BACMCPTLP L29189 g459688 Bacillus subtilis 1423 -11529609 6000684886 mcpb methyl-accepting chemotaxis protein (fn:chemotaxis deficiency toward asparagine,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.) (le:211745) (re:213733) (di:complement) BSUB0016 Z99119 g2635610 Bacillus subtilis 1423 -11529609 7500885389 mcpb methyl-accepting chemotaxis protein (fn:chemotaxis deficiency toward asparagine,) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:12515) (re:14503) (di:complement) BSUB0017 Z99120 g2635622 Bacillus subtilis 1423 -11529609 7000685803 mcpb methyl-accepting chemotaxis protein mcpb (db:pir) H69655 H69655 Bacillus subtilis 1423 -11529609 6500725751 methyl-accepting chemotaxis protein:methyl-accepting chemotaxis protein mcpb:h3 (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) mcpB mcpB Bacillus subtilis 1423 -11529609

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759793	2136	24292	330	109

Description

GTC ORF with score 295 to: (sr:colletotrichum gloeosporioides cdna to mrna) (db:genpept-pln1) (ec:1.2.1.12) (de:colletotrichum gloeosporioides glyceraldehyde-3-phosphatedehydrogenase mrna, complete cds.) (le:39) (re:1055) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759794	2137	24293	234	77

Description

5000688827 flagellar protein:flagellar protein flit (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliT fliT Bacillus subtilis 1423 -11529610 7500881633 flit (de:flagellar protein flit) (db:swissprot) FLIT_BACSU P39740 BACILLUS SUBTILIS 1423 -11529610 7000685303 flit flagellar protein flit (db:pir2.dat) I40399 I40399 Bacillus subtilis 1423 -11529610 219212 flit (db:genpept-bct1) (de:b.subtilis (hb2058) genes for flid, flis, flit proteins.) (le:2592) (re:2933) (di:direct) BSFLIDST Z31376 g499383 Bacillus subtilis 1423 -11529610 6500725752 flit flagellar protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:34120) (re:34461) (di:complement) BSUB0019 Z99122 g2636058 Bacillus subtilis 1423 -11529610 298111 flit flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762347 Bacillus subtilis 1423 -11529610 72030 flit (de:flagellar protein flit) (db:swissprot) FLIT_BACSU P39740 BACILLUS SUBTILIS 1423 -11529610 170001 flit flagellar protein flit (db:pir) I40399 I40399 Bacillus subtilis 1423 -11529610 220128 flit flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762347 Bacillus subtilis 1423 -11529610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759795	2138	24294	666	221

Description

GTC ORF with score 789 to: (sr:colletotrichum gloeosporioides cdna to mrna) (db:genpept-pln1) (ec:1.2.1.12) (de:colletotrichum gloeosporioides glyceraldehyde-3-phosphatedehydrogenase mrna, complete cds.) (le:39) (re:1055) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759986	2139	24295	666	221

Description

5000688826 flagellar protein:flagellar protein flis (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliS fliS Bacillus subtilis 1423 -11529611 7500881632 flis (de:flagellar protein flis) (db:swissprot) FLIS_BACSU P39739 BACILLUS SUBTILIS 1423 -11529611 7000685301 flis flagellar protein flis (cl:flagellar protein flis) (db:pir2.dat) I40398 I40398 Bacillus subtilis 1423 -11529611 219211 flis (db:genpept-bct1) (de:b.subtilis (hb2058) genes for flid, flis, flit proteins.) (le:2194) (re:2595) (di:direct) BSFLIDST Z31376 g499382 Bacillus subtilis 1423 -11529611 6500725753 flis flagellar protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:34458) (re:34859) (di:complement) BSUB0019 Z99122 g2636059 Bacillus subtilis 1423 -11529611 298110 flis flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762346 Bacillus subtilis 1423 -11529611 72027 flis (de:flagellar protein flis) (db:swissprot) FLIS_BACSU P39739 BACILLUS SUBTILIS 1423 -11529611 170000 flis flagellar protein flis (cl:flagellar protein flis) (db:pir) I40398 I40398 Bacillus subtilis 1423 -11529611 220127 flis flagellar protein (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762346 Bacillus subtilis 1423 -11529611

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759991	2140	24296	186	61

Description

GTC ORF with score 139 to: (sr:schizosaccharomyces pombe (strain:972h-) cdna to mrna) (db:genpept-pln1) (ec:2.7.7.6) (de:schizosaccharomyces pombe rpb7 mrna for rna polymerase ii subunitrpb7, complete cds.) (le:26) (re:544) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501759996	2141	24297	207	68

Description

GTC ORF with score 91 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac f18o19 genomic sequence,complete sequence.) (nt:hypothetical protein) (le:25161:26061:26466) (re:25979:26314:26653) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760027	2142	24298	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760028	2143	24299	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760035	2144	24300	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760043	2145	24301	363	120

Description

6500725754 mrgb:flid flagellar hook-associated protein 2:hap2:filament cap protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) fliD fliD Bacillus subtilis 1423 -11529612 7000692992 flid flagellar hook-associated protein 2 hap2 flid (db:pir2.dat) H69623 H69623 Bacillus subtilis 1423 -11529612 220126 flid flagellar hook-associated protein 2 hap2 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:34881) (re:36377) (di:complement) BSUB0019 Z99122 g2636060 Bacillus subtilis 1423 -11529612 298109 flid flagellar hook-associated protein 2 (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762345 Bacillus subtilis 1423 -11529612

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760045	2146	24302	510	169

Description

5000688830 flagellin protein:flagellin (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) hag hag Bacillus subtilis 1423 -11529613 71890 hag (de:flagellin) (db:swissprot) FLA_BACSU P02968 BACILLUS SUBTILIS 1423 -11529613 131134 hag flagellin hag (cl:flagellin) (db:pir1.dat) FLBS68 A44759 Bacillus subtilis 1423 -11529613 215605 (sr:b.subtilis (strain i168) dna) (db:genpept-bct1) (de:b.subtilis flagellin gene, complete cds.) (nt:flagellin) (le:178) (re:1092) (di:direct) BACFLAGA M26947 g142909 Bacillus subtilis 1423 -11529613 215821 (sr:b.subtilis (strain i168) dna, clone pdm67) (db:genpept-bct1) (de:b.subtilis flagellin gene (hag), complete cds.) (nt:flagellin) (le:545) (re:1459) (di:direct) BACHAGFA M26948 g143033 Bacillus subtilis 1423 -11529613 220124 hag flagellin protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:36957) (re:37871) (di:complement) BSUB0019 Z99122 g2636062 Bacillus subtilis 1423 -11529613 298107 hag flagellin (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762343 Bacillus subtilis 1423 -11529613 6500725755 flagellin protein:flagellin (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) hag hag Bacillus subtilis 1423 -11529613

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760050	2147	24303	510	169

Description

6500725756 yvid:flgl flagellar hook-associated protein 3:flagellar-hook associated protein 3:hap3 (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgL flgL Bacillus subtilis 1423 -11529614 5500685223 flgl (de:flagellar hook-associated protein 3 (hap3)) (db:swissprot) FLGL_BACSU P96501 BACILLUS SUBTILIS 1423 -11529614 7000685271 flgl flagellar hook-associated protein 3 hap3 flgl (db:pir2.dat) A69623 A69623 Bacillus subtilis 1423 -11529614 220120 flgl flagellar hook-associated protein 3 hap3 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvid) (le:39308) (re:40204) (di:complement) BSUB0019 Z99122 g2636066 Bacillus subtilis 1423 -11529614 298103 flgl flagellar-hook associated protein 3 hap3 (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762339 Bacillus subtilis 1423 -11529614

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760064	2148	24304	1590	530

Description

6500725757 flagellar hook-associated protein 1:hap1 (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgK flgK Bacillus subtilis 1423 -11529615 71928 flgk (de:flagellar hook-associated protein 1 (hap1)) (db:swissprot) FLGK_BACSU P39810 BACILLUS SUBTILIS 1423 -11529615 7000685270 flgk flagellar hook-associated protein 1 hap1 flgk (db:pir2.dat) H69622 H69622 Bacillus subtilis 1423 -11529615 220119 flgk flagellar hook-associated protein 1 hap1 (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:40215) (re:41738) (di:complement) BSUB0019 Z99122 g2636067 Bacillus subtilis 1423 -11529615 298102 flgk flagellar-hook associated protein 1 hap1 (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762338 Bacillus subtilis 1423 -11529615

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760074	2149	24305	594	197

Description

5000688808 anti-sigma factor repressor of sigma-d-dependent transcription:negative regulator of flagellin synthesis:anti-sigma factor (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgM flgM Bacillus subtilis 1423 -11529616 71933 flgm (de:negative regulator of flagellin synthesis (anti-sigma factor)) (db:swissprot) FLGM_BACSU P39809 BACILLUS SUBTILIS 1423 -11529616 7000685272 flgm flagellin synthesis regulatory protein anti-sigma factor flgm (db:pir2.dat) B69623 B69623 Bacillus subtilis 1423 -11529616 215615 flgm flagellin synthesis regulatory protein (sr:bacillus subtilis (strain w168) (library: lambda gtwes library) (db:genpept-bct1) (de:bacillus subtilis (clones pdm116 and pdm113) flagellin synthesisregulatory protein (flgm) and flagellar hook-filament junctionprotein (flgk) genes and orf139, orf... BACFLGMK L14437 g451869 Bacillus subtilis 1423 -11529616 220117 flgm anti-sigma factor repressor of sigma-d-dependent (fn:responsible for the coupling of late flagellar) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:42255) (re:42521) (di:complement) BSUB0019 Z99122 g2636069 Bacillus subtilis 1423 -11529616 298100 flgm negative regulator of flagellin synthesis (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762336 Bacillus subtilis 1423 -11529616 6500725758 anti-sigma factor repressor of sigma-d-dependent transcription:negative regulator of flagellin synthesis:anti-sigma factor (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flgM flgM Bacillus subtilis 1423 -11529616

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760087	2150	24306	1419	472

Description

6500725759 yvyb:flhp flagellar hook-basal body protein (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flhP flhP Bacillus subtilis 1423 -11529617 220402 flhp (de:flagellar hook-basal body complex protein flhp) (db:swissprot) FLHP_BACSU P39753 BACILLUS SUBTILIS 1423 -11529617 7000692993 flhp flagellar hook-basal body protein flhp (db:pir2.dat) G69623 G69623 Bacillus subtilis 1423 -11529617 7500881577 flhp flagellar hook-basal body protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvyb) (le:147401) (re:148207) (di:complement) BSUB0019 Z99122 g2636164 Bacillus subtilis 1423 -11529617 7502851632 flhp (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:similar to flagellar hook-basal body proteins) (le:1114) (re:1920) (di:direct) BSZ83337 Z83337 g1763701 Bacillus subtilis 1423 -11529617 7500881575 flhp (de:flagellar hook-basal body complex protein flhp) (db:swissprot) FLHP_BACSU P39753 BACILLUS SUBTILIS 1423 -11529617

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760096	2151	24307	1164	387

Description

6500725760 yvya:flho flagellar basal-body rod protein:flagellar hook-basal body complex protein flho (gtcfc:12.9) (keggfc:14.2) (bsorffc:6.3.1) (db:gtc-bacillus subtilis) flhO flhO Bacillus subtilis 1423 -11529618 7000692990 flho flagellar basal-body rod protein flho (db:pir2.dat) F69623 F69623 Bacillus subtilis 1423 -11529618 220401 flho flagellar basal-body rod protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: yvya) (le:148241) (re:149053) (di:complement) BSUB0019 Z99122 g2636165 Bacillus subtilis 1423 -11529618 7500963985 flho (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:similar to flagellar hook-basal body proteins) (le:268) (re:1080) (di:direct) BSZ83337 Z83337 g1763700 Bacillus subtilis 1423 -11529618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760100	2152	24308	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760107	2153	24309	213	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760280	2154	24310	384	127

Description

GTC ORF with score 158 to: (or:Borrelia burgdorferi) (sr:lyme disease spirochete) (db:genpept-bct2) (de:borrelia burgdorferi (section 9 of 70) of the complete genome.) (nt:similar to gb:m33145 sp:p17242 gb:x68192 pid:147935) (le:109) (re:1509) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760281	2155	24311	885	294

Description

6500725761 ykxf:xtma pbsx defective prophage terminase:small subunit:pbsx phage terminase small subunit (gtcfc:13.1) (keggfc:14.2) (bsorffc:7.5.1) (db:gtc-bacillus subtilis) xtmA xtmA Bacillus subtilis 1423 -11529619 108164 xtma (de:pbsx phage terminase small subunit) (db:swissprot) XTMA_BACSU P39785 BACILLUS SUBTILIS 1423 -11529619 7000687051 xtma pbsx terminase small subunit xtma:hypothetical protein 8 xre region (db:pir2.dat) H69734 H69734 Bacillus subtilis 1423 -11529619 219484 xtma pbsx terminase (fn:small subunit of pbsx terminase) (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqas of the skin element) (le:4224) (re:5021) (di:direct) BSPBSXSE Z70177 g1225942 Bacillus subtilis 1423 -11529619 7500894480 xtma pbsx defective prophage terminase small (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykxf) (le:130173) (re:130970) (di:direct) BSUB0007 Z99110 g2633611 Bacillus subtilis 1423 -11529619 5000689137 (de:(xtma) (pn:pbsx phage terminase small subunit) (gtcfc:13.07) (ec:) (xtma_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) xtmA xtmA Bacillus subtilis 1423 10049896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760294	2156	24312	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760306	2157	24313	504	167

Description

6500725762 ykxg:xtmb pbsx defective prophage terminase:large subunit:pbsx phage terminase large subunit (gtcfc:13.1) (keggfc:14.2) (bsorffc:7.5.1) (db:gtc-bacillus subtilis) xtmB xtmB Bacillus subtilis 1423 -11529620 108165 xtmb (de:pbsx phage terminase large subunit) (db:swissprot) XTMB_BACSU P39786 BACILLUS SUBTILIS 1423 -11529620 7000687052 xtmb phage pbsx terminase large chain xtmb (db:pir2.dat) A69735 A69735 Bacillus subtilis 1423 -11529620 219485 xtmb pbsx terminase (fn:large subunit of pbsx terminase) (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqat of the skin element) (le:5018) (re:6319) (di:direct) BSPBSXSE Z70177 g1225943 Bacillus subtilis 1423 -11529620 7500894481 xtmb pbsx defective prophage terminase large (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykxg) (le:130967) (re:132268) (di:direct) BSUB0007 Z99110 g2633612 Bacillus subtilis 1423 -11529620 5000689138 (de:(xtmb) (pn:pbsx phage terminase large subunit) (gtcfc:13.07) (ec:) (xtmb_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) xtmB xtmB Bacillus subtilis 1423 10049897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760309	2158	24314	342	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760311	2159	24315	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760322	2160	24316	483	160

Description

6500725763 xepa:xkdy lytic exoenzyme associated with defective prophage pbsx:phage-like element pbsx protein xkdy:protein (gtcfc:13.1) (keggfc:14.2) (bsorffc:7.5.1) (db:gtc-bacillus subtilis) xkdY xkdY Bacillus subtilis 1423 -11529621 7000694349 xkdy pbsx prophage lytic exoenzyme orf xkdy (db:pir2.dat) H69733 H69733 Bacillus subtilis 1423 -11529621 219505 xepa exported protein (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqxg of the skin element) (le:24971) (re:25810) (di:direct) BSPBSXSE Z70177 g1225962 Bacillus subtilis 1423 -11529621 7500965039 xkdy lytic exoenzyme associated with defective (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: xepa) (le:150920) (re:151759) (di:direct) BSUB0007 Z99110 g2633632 Bacillus subtilis 1423 -11529621

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760323	2161	24317	1059	353

Description

5000689026 hypothetical protein:xhla protein (gtcfc:13.1) (keggfc:14.2) (bsorffc:7.5.1) (db:gtc-bacillus subtilis) xhlA xhlA Bacillus subtilis 1423 -11529622 219510 xhla (de:xhla protein) (db:swissprot) XHLA_BACSU P39798 BACILLUS SUBTILIS 1423 -11529622 170668 xhla holin component xhla:pbsx prophage-mediated lysis protein xhla (db:pir2.dat) G69730 G69730 Bacillus subtilis 1423 -11529622 216443 xhla (sr:bacillus subtilis (strain 168) (library: lambda embl3) dna) (db:genpept-bct1) (de:bacillus subtilis 168 endogenous defective prophage pbsx encodingn-acetylmuramoyl-l-alanine amidase (xlya) gene and xepa, xhla, andxhlb genes, complete cds.) (le:946)... BACPBSX L25924 g496174 Bacillus subtilis 1423 -11529622 219506 xhla protein involved in cell lysis (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (le:25863) (re:26132) (di:direct) BSPBSXSE Z70177 g1225963 Bacillus subtilis 1423 -11529622 7500894442 xhla protein associated with cell lysis upon (db:genpept-bct1) (de:b.subtilis defective prophage pbsx xhla, xhlb, and xyla genes.) (le:1018) (re:1287) (di:direct) BSPBSXXHL Z36941 g535795 Bacillus subtilis 1423 -11529622 7502851633 xhla (fn:involved in cell lysis upon induction of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:151812) (re:152081) (di:direct) BSUB0007 Z99110 g2633633 Bacillus subtilis 1423 -11529622 108103 xhla (de:xhla protein) (db:swissprot) XHLA_BACSU P39798 BACILLUS SUBTILIS 1423 -11529622 7000687023 xhla xhla protein (db:pir) I39936 I39936 Bacillus subtilis 1423 -11529622 6500725764 hypothetical protein:xhla protein (gtcfc:13.1) (keggfc:14.2) (bsorffc:7.5.1) (db:gtc-bacillus subtilis) xhlA xhlA Bacillus subtilis 1423 -11529622

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760344	2162	24318	240	79

Description

GTC ORF with score 90 to: (fn:formation of uridine 5'-monophosphate from) (sr:streptococcus salivarius (library: lambda-a39/atcc 25975) dna) (db:genpept-bct1) (ec:2.4.2.9) (de:streptococcus salivarius fructosyltransferase (ftf) gene, completecds; ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760350	2163	24319	408	136

Description

GTC ORF with score 109 to: (sr:plasmodium falciparum (isolate:thai822a) dna) (db:genpept-inv) (de:plasmodium falciparum gene for thrombospondin-related protein,partial cds, isolate thai822a.) (nt:surface protein 2) (le:1) (re:1677) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760353	2164	24320	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760359	2165	24321	1122	374

Description

6500725765 xpab:xhlb holin (gtcfc:13.1) (keggfc:14.2) (bsorffc:7.5.1) (db:gtc-bacillus subtilis) xhlB xhlB Bacillus subtilis 1423 -11529623 219511 xhlb:xpab (de:holin) (db:swissprot) XHLB_BACSU Q99163 BACILLUS SUBTILIS 1423 -11529623 170037 xpab:xhlb holin component xhlb (db:pir2.dat) (mp:112 deg.) F49754 F49754 Bacillus subtilis 1423 -11529623 216444 xhlb (sr:bacillus subtilis (strain 168) (library: lambda embl3) dna) (db:genpept-bct1) (de:bacillus subtilis 168 endogenous defective prophage pbsx encodingn-acetylmuramoyl-l-alanine amidase (xlya) gene and xepa, xhla, andxhlb genes, complete cds.) (le:1228... BACPBSX L25924 g496175 Bacillus subtilis 1423 -11529623 217057 xpab (sr:b.subtilis (strain 168) dna) (db:genpept-bct1) (de:b.subtilis xpab gene, complete cds.) (le:25) (re:288) (di:direct) BACXPAB M63943 g143827 Bacillus subtilis 1423 -11529623 219507 xhlb holin-like protein (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (le:26145) (re:26408) (di:direct) BSPBSXSE Z70177 g1225964 Bacillus subtilis 1423 -11529623 5000689027 xhlb holin (db:genpept-bct1) (de:b.subtilis defective prophage pbsx xhla, xhlb, and xyla genes.) (nt:gene product involved in cell lysis upon induction) (le:1300) (re:1563) (di:direct) BSPBSXXHL Z36941 g535796 Bacillus subtilis 1423 -11529623 7500894443 xhlb holin (fn:hydrolysis of 5-bromo 4-chloroindolyl phosphate) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: xpab) (le:152094) (re:152357) (di:direct) BSUB0007 Z99110 g2633634 Bacillus subtilis 1423 -11529623 108104 xhlb:xpab (de:holin) (db:swissprot) XHLB_BACSU Q99163 BACILLUS SUBTILIS 1423 -11529623 7000687024 xhlb hydrolysis of 5-bromo 4-chloroindolyl phosphate upon induction xhlb (db:pir) H69730 H69730 Bacillus subtilis 1423 -11529623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760370	2166	24322	426	141

Description

6500725766 ycbs:phod phosphodiesterase/alkaline phosphatase d:alkaline phosphatase d precursor:apased:ran1:bc6 (gtcfc:13.10) (keggfc:14.1) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) phoD phoD Bacillus subtilis 1423 -11529624 110610 phod (ec:3.1.3.1) (de:alkaline phosphatase d precursor, (apased) (ran1) (bc6)) (db:swissprot) PPBD_BACSU P42251 BACILLUS SUBTILIS 1423 -11529624 7000686161 phod phosphodiesterase/alkaline phosphatase phod (db:pir2.dat) D69676 D69676 Bacillus subtilis 1423 -11529624 220041 phod phosphodiesterase/alkaline phosphatase d (db:genpept-bct1) (de:bacillus subtilis phosphodiesterase/alkaline phosphatase dprecursor (phod) gene, complete cds.) (nt:apase d) (le:349) (re:2019) (di:direct) BSU49060 U49060 g1680684 Bacillus subtilis 1423 -11529624 295245 phod phosphodiesterase/alkaline phosphatase d (db:genpept-bct1) (ec:3.1.4.1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ycbs) (le:88905) (re:90575) (di:direct) BSUB0002 Z99105 g2632548 Bacillus subtilis 1423 -11529624

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760379	2167	24323	696	231

Description

6500725767 serine phosphatase:dephosphorylation of rsbv:sigma factor sibg regulation protein rsbu (gtcfc:13.10) (keggfc:14.2) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) rsbU rsbU Bacillus subtilis 1423 -11529625 7500891135 rsbu (de:sigma factor sibg regulation protein rsbu) (db:swissprot) RSBU_BACSU P40399 BACILLUS SUBTILIS 1423 -11529625 7000694105 rsbu regulator of sigma-b activity rsbu (db:pir2.dat) H69701 H69701 Bacillus subtilis 1423 -11529625 302725 rsbu sigma factor sigb regulation protein rsbu (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar product in synechocystis.) (le:54082) (re:55089) (di:direct) AB001488 AB001488 g1881280 Bacillus subtilis 1423 -11529625 216653 rsbu sigma-b regulator (sr:bacillus subtilis (strain 168 marburg) dna) (db:genpept-bct1) (de:bacillus subtilis (clones paw10, paw50) regulator (rsbu) gene,complete cds, positive regulator (rsbv), 5' end.) (nt:predicted rsbu product has significant similarity) (le:1969) (re:2... BACRSBU L35574 g1146194 Bacillus subtilis 1423 -11529625 7500891138 rsbu serine phosphatase dephosphorylation of rsbv (fn:indirect positive regulation necessary for the) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:117826) (re:118833) (di:direct) BSUB0003 Z99106 g2632770 Bacillus subtilis 1423 -11529625

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760381	2168	24324	900	299

Description

5000688866 serine phosphatase:dephosphorylation of rsbs:sigma-b negative effector:orf x in sigb region (gtcfc:13.10) (keggfc:14.2) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) rsbX rsbX Bacillus subtilis 1423 -11529626 97455 rsbx (de:sigma-b negative effector) (db:swissprot) RSBX_BACSU P17906 BACILLUS SUBTILIS 1423 -11529626 7000686524 rsbx sigma-b activity indirect negative regulator rsbx:serine phosphatase rsbx (db:pir2.dat) D36131 D36131 Bacillus subtilis 1423 -11529626 7500891141 rsbx sigma-b negative effector orf x in sigb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:56713) (re:57312) (di:direct) AB001488 AB001488 g1881284 Bacillus subtilis 1423 -11529626 216644 (sr:b.subtilis (strains 168 and marburg), clone) (db:genpept-bct1) (de:b.subtilis minor sigma-37 factor of rna polymerase (rpof, sigb),complete cds.) (nt:orf x) (le:1762) (re:2361) (di:direct) BACRPOF M34995 g143461 Bacillus subtilis 1423 -11529626 302729 rsbx serine phosphatase dephosphorylation of rsbs (fn:indirect negative regulation of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:120457) (re:121056) (di:direct) BSUB0003 Z99106 g2632774 Bacillus subtilis 1423 -11529626 170260 rsbx sigma-b activity indirect negative regulator rsbx:serine phosphatase rsbx (db:pir) D36131 D36131 Bacillus subtilis 1423 -11529626 6500725768 serine phosphatase:dephosphorylation of rsbs:sigma-b negative effector:orf x in sigb region (gtcfc:13.10) (keggfc:14.2) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) rsbX rsbX Bacillus subtilis 1423 -11529626

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760390	2169	24325	1086	361

Description

6500725769 papq:cwlf:lyte phosphatase-associated protein:cwbp33 (gtcfc:13.10) (keggfc:14.2) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) lytE lytE Bacillus subtilis 1423 -11529627 7000692334 lyte cell wall lytic activity lyte (db:pir2.dat) G69654 G69654 Bacillus subtilis 1423 -11529627 4000714605 lyte phosphatase-associated protein cwbp33 (fn:cell wall lytic activity) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: papq, cwlf) (le:18952) (re:19983) (di:direct) BSUB0006 Z99109 g2633277 Bacillus subtilis 1423 -11529627 7500963501 papq phosphatase-associated protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:see subtilist bg11406 and embl u38819.) (le:5600) (re:6631) (di:direct) BSY14082 Y14082 g2226198 Bacillus subtilis 1423 -11529627

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760590	2170	24326	423	140

Description

6500725770 gtp pyrophosphokinase (gtcfc:13.10) (ec:2.7.6.5) (keggfc:14.1) (bsorffc:2.3.1) (db:gtc-bacillus subtilis) relA relA Bacillus subtilis 1423 -11529628 7000693074 rela gtp pyrophosphokinase stringent response rela (cl:guanosine 3',5'-bis(diphosphate) 3'-pyrophosphatase) (db:pir2.dat) C69691 C69691 Bacillus subtilis 1423 -11529628 7500964040 rela gtp pyrophosphokinase (fn:stringent response) (db:genpept-bct1) (ec:2.7.6.5) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:24664) (re:26868) (di:complement) BSUB0015 Z99118 g2635224 Bacillus subtilis 1423 -11529628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760592	2171	24327	612	203

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760608	2172	24328	663	220

Description

5000689927 hypothetical protein:competence protein s (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comS comS Bacillus subtilis 1423 -11529629 65418 coms (de:competence protein s) (db:swissprot) COMS_BACSU P80355 BACILLUS SUBTILIS 1423 -11529629 7000684869 coms competence factor coms (db:pir2.dat) S65598 S65598 Bacillus subtilis 1423 -11529629 7500879082 coms coms (fn:regulation of genetic competence) (db:genpept-bct1) (de:bacillus subtilis 168 genetic competence regulation (coms) gene,complete cds.) (le:211) (re:351) (di:direct) BSU10926 U10926 g508740 Bacillus subtilis 1423 -11529629 219782 coms (fn:regulation of genetic competence; assembly link) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:195802) (re:195942) (di:direct) BSUB0002 Z99105 g2632636 Bacillus subtilis 1423 -11529629 222616 coms regulation of genetic competence (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:70105) (re:70245) (di:direct) D50453 D50453 g1805422 Bacillus subtilis 1423 -11529629 1500685160 coms competence factor coms (db:pir) S65598 S65598 Bacillus subtilis 1423 -11529629 6500725771 hypothetical protein:competence protein s (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comS comS Bacillus subtilis 1423 -11529629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760619	2173	24329	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760628	2174	24330	402	133

Description

5000689926 competence transcription factor:ctf:competence protein k (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comK comK Bacillus subtilis 1423 -11529630 65412 comk (de:competence transcription factor (ctf) (competence protein k)) (db:swissprot) COMK_BACSU P40396 BACILLUS SUBTILIS 1423 -11529630 7000684867 comk competence transcription factor ctf comk (db:pir2.dat) S43611 S43611 Bacillus subtilis 1423 -11529630 7500879080 comk competence transcription factor ctf (fn:final autoregulatory control switch prior to) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:117081) (re:117659) (di:direct) BSUB0006 Z99109 g2633378 Bacillus subtilis 1423 -11529630 258693 comk (sr:bacillus subtilis e26) (db:genpept-bct1) (de:comk (bacillus subtilis, e26, genomic, 3 genes, 1947 nt).) (nt:this sequence comes from fig. 3.) (le:900) (re:1478) (di:direct) S70734 S70734 g546917 Bacillus subtilis 1423 -11529630 169935 comk competence transcription factor ctf comk (db:pir) S43611 S43611 Bacillus subtilis 1423 -11529630 6500725772 competence transcription factor:ctf:competence protein k (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comK comK Bacillus subtilis 1423 -11529630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760631	2175	24331	918	305

Description

5000689929 hypothetical protein:negative regulator of genetic competence meca (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) mecA mecA Bacillus subtilis 1423 -11529631 83390 meca (de:negative regulator of genetic competence meca) (db:swissprot) MECA_BACSU P37958 BACILLUS SUBTILIS 1423 -11529631 7000685813 meca competence negative regulator meca (db:pir2.dat) S35289 S35289 Bacillus subtilis 1423 -11529631 7500885448 meca (fn:negative regulator of competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:34150) (re:34806) (di:direct) BSUB0007 Z99110 g2633506 Bacillus subtilis 1423 -11529631 216325 meca (sr:bacillus subtilis (strain 168) dna) (db:genpept-bct2) (de:bacillus subtilis negative regulator (meca) gene, complete cds.) (nt:putative) (le:604) (re:1260) (di:direct) BACMECA L06059 g143177 Bacillus subtilis 1423 -11529631 170336 meca competence negative regulator meca (db:pir) S35289 S35289 Bacillus subtilis 1423 -11529631 6500725773 hypothetical protein:negative regulator of genetic competence meca (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) mecA mecA Bacillus subtilis 1423 -11529631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760636	2176	24332	450	150

Description

6500725774 comg7:comgg probably part of the dna transport machinery:comg operon protein 7 (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comGG comGG Bacillus subtilis 1423 -11529632 64882 comgg:comg7 (de:comg operon protein 7) (db:swissprot) CMG7_BACSU P25959 BACILLUS SUBTILIS 1423 -11529632 7000684853 comgg dna transport machinery protein comgg:comg operon protein 7 (db:pir2.dat) H30338 H30338 Bacillus subtilis 1423 -11529632 7500878912 comg7 (sr:bacillus subtilis (strain 168) (clone: ped4) dna) (db:genpept-bct1) (de:bacillus subtilis (clone ped4) comg-(1,2,3,4,5,6,and 7) proteins incomg operon, complete cds.) (le:4863) (re:5237) (di:direct) BACCOMGA M29691 g142711 Bacillus subtilis 1423 -11529632 215378 comgg (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:163093) (re:163467) (di:direct) BACJH642 D84432 g1303882 Bacillus subtilis 1423 -11529632 216126 comgg probably part of the dna transport machinery (fn:competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:160154) (re:160528) (di:complement) BSUB0013 Z99116 g2634901 Bacillus subtilis 1423 -11529632 169934 comgg dna transport machinery protein comgg:comg operon protein 7 (db:pir) H30338 H30338 Bacillus subtilis 1423 -11529632 5000689923 (de:(comgg) (pn:comg operon protein 7:comg operon protein 7) (gn:comg7) (gtcfc:13.12) (ec:) (cmg7_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comGG comGG Bacillus subtilis 1423 10007543

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760663	2177	24333	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760665	2178	24334	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760668	2179	24335	303	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760670	2180	24336	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760690	2181	24337	843	280

Description

6500725775 probably part of the dna transport machinery (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comGF comGF Bacillus subtilis 1423 -11529633 7000692948 comgf dna transport machinery comgf (db:pir2.dat) G69603 G69603 Bacillus subtilis 1423 -11529633 7500963959 comgf probably part of the dna transport machinery (fn:competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:160529) (re:160912) (di:complement) BSUB0013 Z99116 g2634902 Bacillus subtilis 1423 -11529633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760692	2182	24338	609	202

Description

6500725776 comg5:comge probably part of the dna transport machinery:comg operon protein 5 precursor (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comGE comGE Bacillus subtilis 1423 -11529634 7000692381 comge dna transport machinery protein comge:comg operon protein 5 (db:pir2.dat) F30338 F30338 Bacillus subtilis 1423 -11529634 7500963960 comge (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:162336) (re:162683) (di:direct) BACJH642 D84432 g1303881 Bacillus subtilis 1423 -11529634 216125 comge probably part of the dna transport machinery (fn:competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:160938) (re:161285) (di:complement) BSUB0013 Z99116 g2634903 Bacillus subtilis 1423 -11529634 169932 comge dna transport machinery protein comge:comg operon protein 5 (db:pir) F30338 F30338 Bacillus subtilis 1423 -11529634

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760713	2183	24339	1317	439

Description

6500725777 comg4:comgd probably part of the dna transport machinery:comg operon protein 4 precursor (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comGD comGD Bacillus subtilis 1423 -11529635 64879 comgd:comg4 (de:comg operon protein 4 precursor) (db:swissprot) CMG4_BACSU P25956 BACILLUS SUBTILIS 1423 -11529635 7000684852 comgd dna transport machinery protein comgd:comg operon protein 4 (db:pir2.dat) E30338 E30338 Bacillus subtilis 1423 -11529635 7500878911 comg4 (sr:bacillus subtilis (strain 168) (clone: ped4) dna) (db:genpept-bct1) (de:bacillus subtilis (clone ped4) comg-(1,2,3,4,5,6,and 7) proteins incomg operon, complete cds.) (le:3691) (re:4122) (di:direct) BACCOMGA M29691 g142709 Bacillus subtilis 1423 -11529635 215375 comgd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:161921) (re:162352) (di:direct) BACJH642 D84432 g1303880 Bacillus subtilis 1423 -11529635 216124 comgd probably part of the dna transport machinery (fn:competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:161269) (re:161700) (di:complement) BSUB0013 Z99116 g2634904 Bacillus subtilis 1423 -11529635 169931 comgd dna transport machinery protein comgd:comg operon protein 4 (db:pir) E30338 E30338 Bacillus subtilis 1423 -11529635 5000689920 (de:(comgd) (pn:comg operon protein 4 precursor:comg operon protein 4 precursor) (gn:comg4) (gtcfc:13.12) (ec:) (cmg4_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comGD comGD Bacillus subtilis 1423 10007540

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760720	2184	24340	699	233

Description

6500725778 comg3:comgc hypothetical protein:comg operon protein 3 precursor (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comGC comGC Bacillus subtilis 1423 -11529636 64878 comgc:comg3 (de:comg operon protein 3 precursor) (db:swissprot) CMG3_BACSU P25955 BACILLUS SUBTILIS 1423 -11529636 7000684851 comgc exogenous dna-binding protein comgc:comg operon protein 3 (db:pir2.dat) D30338 D30338 Bacillus subtilis 1423 -11529636 7500878910 comg3 (sr:bacillus subtilis (strain 168) (clone: ped4) dna) (db:genpept-bct1) (de:bacillus subtilis (clone ped4) comg-(1,2,3,4,5,6,and 7) proteins incomg operon, complete cds.) (le:3405) (re:3701) (di:direct) BACCOMGA M29691 g142708 Bacillus subtilis 1423 -11529636 215374 comgc (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:161635) (re:161931) (di:direct) BACJH642 D84432 g1303879 Bacillus subtilis 1423 -11529636 216123 comgc (fn:exogenous dna-binding (competence)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:161690) (re:161986) (di:complement) BSUB0013 Z99116 g2634905 Bacillus subtilis 1423 -11529636 169930 comgc exogenous dna-binding protein comgc:comg operon protein 3 (db:pir) D30338 D30338 Bacillus subtilis 1423 -11529636 5000689919 (de:(comgc) (pn:comg operon protein 3 precursor:comg operon protein 3 precursor) (gn:comg3) (gtcfc:13.12) (ec:) (cmg3_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comGC comGC Bacillus subtilis 1423 10007539

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760907	2185	24341	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760908	2186	24342	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760916	2187	24343	684	227

Description

6500725779 comg2:comgb probably part of the dna transport machinery:comg operon protein 2 (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comGB comGB Bacillus subtilis 1423 -11529637 64877 comgb:comg2 (de:comg operon protein 2) (db:swissprot) CMG2_BACSU P25954 BACILLUS SUBTILIS 1423 -11529637 7000684850 comgb dna transport machinery protein comgb:comg operon protein 2 (db:pir2.dat) C30338 C30338 Bacillus subtilis 1423 -11529637 7500878909 comg2 (sr:bacillus subtilis (strain 168) (clone: ped4) dna) (db:genpept-bct1) (de:bacillus subtilis (clone ped4) comg-(1,2,3,4,5,6,and 7) proteins incomg operon, complete cds.) (le:2420) (re:3391) (di:direct) BACCOMGA M29691 g142707 Bacillus subtilis 1423 -11529637 215373 comgb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:160650) (re:161621) (di:direct) BACJH642 D84432 g1303878 Bacillus subtilis 1423 -11529637 216122 comgb probably part of the dna transport machinery (fn:competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:162000) (re:162971) (di:complement) BSUB0013 Z99116 g2634906 Bacillus subtilis 1423 -11529637 169929 comgb dna transport machinery protein comgb:comg operon protein 2 (db:pir) C30338 C30338 Bacillus subtilis 1423 -11529637 5000689918 (de:(comgb) (pn:comg operon protein 2:comg operon protein 2) (gn:comg2) (gtcfc:13.12) (ec:) (cmg2_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comGB comGB Bacillus subtilis 1423 10007538

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760924	2188	24344	531	176

Description

6500725780 comg1:comga hypothetical protein:comg operon protein 1 (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comGA comGA Bacillus subtilis 1423 -11529638 64876 comga:comg1 (de:comg operon protein 1) (db:swissprot) CMG1_BACSU P25953 BACILLUS SUBTILIS 1423 -11529638 7000684849 comga late competence protein comga:comg operon protein 1 (db:pir2.dat) B30338 B30338 Bacillus subtilis 1423 -11529638 7500878908 comg1 (sr:bacillus subtilis (strain 168) (clone: ped4) dna) (db:genpept-bct1) (de:bacillus subtilis (clone ped4) comg-(1,2,3,4,5,6,and 7) proteins incomg operon, complete cds.) (le:1298) (re:2368) (di:direct) BACCOMGA M29691 g142706 Bacillus subtilis 1423 -11529638 215372 comga (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:159527) (re:160597) (di:direct) BACJH642 D84432 g1303877 Bacillus subtilis 1423 -11529638 216121 comga (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:late competence gene) (le:163024) (re:164094) (di:complement) BSUB0013 Z99116 g2634907 Bacillus subtilis 1423 -11529638 169928 comga late competence protein comga:comg operon protein 1 (db:pir) B30338 B30338 Bacillus subtilis 1423 -11529638 5000689917 (de:(comga) (pn:comg operon protein 1:comg operon protein 1) (gn:comg1) (gtcfc:13.12) (ec:) (cmg1_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comGA comGA Bacillus subtilis 1423 10007537

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760927	2189	24345	798	265

Description

6500725781 comd:comed:come4:comer hypothetical protein:come operon protein 4 (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comER comER Bacillus subtilis 1423 -11529639 7000694328 comer pyrroline-5-carboxylate reductase homolog comer:non-essential gene for competence comer (cl:pyrroline-5-carboxylate reductase) (db:pir2.dat) F69602 F69602 Bacillus subtilis 1423 -11529639 216039 comed (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:77579) (re:78400) (di:complement) BACJH642 D84432 g1303795 Bacillus subtilis 1423 -11529639 7500953852 comer (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: comd, comed; non-essential) (le:41030) (re:41851) (di:direct) BSUB0014 Z99117 g2635006 Bacillus subtilis 1423 -11529639

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760931	2190	24346	735	244

Description

6500725782 dna-binding protein:type 4 prepilin-like protein specific leader peptidase:late competence protein comc (gtcfc:13.12) (ec:3.4.99.-) (keggfc:14.1) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comC comC Bacillus subtilis 1423 -11529640 81877 comc (ec:3.4.99.-) (de:(late competence protein comc)) (db:swissprot) LEP3_BACSU P15378 BACILLUS SUBTILIS 1423 -11529640 7000685725 comc genetic transformation late competence protein comc (cl:hypothetical protein b2972) (db:pir2.dat) A33490 A33490 Bacillus subtilis 1423 -11529640 7500884915 comc late competence protein (sr:bacillus subtilis (strain is75) dna) (db:genpept-bct1) (de:bacillus subtilis late competence protein (comc) gene, completecds.) (le:819) (re:1565) (di:direct) BACCOMC M30805 g142704 Bacillus subtilis 1423 -11529640 215366 comc dna-binding protein (fn:required for the processing and translocation) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:68557) (re:69303) (di:complement) BSUB0015 Z99118 g2635272 Bacillus subtilis 1423 -11529640 170008 comc genetic transformation late competence protein comc (db:pir) A33490 A33490 Bacillus subtilis 1423 -11529640 5000689909 (de:(comc) (pn:type 4 prepilin-like protein specific leader peptidase:type 4 prepilin-like protein specific leader peptidase :late competence protein comc) (gtcfc:13.12) (ec:3.4.99.-) (lep3_bacsu) (keggfc:11.1) (bsorffc:6.6.0)) comC comC Bacillus subtilis 1423 10024111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760932	2191	24347	432	143

Description

5000689928 pheromone peptide aa 46-:competence pheromone precursor (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comX comX Bacillus subtilis 1423 -11529641 65424 comx (de:competence pheromone precursor) (db:swissprot) COMX_BACSU P45453 BACILLUS SUBTILIS 1423 -11529641 7000684870 comx competence pheromone comx precursor (db:pir2.dat) B38111 B38111 Bacillus subtilis 1423 -11529641 7500879083 comx competence pheromone precursor pheromone (fn:required for the development of genetic) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:57929) (re:58096) (di:complement) BSUB0017 Z99120 g2635665 Bacillus subtilis 1423 -11529641 169937 comx competence pheromone comx precursor (db:pir) B38111 B38111 Bacillus subtilis 1423 -11529641 6500725783 pheromone peptide aa 46-:competence pheromone precursor (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comX comX Bacillus subtilis 1423 -11529641

Jc542 U.S. PTO 09/417507 10/14/99

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760947	2192	24348	543	180

Description

GTC ORF with score 138 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid w03d2.) (nt:weak similarity to collagens; glycine- and) (le:27621:27799:27989:28126) (re:27740:27942:28069:28218) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760948	2193	24349	861	286

Description

6500725784 comf3:comfc hypothetical protein:comf operon protein 3 (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comFC comFC Bacillus subtilis 1423 -11529642 64874 comfc:comf3 (de:comf operon protein 3) (db:swissprot) CMF3_BACSU P39147 BACILLUS SUBTILIS 1423 -11529642 7000684848 comfc:comf3 late competence gene comfc (db:pir2.dat) S77621 S77621 Bacillus subtilis 1423 -11529642 7500878906 comforf3 f3 (db:genpept-bct1) (de:b.subtilis comf gene.) (le:2696) (re:3385) (di:direct) BSCOMFG Z18629 g580842 Bacillus subtilis 1423 -11529642 7500878907 comfc (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:late competence gene) (le:43095) (re:43784) (di:complement) BSUB0019 Z99122 g2636071 Bacillus subtilis 1423 -11529642 298098 comfc (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762334 Bacillus subtilis 1423 -11529642 170243 comfc:comf3 late competence gene comfc (db:pir) S77621 S77621 Bacillus subtilis 1423 -11529642 219085 comfc (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762334 Bacillus subtilis 1423 -11529642 5000689916 (de:(comfc) (pn:comf operon protein 3:comf operon protein 3) (gn:comf3) (gtcfc:13.12) (ec:) (cmf3_bacsu) (keggfc:11.2) (bsorffc:6.6.0) (db:gtc-bacillus subtilis)) comFC comFC Bacillus subtilis 1423 10007535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760950	2194	24350	669	223

Description

6500725785 comf2:comfb hypothetical protein:comf operon protein 2 (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comFB comFB Bacillus subtilis 1423 -11529643 7500878905 comfb:comf2 (de:comf operon protein 2) (db:swissprot) CMF2_BACSU P39146 BACILLUS SUBTILIS 1423 -11529643 7000684847 comfb:comf2 late competence gene comfb (db:pir2.dat) I40388 I40388 Bacillus subtilis 1423 -11529643 5000689915 comforf2 f2 (db:genpept-bct1) (de:b.subtilis comf gene.) (le:2403) (re:2699) (di:direct) BSCOMFG Z18629 g39850 Bacillus subtilis 1423 -11529643 219084 comfb (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:late competence gene) (le:43781) (re:44077) (di:complement) BSUB0019 Z99122 g2636072 Bacillus subtilis 1423 -11529643 298097 comfb (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762333 Bacillus subtilis 1423 -11529643 64873 comfb:comf2 (de:comf operon protein 2) (db:swissprot) CMF2_BACSU P39146 BACILLUS SUBTILIS 1423 -11529643 170242 comfb:comf2 late competence gene comfb (db:pir) I40388 I40388 Bacillus subtilis 1423 -11529643 220114 comfb (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762333 Bacillus subtilis 1423 -11529643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760953	2195	24351	471	156

Description

6500725786 comf1:comfa late competence protein:comf operon protein 1 (gtcfc:13.12) (keggfc:14.2) (bsorffc:6.6.1) (db:gtc-bacillus subtilis) comFA comFA Bacillus subtilis 1423 -11529644 7500878903 comfa:comf1 (de:comf operon protein 1) (db:swissprot) CMF1_BACSU P39145 BACILLUS SUBTILIS 1423 -11529644 7000684846 comfa:comf1 late competence protein required for dna uptake comfa:atp-dependent dna helicase/translocase comf1 (cl:dead/h box helicase homology) (db:pir2.dat) G69602 G69602 Bacillus subtilis 1423 -11529644 5000689914 comforf1 f1 (db:genpept-bct1) (de:b.subtilis comf gene.) (le:952) (re:2343) (di:direct) BSCOMFG Z18629 g580841 Bacillus subtilis 1423 -11529644 7500878904 comfa late competence protein (fn:required for dna uptake (competence)) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (le:44137) (re:45528) (di:complement) BSUB0019 Z99122 g2636073 Bacillus subtilis 1423 -11529644 298096 comfa (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762332 Bacillus subtilis 1423 -11529644 64872 comfa:comf1 (de:comf operon protein 1) (db:swissprot) CMF1_BACSU P39145 BACILLUS SUBTILIS 1423 -11529644 170241 comfa:comf1 late competence protein required for dna uptake comfa:atp-dependent dna helicase/translocase comf1 (cl:dead/h box helicase homology) (db:pir) G69602 G69602 Bacillus subtilis 1423 -11529644 219083 comfa (db:genpept-bct2) (de:bacillus subtilis putative transcriptional regulator (yvhj),ycr59c/yigz homolog (yvhk), histidine kinase (degs),transcriptionalregulator of degradation enzyme (degu), (degv), (comfa), (comfb),(comfc), flagellar protein (yvib), neg... BSU56901 U56901 g1762332 Bacillus subtilis 1423 -11529644

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760960	2196	24352	471	156

Description

6500725787 general stress protein:general stress protein ctc (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) ctc ctc Bacillus subtilis 1423 -11529645 7000692882 ctc general stress protein ctc (db:pir2.dat) S66082 S66082 Bacillus subtilis 1423 -11529645 7500964004 ctc expressed at the end of exponential growyh under (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:122383) (re:122997) (di:direct) BAC180K D26185 g467441 Bacillus subtilis 1423 -11529645 215041 ctc general stress protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:58781) (re:59395) (di:direct) BSUB0001 Z99104 g2632319 Bacillus subtilis 1423 -11529645 206164 ctc general stress protein ctc (db:pir) S66082 S66082 Bacillus subtilis 1423 -11529645

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760966	2197	24353	501	167

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760986	2198	24354	621	206

Description

5000689930 mecb:clpc class iii stress response related atpase:negative regulator of genetic competence (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) clpC clpC Bacillus subtilis 1423 -11529646 83391 mecb:clpc (de:negative regulator of genetic competence mecb) (db:swissprot) MECB_BACSU P37571 BACILLUS SUBTILIS 1423 -11529646 7000685814 clpc:mecb class iii stress response-related atpase clpc:adenosine triphosphatase clpc:clpa/clpb protein homolog (cl:atp-dependent clp proteinase chain a) (db:pir2.dat) I40508 I40508 Bacillus subtilis 1423 -11529646 7500885449 clpa/clpb family (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:167171) (re:169603) (di:direct) BAC180K D26185 g467474 Bacillus subtilis 1423 -11529646 215074 mecb clpc adenosine triphosphatase (fn:competence gene repressor; required for cell) (db:genpept-bct1) (de:bacillus subtilis marburg 168 clpc adenosine triphosphatase (mecb)gene, complete cds, orfx and orfy, partial cds.) (le:335) (re:2767) (di:direct) BSU02604 U02604 g442360 Bacillus subtilis 1423 -11529646 219762 clpc class iii stress response-related atpase (fn:negative regulator of late competence genes;) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: mecb) (le:103569) (re:106001) (di:direct) BSUB0001 Z99104 g2632353 Bacillus subtilis 1423 -11529646 169851 clpc:mecb class iii stress response-related atpase clpc:adenosine triphosphatase clpc:clpa/clpb protein homolog (cl:atp-dependent clp proteinase chain a) (db:pir) I40508 I40508 Bacillus subtilis 1423 -11529646 6500725788 mecb class iii stress response related atpase:negative regulator of genetic competence (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) clpC clpC Bacillus subtilis 1423 -11529646

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760988	2199	24355	309	102

Description

6500725789 ycde:rapj response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapJ rapJ Bacillus subtilis 1423 -11529647 7000694503 rapj response regulator aspartate phosphatase rapj (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) E69689 E69689 Bacillus subtilis 1423 -11529647 5500687020 rapj rapj (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:a member protein of the response-regulator) (le:17519) (re:18640) (di:direct) AB000617 AB000617 g2415733 Bacillus subtilis 1423 -11529647 7500965141 rapj response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ycde) (le:109334) (re:110455) (di:direct) BSUB0002 Z99105 g2632568 Bacillus subtilis 1423 -11529647

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501760993	2200	24356	702	233

Description

6500725790 ycll:rapc response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapC rapC Bacillus subtilis 1423 -11529648 7000694497 rapc response regulator aspartate phosphatase rapc (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) F69688 F69688 Bacillus subtilis 1423 -11529648 222641 rapc response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ycll) (le:25661) (re:26809) (di:direct) BSUB0003 Z99106 g2632678 Bacillus subtilis 1423 -11529648 7500965135 rapc response-regulator aspartate phosphatase c (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:108064) (re:109212) (di:direct) D50453 D50453 g1805447 Bacillus subtilis 1423 -11529648

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761007	2201	24357	1458	486

Description

6500725791 general stress protein:glucose starvation-inducible protein b:general stress protein b (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) gsiB gsiB Bacillus subtilis 1423 -11529649 131477 gsib general stress protein gsib:glucose starvation inducible b (cl:gsib protein) (db:pir1.dat) S26183 S26183 Bacillus subtilis 1423 -11529649 219350 gsib glucose starvation-inducible protein b general (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (le:27563) (re:27934) (di:direct) AB001488 AB001488 g1881250 Bacillus subtilis 1423 -11529649 302695 gsib (db:genpept-bct1) (de:b.subtilis gsib gene.) (le:372) (re:743) (di:direct) BSGSIB X56680 g39934 Bacillus subtilis 1423 -11529649 7500953662 gsib general stress protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:91307) (re:91678) (di:direct) BSUB0003 Z99106 g2632740 Bacillus subtilis 1423 -11529649

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761024	2202	24358	648	216

Description

6500725792 yddl:rapi response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapI rapI Bacillus subtilis 1423 -11529650 7000694502 rapi response regulator aspartate phosphatase rapi (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) D69689 D69689 Bacillus subtilis 1423 -11529650 302756 yddl (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable protein asp-phosphatase.) (le:80542) (re:81717) (di:direct) AB001488 AB001488 g1881311 Bacillus subtilis 1423 -11529650 7500965140 rapi response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: yddl) (le:144287) (re:145462) (di:direct) BSUB0003 Z99106 g2632801 Bacillus subtilis 1423 -11529650

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761033	2203	24359	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761040	2204	24360	681	227

Description

6500725793 regulator of the activity of phosphatase rapi (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) phrI phrI Bacillus subtilis 1423 -11529651 7000694397 phri phosphatase rapi regulator phri (db:pir2.dat) E69677 E69677 Bacillus subtilis 1423 -11529651 7500965063 phri regulator of the activity of phosphatase rapi (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:145419) (re:145538) (di:direct) BSUB0003 Z99106 g2632802 Bacillus subtilis 1423 -11529651

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761055	2205	24361	279	92

Description

5000689030 cold-shock protein:cold shock protein cspc (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) cspC cspC Bacillus subtilis 1423 -11529652 66660 cspc (de:cold shock protein cspc) (db:swissprot) CSPC_BACSU P39158 BACILLUS SUBTILIS 1423 -11529652 7000684923 cspc cold shock protein cspc (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) E69608 E69608 Bacillus subtilis 1423 -11529652 215436 cspc cold shock protein (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:conserved in many organisms.) (le:92483) (re:92683) (di:direct) AB001488 AB001488 g1881321 Bacillus subtilis 1423 -11529652 302766 cspc cold shock protein (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis cspc gene for cold shock protein, partial cds.) (le:49) (re:247) (di:direct) BACCSPC D25230 g1230546 Bacillus subtilis 1423 -11529652 5500684522 cspc cold-shock protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:156228) (re:156428) (di:direct) BSUB0003 Z99106 g2632812 Bacillus subtilis 1423 -11529652 7500879492 cspc cold shock protein c (db:genpept-bct2) (de:bacillus subtilis cold shock protein c (cspc) gene, complete cds.) (nt:cspc; rna-binding protein) (le:1067) (re:1267) (di:direct) BSU92976 U92976 g2393787 Bacillus subtilis 1423 -11529652 6500725794 cold-shock protein:cold shock protein cspc (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) cspC cspC Bacillus subtilis 1423 -11529652

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761240	2206	24362	837	279

Description

6500725795 nuclease inhibitor:dinb protein (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) dinB dinB Bacillus subtilis 1423 -11529653 68660 dinb (de:dinb protein) (db:swissprot) DINB_BACSU Q02886 BACILLUS SUBTILIS 1423 -11529653 7000685050 dinb nuclease inhibitor dinb:hypothetical protein dna damage-inducible b7 promoter region (cl:nuclease inhibitor dinb) (db:pir2.dat) F69615 F69615 Bacillus subtilis 1423 -11529653 302814 dinb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:dna damage-inducible dinb protein, similar product) (le:141465) (re:141983) (di:complement) AB001488 AB001488 g1881369 Bacillus subtilis 1423 -11529653 6000686386 dinb nuclease inhibitor (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:205211) (re:205729) (di:complement) BSUB0003 Z99106 g2632863 Bacillus subtilis 1423 -11529653 7500880321 dinb nuclease inhibitor (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:7261) (re:7779) (di:complement) BSUB0004 Z99107 g2632876 Bacillus subtilis 1423 -11529653

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761257	2207	24363	672	224

Description

6500725796 yeeh:yzqa:raph response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapH rapH Bacillus subtilis 1423 -11529654 7000694501 raph response regulator aspartate phosphatase raph (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) C69689 C69689 Bacillus subtilis 1423 -11529654 7500965139 raph response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yeeh, yzqa) (le:149760) (re:151055) (di:direct) BSUB0004 Z99107 g2632997 Bacillus subtilis 1423 -11529654

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761260	2208	24364	489	163

Description

6500725797 yfhn:csbb stress response protein:csbb protein (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) csbB csbB Bacillus subtilis 1423 -11529655 120138 csbb (de:csbb protein) (db:swissprot) CSBB_BACSU Q45539 BACILLUS SUBTILIS 1423 -11529655 7000684911 csbb stress response protein csbb (cl:stress response protein csbb) (db:pir2.dat) JC5173 JC5173 Bacillus subtilis 1423 -11529655 7500879442 csbb (db:genpept-bct1) (de:bacillus subtilis csbb gene, complete cds.) (nt:similar to hypothetical protein from synechocystis) (le:310) (re:1299) (di:direct) BACCSBB L77099 g1387979 Bacillus subtilis 1423 -11529655 215435 csbb stress response protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yfhn) (le:127505) (re:128494) (di:direct) BSUB0005 Z99108 g2633183 Bacillus subtilis 1423 -11529655 7000684912 yfhn (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:20396) (re:21385) (di:direct) D85082 D85082 g2804544 Bacillus subtilis 1423 -11529655 1500686915 csbb stress response protein csbb (db:pir) JC5173 JC5173 Bacillus subtilis 1423 -11529655

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761267	2209	24365	999	332

Description

5000689029 major cold-shock protein:cold shock protein cspb:major cold shock protein (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) cspB cspB Bacillus subtilis 1423 -11529656 218972 cspb:cspa (de:cold shock protein cspb (major cold shock protein)) (db:swissprot) CSPB_BACSU P32081 BACILLUS SUBTILIS 1423 -11529656 7000684922 cspb major cold shock protein cspb (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) A45723 A45723 Bacillus subtilis 1423 -11529656 308488 cspb cold shock protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:see embl x59715) (le:5145) (re:5348) (di:complement) BS75DGREG X96983 g1239985 Bacillus subtilis 1423 -11529656 220133 cspb cold shock protein cspb (db:genpept-bct1) (de:b.subtilis cspb gene for cold shock protein.) (le:269) (re:472) (di:direct) BSCSPBG X59715 g297761 Bacillus subtilis 1423 -11529656 219105 cspb cold shock protein cspb (fn:ss-dna binding; rna binding) (sr:bacillus subtilis strain=jh642) (db:genpept-bct1) (de:bacillus subtilis putative lipoprotein and cold shock protein cspb(cspb) genes, complete cds, and orf1 gene, partial cds.) (nt:similar to y-box protein) (le:1868... BSU58859 U58859 g1336658 Bacillus subtilis 1423 -11529656 6500725798 cspb major cold-shock protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:180951) (re:181154) (di:complement) BSUB0005 Z99108 g2633233 Bacillus subtilis 1423 -11529656 66658 cspb:cspa (de:cold shock protein cspb (major cold shock protein)) (db:swissprot) CSPB_BACSU P32081 BACILLUS SUBTILIS 1423 -11529656 152149 cspb major cold shock protein cspb (cl:major cold shock protein:cold shock domain homology) (db:pir) A45723 A45723 Bacillus subtilis 1423 -11529656

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761278	2210	24366	435	144

Description

6500725799 gsiaa:spo0l:rapa response regulator aspartate phosphatase:glucose starvation-inducible protein a (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapA rapA Bacillus subtilis 1423 -11529657 7000694495 rapa:gsiaa response regulator aspartate phosphatase rapa:gsiaa protein (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) D69688 D69688 Bacillus subtilis 1423 -11529657 6000689463 rapa aspartate phosphatase of the phosphorelay (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (le:5... AF034138 AF034138 g2645863 Bacillus subtilis 1423 -11529657 7500965134 rapa response regulator aspartate phosphatase (fn:prevents sporulation by dephosphorylating) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: gsiaa, spo0l) (le:120948) (re:122084) (di:direct) BSUB0007 Z99110 g2633597 Bacillus subtilis 1423 -11529657

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761279	2211	24367	465	155

Description

6500725800 ymfo:yzlb:cina competence-damage inducible protein:putative competence-damage protein (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) cinA cinA Bacillus subtilis 1423 -11529658 64632 cina (de:putative competence-damage protein) (db:swissprot) CINA_BACSU P46323 BACILLUS SUBTILIS 1423 -11529658 7000684817 cina competence-damage inducible protein cina (db:pir2.dat) E69599 E69599 Bacillus subtilis 1423 -11529658 220106 cina cina (fn:putative competence-damage inducible function) (db:genpept-bct1) (de:bacillus subtilis cina gene, complete cds, and reca gene, partialcds.) (nt:similar to s. pneumoniae cina) (le:266) (re:1516) (di:direct) BSU56238 U56238 g1314847 Bacillus subtilis 1423 -11529658 7500878752 cina competence-damage inducible protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymfo, yzlb) (le:164172) (re:165422) (di:direct) BSUB0009 Z99112 g2634065 Bacillus subtilis 1423 -11529658 5000689068 (de:(cina) (pn:putative competence-damage protein) (gtcfc:13.07) (ec:) (cina_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) cinA cinA Bacillus subtilis 1423 10007294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761287	2212	24368	321	106

Description

6500725801 yobg:rapk response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapK rapK Bacillus subtilis 1423 -11529659 7000694504 rapk response regulator aspartate phosphatase rapk (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) F69689 F69689 Bacillus subtilis 1423 -11529659 5500701890 yobg yobg (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis gsia glucose starvation) (le:42144) (re:43259) (di:direct) AF027868 AF027868 g2619005 Bacillus subtilis 1423 -11529659 7500965142 rapk response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yobg) (le:61235) (re:62350) (di:direct) BSUB0011 Z99114 g2634284 Bacillus subtilis 1423 -11529659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761288	2213	24369	390	130

Description

6500725802 regulator of the activity of phosphatase rapk (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) phrK phrK Bacillus subtilis 1423 -11529660 7000694398 phrk phosphatase rapk regulator phrk (db:pir2.dat) F69677 F69677 Bacillus subtilis 1423 -11529660 7500965064 phrk regulator of the activity of phosphatase rapk (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:62347) (re:62469) (di:direct) BSUB0011 Z99114 g2634285 Bacillus subtilis 1423 -11529660

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761304	2214	24370	189	63

Description

5000689072 cold-shock protein:cold shock protein cspd (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) cspD cspD Bacillus subtilis 1423 -11529661 66662 cspd (de:cold shock protein cspd) (db:swissprot) CSPD_BACSU P51777 BACILLUS SUBTILIS 1423 -11529661 7000684924 cspd cold shock protein cspd (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) F69608 F69608 Bacillus subtilis 1423 -11529661 217086 cspd cold-shock protein (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:81.5% identity to the bacillus subtilis cold-shock) (le:13345) (re:13545) (di:complement) BACYACA L77246 g1256629 Bacillus subtilis 1423 -11529661 7500879493 cspd cold-shock protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:111607) (re:111807) (di:direct) BSUB0012 Z99115 g2634613 Bacillus subtilis 1423 -11529661 6500725803 cold-shock protein:cold shock protein cspd (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) cspD cspD Bacillus subtilis 1423 -11529661

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761306	2215	24371	228	75

Description

6500725804 yqfe:phoh phosphate starvation-induced protein:phoh protein homolog (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) phoH phoH Bacillus subtilis 1423 -11529662 89636 phoh (de:phoh-like protein) (db:swissprot) PHOL_BACSU P46343 BACILLUS SUBTILIS 1423 -11529662 7000686137 phoh phosphate starvation-induced protein phoh (cl:phosphate starvation-induced protein) (db:pir2.dat) E69676 E69676 Bacillus subtilis 1423 -11529662 216065 yqfe (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:104150) (re:105109) (di:direct) BACJH642 D84432 g1303821 Bacillus subtilis 1423 -11529662 7500888043 phoh phosphate starvation-induced protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqfe) (le:14321) (re:15280) (di:complement) BSUB0014 Z99117 g2634980 Bacillus subtilis 1423 -11529662 5000689039 (de:(phoh) (pn:phoh protein homolog:fragment) (gtcfc:13.02) (ec:) (phoh_bacsu) (keggfc:11.2) (bsorffc:7.1.0) (db:gtc-bacillus subtilis)) phoH phoH Bacillus subtilis 1423 10031758

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761311	2216	24372	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761316	2217	24373	570	190

Description

5000689671 yqch:rape response regulator aspartate phosphatase:hypothetical 44.6 kd protein in cwla-cisa intergenic region:orf5 (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapE rapE Bacillus subtilis 1423 -11529663 115842 rape (de:response regulator aspartate phosphatase) (db:swissprot) RAPE_BACSU P45943 BACILLUS SUBTILIS 1423 -11529663 7000688338 rape response regulator aspartate phosphatase rape (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) H69688 H69688 Bacillus subtilis 1423 -11529663 216017 yqch (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:59270) (re:60397) (di:complement) BACJH642 D84432 g1303773 Bacillus subtilis 1423 -11529663 216804 orf5 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (nt:similarity to gsiaa protein) (le:41025) (re:42152) (di:complement) BACSKIN D32216 g1217880 Bacillus subtilis 1423 -11529663 7500889369 rape response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqch) (le:59033) (re:60160) (di:direct) BSUB0014 Z99117 g2635028 Bacillus subtilis 1423 -11529663 6500725805 yqch response regulator aspartate phosphatase:hypothetical 44.6 kd protein in cwla-cisa intergenic region:orf5 (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapE rapE Bacillus subtilis 1423 -11529663

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761322	2218	24374	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761330	2219	24375	447	148

Description

5000689040 hypothetical protein:dna repair protein radc homolog:orfb (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) ysxA ysxA Bacillus subtilis 1423 -11529664 92959 ysxa (de:dna repair protein radc homolog (orfb)) (db:swissprot) RADC_BACSU Q02170 BACILLUS SUBTILIS 1423 -11529664 7000686266 ysxa dna repair protein homolog ysxa (cl:dna repair protein radc) (db:pir2.dat) B45239 B45239 Bacillus subtilis 1423 -11529664 7500889341 orfb (sr:bacillus subtilis (sub_strain py79, strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orfa, orfb, mreb, mrec, mred, minc, and mindgenes, complete coding regions.) (nt:homologous to e. coli radc gene product and to) (le:762) (re:1457) (di:di... BACDIVREG M96343 g142854 Bacillus subtilis 1423 -11529664 215541 (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis maf gene, complete cds; orfb, complete cds; mrebgene, 5' end.) (nt:putative) (le:1557) (re:2252) (di:direct) BACMAFMREB L08793 g143162 Bacillus subtilis 1423 -11529664 216305 ysxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (nt:similar to dna repair protein) (le:65971) (re:66666) (di:complement) BSUB0015 Z99118 g2635269 Bacillus subtilis 1423 -11529664 170233 ysxa dna repair protein homolog ysxa (db:pir) B45239 B45239 Bacillus subtilis 1423 -11529664 6500725806 hypothetical protein:dna repair protein radc homolog:orfb (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) ysxA ysxA Bacillus subtilis 1423 -11529664

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761335	2220	24376	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761337	2221	24377	873	290

Description

6500725807 carbon starvation-induced protein:carbon starvation protein a homolog (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) cstA cstA Bacillus subtilis 1423 -11529665 5500685029 csta (de:carbon starvation protein a homolog) (db:swissprot) CSTA_BACSU P94532 BACILLUS SUBTILIS 1423 -11529665 7000684930 csta carbon starvation-induced protein csta (cl:carbon starvation protein) (db:pir2.dat) A69609 A69609 Bacillus subtilis 1423 -11529665 220299 csta carbon starvation-induced protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.) (le:140354) (re:142150) (di:complement) BSUB0015 Z99118 g2635336 Bacillus subtilis 1423 -11529665 304172 csta carbon starvation induced protein (db:genpept-bct1) (de:b.subtilis genomic sequence 89009bp.) (nt:homology to csta of escherichia coli; identified by) (le:27757) (re:29553) (di:direct) BSZ75208 Z75208 g1770023 Bacillus subtilis 1423 -11529665

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761348	2222	24378	600	199

Description

5000689467 metalloregulation dna-binding stress protein:mrga protein (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) mrgA mrgA Bacillus subtilis 1423 -11529666 84216 mrga (de:metalloregulation dna-binding stress protein) (db:swissprot) MRGA_BACSU P37960 BACILLUS SUBTILIS 1423 -11529666 7000685870 mrga metal-regulated protein mrga:metalloregulation dna-binding stress protein mrga (cl:hypothetical protein hi1349) (db:pir2.dat) G69660 G69660 Bacillus subtilis 1423 -11529666 216362 mrga mrga (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis mrga (mrga) gene, complete cds and orf, partialcds.) (le:467) (re:928) (di:direct) BACMRGA L19547 g852076 Bacillus subtilis 1423 -11529666 6000684907 mrga metalloregulation dna-binding stress protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.) (le:185624) (re:186085) (di:direct) BSUB0017 Z99120 g2635795 Bacillus subtilis 1423 -11529666 7500885870 mrga (db:genpept-bct1) (de:b.subtilis genomic dna fragment from citg to yirg.) (le:5719) (re:6180) (di:complement) BSZ93941 Z93941 g2624001 Bacillus subtilis 1423 -11529666 6500725808 metalloregulation dna-binding stress protein:mrga protein (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) mrgA mrgA Bacillus subtilis 1423 -11529666

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761353	2223	24379	339	112

Description

6500725809 ywpa:rapd response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapD rapD Bacillus subtilis 1423 -11529667 7000694498 rapd response regulator aspartate phosphatase rapd (db:pir2.dat) G69688 G69688 Bacillus subtilis 1423 -11529667 220403 rapd response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: ywpa) (le:146314) (re:147378) (di:direct) BSUB0019 Z99122 g2636163 Bacillus subtilis 1423 -11529667 7500965136 rapd (db:genpept-bct1) (de:b.subtilis mbl, flh(o,p), rapd, ywp(b,c,d,e,f,g,h,i,j) and ywqagenes.) (nt:similar to phosphatases) (le:1943) (re:3007) (di:complement) BSZ83337 Z83337 g1763702 Bacillus subtilis 1423 -11529667

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761359	2224	24380	1221	407

Description

6500725810 spo0p:ywme:rapb response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapB rapB Bacillus subtilis 1423 -11529668 7000694496 rapb response regulator aspartate phosphatase rapb (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) E69688 E69688 Bacillus subtilis 1423 -11529668 219034 rapb aspartyl-phosphate phosphatases (db:genpept-bct1) (de:b.subtilis atpc gene.) (le:9069) (re:10202) (di:direct) BSATPC Z81356 g1648857 Bacillus subtilis 1423 -11529668 304087 rapb response regulator aspartate phosphatase (fn:dephosphorylates spo0f-p) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:alternate gene name: spo0p, ywme) (le:172965) (re:174098) (di:complement) BSUB0019 Z99122 g2636194 Bacillus subtilis 1423 -11529668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761376	2225	24381	372	123

Description

6500725811 ywhj:rapf response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapF rapF Bacillus subtilis 1423 -11529669 7000694499 rapf response regulator aspartate phosphatase rapf (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) A69689 A69689 Bacillus subtilis 1423 -11529669 7500965137 rapf unknown:highly similar to b. subtilis rapa and (db:genpept-bct1) (de:b.subtilis thrz downstream chromosomal region.) (le:8915) (re:10060) (di:complement) BSTHRZ Z80360 g1565245 Bacillus subtilis 1423 -11529669 219710 rapf response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ywhj) (le:46654) (re:47799) (di:direct) BSUB0020 Z99123 g2636282 Bacillus subtilis 1423 -11529669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761377	2226	24382	231	76

Description

6500725812 ipa-12d:ywag:gspa general stress protein:general stress protein a (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) gspA gspA Bacillus subtilis 1423 -11529670 7500882804 gspa:ipa-12d (de:general stress protein a) (db:swissprot) GSPA_BACSU P25148 BACILLUS SUBTILIS 1423 -11529670 7000685461 gspa general stress protein gspa (db:pir2.dat) S16423 S16423 Bacillus subtilis 1423 -11529670 5000689035 ipa-12d (db:genpept-bct1) (de:b.subtilis genomic region (325 to 333).) (le:12145) (re:13005) (di:direct) BSGENR X73124 g580866 Bacillus subtilis 1423 -11529670 219249 gspa general stress protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (nt:alternate gene name: ipa-12d, ywag) (le:144954) (re:145814) (di:complement) BSUB0020 Z99123 g2636378 Bacillus subtilis 1423 -11529670 74686 gspa:ipa-12d (de:general stress protein a) (db:swissprot) GSPA_BACSU P25148 BACILLUS SUBTILIS 1423 -11529670 170197 gspa general stress protein gspa (db:pir) S16423 S16423 Bacillus subtilis 1423 -11529670

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761581	2227	24383	525	174

Description

6500725813 yycm:rapg response regulator aspartate phosphatase (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) rapG rapG Bacillus subtilis 1423 -11529671 7000694500 rapg response regulator aspartate phosphatase rapg (cl:response regulator aspartate phosphatase rapa) (db:pir2.dat) B69689 B69689 Bacillus subtilis 1423 -11529671 7500965138 rapg response regulator aspartate phosphatase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yycm) (le:140189) (re:141286) (di:direct) BSUB0021 Z99124 g2636577 Bacillus subtilis 1423 -11529671

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761582	2228	24384	444	147

Description

6500725814 yycl:phrg regulator of the activity of phosphatase rapg (gtcfc:13.2) (keggfc:14.2) (bsorffc:7.1.1) (db:gtc-bacillus subtilis) phrG phrG Bacillus subtilis 1423 -11529672 7000694396 phrg phosphatase rapg regulator phrg (db:pir2.dat) D69677 D69677 Bacillus subtilis 1423 -11529672 7500965062 phrg regulator of the activity of phosphatase rapg (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: yycl) (le:141287) (re:141403) (di:direct) BSUB0021 Z99124 g2636578 Bacillus subtilis 1423 -11529672

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761584	2229	24385	492	163

Description

6500725815 coml:srfa1:srfa:srfaa surfactin synthetase:surfactin synthetase subunit 1 (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) srfAA srfAA Bacillus subtilis 1423 -11529673 7000694632 srfaa:srfa1 surfactin synthetase component i:competence protein srfaa:surfactin production protein srfaa:surfactin synthetase srfa1 (cl:surfactin synthetase:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) I40485 I40485 Bacillus subtilis 1423 -11529673 7500955889 srfa1 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (le:1) (re:10767) (di:direct) BSSRFAP X70356 g396481 Bacillus subtilis 1423 -11529673 219680 srfaa surfactin synthetase (fn:surfactin production and competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: coml) (le:181887) (re:192653) (di:direct) BSUB0002 Z99105 g2632634 Bacillus subtilis 1423 -11529673 222614 srfaa surfactin production (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:56190) (re:66956) (di:direct) D50453 D50453 g1805420 Bacillus subtilis 1423 -11529673 170596 srfaa:srfa1 surfactin synthetase / competence protein srfaa:surfactin synthetase srfa1 (cl:surfactin synthetase:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir) I40485 I40485 Bacillus subtilis 1423 -11529673

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761599	2230	24386	1197	399

Description

6500725816 coml:srfab surfactin synthetase (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) srfAB srfAB Bacillus subtilis 1423 -11529674 219681 srfab:srfa2:coml (de:surfactin synthetase subunit 2) (db:swissprot) SRF2_BACSU Q04747 BACILLUS SUBTILIS 1423 -11529674 170597 srfab:srfa2 surfactin synthetase component ii:surfactin synthetase srfa2:surfactin synthetase/competence protein srfab (cl:surfactin synthetase:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) I40486 I40486 Bacillus subtilis 1423 -11529674 7500892071 srfa2 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (le:10780) (re:21543) (di:direct) BSSRFAP X70356 g396482 Bacillus subtilis 1423 -11529674 222615 srfab surfactin synthetase (fn:surfactin production and competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: coml) (le:192666) (re:203429) (di:direct) BSUB0002 Z99105 g2632635 Bacillus subtilis 1423 -11529674 7502851634 srfab surfactin production (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:66969) (re:77732) (di:direct) D50453 D50453 g1805421 Bacillus subtilis 1423 -11529674 7500892070 srfab:srfa2:coml (de:surfactin synthetase subunit 2) (db:swissprot) SRF2_BACSU Q04747 BACILLUS SUBTILIS 1423 -11529674 7000694664 srfab:srfa2 surfactin synthetase / competence protein srfab:surfactin synthetase srfa2 (cl:acyl carrier protein homology:acetate--coa ligase homology:gramicidin s synthetase i repeat homology) (db:pir) I40486 I40486 Bacillus subtilis 1423 -11529674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761601	2231	24387	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761602	2232	24388	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761609	2233	24389	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761627	2234	24390	351	116

Description

6500725817 coml:srfa3:srfac surfactin synthetase:surfactin synthetase subunit 3 (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) srfAC srfAC Bacillus subtilis 1423 -11529675 7500892072 srfac:srfa3 (de:surfactin synthetase subunit 3) (db:swissprot) SRF3_BACSU Q08787 BACILLUS SUBTILIS 1423 -11529675 7000686676 srfac:srfa3 surfactin synthetase / competence protein srfac:surfactin synthetase srfa3 (cl:peptide synthetase ppse:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) I40487 I40487 Bacillus subtilis 1423 -11529675 5000689064 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (nt:srfa3) (le:21580) (re:25404) (di:direct) BSSRFAP X70356 g396483 Bacillus subtilis 1423 -11529675 219682 srfac surfactin synthetase (fn:surfactin production and competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: coml) (le:203466) (re:207290) (di:direct) BSUB0002 Z99105 g2632637 Bacillus subtilis 1423 -11529675 222617 srfac surfactin production (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:77769) (re:81593) (di:direct) D50453 D50453 g1805423 Bacillus subtilis 1423 -11529675 99453 srfac:srfa3 (de:surfactin synthetase subunit 3) (db:swissprot) SRF3_BACSU Q08787 BACILLUS SUBTILIS 1423 -11529675 170598 srfac:srfa3 surfactin synthetase / competence protein srfac:surfactin synthetase srfa3 (cl:peptide synthetase ppse:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir) I40487 I40487 Bacillus subtilis 1423 -11529675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761638	2235	24391	558	185

Description

6500725818 coml:srfa4:srfad surfactin synthetase:surfactin synthetase subunit 4 (gtcfc:13.3) (ec:3.1.2.-) (keggfc:14.1) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) srfAD srfAD Bacillus subtilis 1423 -11529676 7000686677 srfad:srfa4 surfactin synthetase / competence protein srfad:surfactin synthetase srfa4 (cl:oleoyl-(acyl-carrier-protein) hydrolase:oleoyl-(acyl-carrier-protein) hydrolase homology) (db:pir2.dat) I40488 I40488 Bacillus subtilis 1423 -11529676 7500965246 srfa4 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (le:25433) (re:26161) (di:direct) BSSRFAP X70356 g396484 Bacillus subtilis 1423 -11529676 7500965247 srfad surfactin synthetase (fn:surfactin production and competence) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: coml) (le:207319) (re:208047) (di:direct) BSUB0002 Z99105 g2632638 Bacillus subtilis 1423 -11529676 222618 srfad surfactin production (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:81622) (re:82350) (di:direct) D50453 D50453 g1805424 Bacillus subtilis 1423 -11529676 219683 srfad surfactin production (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:81622) (re:82350) (di:direct) D50453 D50453 g1805424 Bacillus subtilis 1423 -11529676 99454 srf4_bacsu (de:surfactin synthetase subunit 4 (ec 3.1.2.-).) Q08788 Q08788 Bacillus subtilis 1423 -11529676 5000689065 (de:(srfad) (pn:surfactin synthetase subunit 4) (gn:srfa4) (gtcfc:13.03) (ec:3.1.2.-) (srf4_bacsu) (keggfc:11.1) (bsorffc:7.3.0) (db:gtc-bacillus subtilis)) srfAD srfAD Bacillus subtilis 1423 10041312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761641	2236	24392	1215	405

Description

6500725819 surfactin (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) sfp sfp Bacillus subtilis 1423 -11529677 6000690105 sfp surfactin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:212572) (re:213069) (di:complement) BSUB0002 Z99105 g2632643 Bacillus subtilis 1423 -11529677 7500965181 sfp surfactin (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:4472) (re:4969) (di:complement) BSUB0003 Z99106 g2632658 Bacillus subtilis 1423 -11529677 7000694582 sfp siderophore biosynthesis regulatory protein sfp 0 (db:pir) F69705 F69705 Bacillus subtilis 1423 -11529677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761654	2237	24393	726	241

Description

6500725820 hypothetical protein:putative polyketide beta-ketoacyl synthase (gtcfc:13.3) (ec:2.3.1.-) (keggfc:14.1) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksF pksF Bacillus subtilis 1423 -11529678 89886 pksf (ec:2.3.1.-) (de:putative polyketide beta-ketoacyl synthase,) (db:swissprot) PKSF_BACSU P40804 BACILLUS SUBTILIS 1423 -11529678 7000686146 pksf involved in polyketide synthesis pksf (cl:3-oxoacyl-(acyl-carrier-protein) synthase i homology) (db:pir2.dat) D69678 D69678 Bacillus subtilis 1423 -11529678 219783 unknown (db:genpept-bct1) (de:bacillus subtilis w168 polyketide synthase (pksx and pksorfx6)genes, complete cds.) (nt:pksorfx1; similar to rhizobium leguminosarum) (le:795) (re:2045) (di:direct) BSU11039 U11039 g602657 Bacillus subtilis 1423 -11529678 6000685003 pksf (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:189560) (re:190810) (di:direct) BSUB0009 Z99112 g2634084 Bacillus subtilis 1423 -11529678 7500888135 pksf (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:6780) (re:8030) (di:direct) BSUB0010 Z99113 g2634096 Bacillus subtilis 1423 -11529678 5000688375 (de:(pksf) (pn:putative polyketide beta-ketoacyl synthase) (gtcfc:1.11:5.12:5.13:6.08:6.14:6.16:7.01) (ec:2.3.1.-) (pksf_bacsu) (keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7:6.9:8.1) (bsorffc:7.3.0) (db:gtc-bacillus subtilis)) pksF pksF Bacillus subtilis 1423 10032006

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761668	2238	24394	768	255

Description

5000689051 hypothetical protein:putative polyketide biosynthesis protein pksg (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksG pksG Bacillus subtilis 1423 -11529679 89887 pksg (de:putative polyketide biosynthesis protein pksg) (db:swissprot) PKSG_BACSU P40830 BACILLUS SUBTILIS 1423 -11529679 7000686147 pksg involved in polyketide synthesis pksg (db:pir2.dat) E69678 E69678 Bacillus subtilis 1423 -11529679 219784 unknown (db:genpept-bct1) (de:bacillus subtilis w168 polyketide synthase (pksx and pksorfx6)genes, complete cds.) (nt:pksorfx2; similar to hamster) (le:2270) (re:3307) (di:direct) BSU11039 U11039 g528991 Bacillus subtilis 1423 -11529679 6000685005 pksg (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:191035) (re:192072) (di:direct) BSUB0009 Z99112 g2634085 Bacillus subtilis 1423 -11529679 7500888136 pksg (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:8255) (re:9292) (di:direct) BSUB0010 Z99113 g2634097 Bacillus subtilis 1423 -11529679 6500725821 hypothetical protein:putative polyketide biosynthesis protein pksg (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksG pksG Bacillus subtilis 1423 -11529679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761669	2239	24395	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761671	2240	24396	456	151

Description

5000689052 hypothetical protein:putative polyketide biosynthesis enoyl-coa hydratase homolog pksh (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksH pksH Bacillus subtilis 1423 -11529680 89888 pksh (de:putative polyketide biosynthesis enoyl-coa hydratase homolog pksh) (db:swissprot) PKSH_BACSU P40805 BACILLUS SUBTILIS 1423 -11529680 7000686148 pksh involved in polyketide synthesis pksh (db:pir2.dat) F69678 F69678 Bacillus subtilis 1423 -11529680 219785 unknown (db:genpept-bct1) (de:bacillus subtilis w168 polyketide synthase (pksx and pksorfx6)genes, complete cds.) (nt:pksorfx3; similar to rhodobacter capsulatus) (le:3295) (re:4074) (di:direct) BSU11039 U11039 g528992 Bacillus subtilis 1423 -11529680 6000685007 pksh (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:192060) (re:192839) (di:direct) BSUB0009 Z99112 g2634086 Bacillus subtilis 1423 -11529680 7500888137 pksh (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:9280) (re:10059) (di:direct) BSUB0010 Z99113 g2634098 Bacillus subtilis 1423 -11529680 6500725822 hypothetical protein:putative polyketide biosynthesis enoyl-coa hydratase homolog pksh (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksH pksH Bacillus subtilis 1423 -11529680

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761674	2241	24397	993	331

Description

GTC ORF with score 266 to: (fn:catalyzes the first methylation step from pe to) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe phosphatidylethanolaminemethyltransferase (cho2+) gene, complete cds.) (nt:cho2p) (le:1018) (re:3348) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761676	2242	24398	462	154

Description

GTC ORF with score 388 to: (fn:enzyme; energy metabolism, carbon:) (db:genpept-bct2) (ec:1.1.1.28) (de:escherichia coli k-12 mg1655 section 125 of 400 of the completegenome.) (nt:f329; 100 pct identical to ldhd_ecoli sw: p52643;) (le:832) (re:1821) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761686	2243	24399	330	109

Description

5000689053 hypothetical protein:putative polyketide biosynthesis enoyl-coa hydratase homolog pksi (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksI pksI Bacillus subtilis 1423 -11529681 89889 pksi (de:putative polyketide biosynthesis enoyl-coa hydratase homolog pksi) (db:swissprot) PKSI_BACSU P40802 BACILLUS SUBTILIS 1423 -11529681 7000686149 pksi involved in polyketide synthesis pksi (db:pir2.dat) G69678 G69678 Bacillus subtilis 1423 -11529681 219786 unknown (db:genpept-bct1) (de:bacillus subtilis w168 polyketide synthase (pksx and pksorfx6)genes, complete cds.) (nt:pksorfx4; similar to rhodobacter capsulatus) (le:4114) (re:4863) (di:direct) BSU11039 U11039 g528993 Bacillus subtilis 1423 -11529681 6000685009 pksi (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:192879) (re:193628) (di:direct) BSUB0009 Z99112 g2634087 Bacillus subtilis 1423 -11529681 7500888138 pksi (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:10099) (re:10848) (di:direct) BSUB0010 Z99113 g2634099 Bacillus subtilis 1423 -11529681 6500725823 hypothetical protein:putative polyketide biosynthesis enoyl-coa hydratase homolog pksi (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksI pksI Bacillus subtilis 1423 -11529681

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761687	2244	24400	624	208

Description

5000689054 hypothetical protein:putative polyketide biosynthesis protein pksj (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksJ pksJ Bacillus subtilis 1423 -11529682 89890 pksj (de:putative polyketide biosynthesis protein pksj) (db:swissprot) PKSJ_BACSU P40806 BACILLUS SUBTILIS 1423 -11529682 7000686150 pksj involved in polyketide synthesis pksj (db:pir2.dat) H69678 H69678 Bacillus subtilis 1423 -11529682 219787 unknown (db:genpept-bct1) (de:bacillus subtilis w168 polyketide synthase (pksx and pksorfx6)genes, complete cds.) (nt:pksorfx5; similar to bacillus brevis gramicidin s) (le:4908) (re:6581) (di:direct) BSU11039 U11039 g528994 Bacillus subtilis 1423 -11529682 6000685011 pksj (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:193673) (re:195346) (di:direct) BSUB0009 Z99112 g2634088 Bacillus subtilis 1423 -11529682 7500888139 pksj (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:10893) (re:12566) (di:direct) BSUB0010 Z99113 g2634100 Bacillus subtilis 1423 -11529682 6500725824 hypothetical protein:putative polyketide biosynthesis protein pksj (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) pksJ pksJ Bacillus subtilis 1423 -11529682

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761693	2245	24401	273	90

Description

6500725825 peptide synthetase (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) ppsC ppsC Bacillus subtilis 1423 -11529683 7000694359 ppsc:pps3 peptide synthetase ppsc:peptide synthetase 3 (cl:peptide synthetase ppsd:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) C69681 C69681 Bacillus subtilis 1423 -11529683 219525 pps3 peptide-synthetase orf3 (db:genpept-bct1) (de:b.subtilis genes for peptide synthetase and penicillin bindingprotein.) (le:17430) (re:25097) (di:direct) BSPEPSYN Z34883 g1805668 Bacillus subtilis 1423 -11529683 7500954530 ppsc peptide synthetase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:192936) (re:200603) (di:complement) BSUB0010 Z99113 g2634215 Bacillus subtilis 1423 -11529683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761694	2246	24402	516	171

Description

6500725826 pps2:ppsb peptide synthetase:peptide synthetase 2 (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) ppsB ppsB Bacillus subtilis 1423 -11529684 7500888377 ppsb:pps2 (de:peptide synthetase 2) (db:swissprot) PPS2_BACSU P39846 BACILLUS SUBTILIS 1423 -11529684 7000686167 ppsb:pps2 peptide synthetase ppsb:pps2 (cl:peptide synthetase ppsd:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) I40457 I40457 Bacillus subtilis 1423 -11529684 5000689059 pps2 peptide synthetase orf2 (db:genpept-bct1) (de:b.subtilis genes for peptide synthetase and penicillin bindingprotein.) (le:9731) (re:17413) (di:direct) BSPEPSYN Z34883 g509469 Bacillus subtilis 1423 -11529684 219524 ppsb peptide synthetase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:200620) (re:208302) (di:complement) BSUB0010 Z99113 g2634216 Bacillus subtilis 1423 -11529684 90815 ppsb:pps2 (de:peptide synthetase 2) (db:swissprot) PPS2_BACSU P39846 BACILLUS SUBTILIS 1423 -11529684 170431 ppsb:pps2 peptide synthetase ppsb:pps2 (cl:peptide synthetase ppsd:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir) I40457 I40457 Bacillus subtilis 1423 -11529684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761695	2247	24403	300	100

Description

6500725827 pps1:ppsa peptide synthetase:peptide synthetase 1 (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.3.1) (db:gtc-bacillus subtilis) ppsA ppsA Bacillus subtilis 1423 -11529685 7500888376 ppsa:pps1 (de:peptide synthetase 1) (db:swissprot) PPS1_BACSU P39845 BACILLUS SUBTILIS 1423 -11529685 7000686166 ppsa:pps1 peptide synthetase ppsa:pps1 (cl:peptide synthetase ppsd:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir2.dat) I40456 I40456 Bacillus subtilis 1423 -11529685 5000689058 pps1 putative fengycin synthetase orf1 (db:genpept-bct1) (de:b.subtilis genes for peptide synthetase and penicillin bindingprotein.) (le:2021) (re:9706) (di:direct) BSPEPSYN Z34883 g580910 Bacillus subtilis 1423 -11529685 219523 ppsa peptide synthetase (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:208327) (re:216012) (di:complement) BSUB0010 Z99113 g2634217 Bacillus subtilis 1423 -11529685 90813 ppsa:pps1 (de:peptide synthetase 1) (db:swissprot) PPS1_BACSU P39845 BACILLUS SUBTILIS 1423 -11529685 170430 ppsa:pps1 peptide synthetase ppsa:pps1 (cl:peptide synthetase ppsd:acetate--coa ligase homology:acyl carrier protein homology:gramicidin s synthetase i repeat homology) (db:pir) I40456 I40456 Bacillus subtilis 1423 -11529685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761705	2248	24404	369	122

Description

6500725828 dimethyladenosine transferase:s-adenosylmethionine-6-n:n-adenosyl:rrna dimethyltransferase:16s rrna dimethylase:high level kasugamycin resistance protein ksga:kasugamycin dimethyltransferase (gtcfc:13.3) (ec:2.1.1.-) (keggfc:14.1) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) ksgA ksgA Bacillus subtilis 1423 -11529686 81176 ksga (ec:2.1.1.-) (de:dimethyltransferase)) (db:swissprot) KSGA_BACSU P37468 BACILLUS SUBTILIS 1423 -11529686 7000685703 ksga dimethyladenosine transferase ksga:high level kasgamycin resistance protein ksga (cl:rrna (adenine-n6-)-methyltransferase) (db:pir2.dat) S66071 S66071 Bacillus subtilis 1423 -11529686 7500884746 ksga high level kasgamycin resistance (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:114240) (re:115118) (di:direct) BAC180K D26185 g467431 Bacillus subtilis 1423 -11529686 215031 ksga dimethyladenosine transferase (fn:high level kasugamycin resistance) (db:genpept-bct1) (ec:2.1.1.-) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:50638) (re:51516) (di:direct) BSUB0001 Z99104 g2632309 Bacillus subtilis 1423 -11529686 206172 ksga dimethyladenosine transferase ksga:high level kasgamycin resistance protein ksga (cl:rrna (adenine-n6-)-methyltransferase) (db:pir) S66071 S66071 Bacillus subtilis 1423 -11529686 5000688432 (de:(ksga) (pn:dimethyladenosine transferase:s-adenosylmethionine-6-n", n"-adenosyl:rrna dimethyltransferase:dimethyladenosine transferase :s-adenosylmethionine-6-n", n"-adenosyl:rrna dimethyltransferase:16s rrna dimethylase:high level) ksgA ksgA Bacillus subtilis 1423 10023412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761714	2249	24405	972	323

Description

6500725829 cephalosporin c deacetylase (gtcfc:13.3) (ec:3.1.1.41) (keggfc:14.1) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) cah cah Bacillus subtilis 1423 -11529687 7000692355 cah cephalosporin-c deacetylase (cl:cephalosporin-c deacetylase) (ec:3.1.1.41) (db:pir2.dat) G69596 G69596 Bacillus subtilis 1423 -11529687 222584 cah cephalosporin c deacetylase (db:genpept-bct1) (ec:3.1.1.41) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:147460) (re:148416) (di:direct) BSUB0002 Z99105 g2632604 Bacillus subtilis 1423 -11529687 7500963519 cah cephalosporin c deacetylase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:21761) (re:22717) (di:direct) D50453 D50453 g1805390 Bacillus subtilis 1423 -11529687

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761730	2250	24406	183	61

Description

6500725830 multidrug resistance protein (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) ebrB ebrB Bacillus subtilis 1423 -11529688 7000694239 ebrb multidrug resistance protein ebrb (cl:suge protein) (db:pir2.dat) E69619 E69619 Bacillus subtilis 1423 -11529688 7500964966 ebrb multidrug resistance protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:82733) (re:83086) (di:complement) BSUB0010 Z99113 g2634113 Bacillus subtilis 1423 -11529688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761731	2251	24407	957	318

Description

6500725831 multidrug resistance protein (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) ebrA ebrA Bacillus subtilis 1423 -11529689 7000694238 ebra multidrug resistance protein ebra (cl:suge protein) (db:pir2.dat) D69619 D69619 Bacillus subtilis 1423 -11529689 7500964965 ebra multidrug resistance protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:83100) (re:83417) (di:complement) BSUB0010 Z99113 g2634114 Bacillus subtilis 1423 -11529689

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761736	2252	24408	846	282

Description

5000689050 hypothetical protein:putative arsenate reductase (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) yqcM yqcM Bacillus subtilis 1423 -11529690 60284 yqcm (de:putative arsenate reductase) (db:swissprot) ARSC_BACSU P45947 BACILLUS SUBTILIS 1423 -11529690 7000684636 yqcm arsenate reductase homolog yqcm (cl:protein-tyrosine-phosphatase, low molecular weight) (db:pir2.dat) C69950 C69950 Bacillus subtilis 1423 -11529690 216022 yqcm (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:63870) (re:64289) (di:direct) BACJH642 D84432 g1303778 Bacillus subtilis 1423 -11529690 216809 orf109 (sr:bacillus subtilis (strain:jh642 (trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis 48 kb region including a skin element which islocated between spoivcb and spoiiic.) (nt:similarity to arsenate reductase (arsc) of s.) (le:45625) (re:46044)... BACSKIN D32216 g1217885 Bacillus subtilis 1423 -11529690 7500877211 yqcm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to arsenate reductase) (le:55141) (re:55560) (di:complement) BSUB0014 Z99117 g2635023 Bacillus subtilis 1423 -11529690 6500725832 hypothetical protein:putative arsenate reductase (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) yqcM yqcM Bacillus subtilis 1423 -11529690

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761750	2253	24409	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761950	2254	24410	438	145

Description

5000689046 methylenomycin a resistance protein:mmr peptide (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) mmr mmr Bacillus subtilis 1423 -11529691 219720 mmr (de:methylenomycin a resistance protein (mmr peptide)) (db:swissprot) MMR_BACSU Q00538 BACILLUS SUBTILIS 1423 -11529691 131188 mmr methylenomycin a resistance protein mmr (cl:tetracycline resistance protein) (db:pir1.dat) YTBSMA I40493 Bacillus subtilis 1423 -11529691 7500885695 mmr methylenomycinaresistance protein (db:genpept-bct1) (de:b.subtilis thrz and mmr genes.) (le:478) (re:1878) (di:direct) BSTHRZMMR X66121 g40215 Bacillus subtilis 1423 -11529691 7502851635 mmr methylenomycin a resistance protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.) (le:57416) (re:58816) (di:complement) BSUB0020 Z99123 g2636293 Bacillus subtilis 1423 -11529691 83920 mmr (de:methylenomycin a resistance protein (mmr peptide)) (db:swissprot) MMR_BACSU Q00538 BACILLUS SUBTILIS 1423 -11529691 6500725833 methylenomycin a resistance protein:mmr peptide (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) mmr mmr Bacillus subtilis 1423 -11529691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761951	2255	24411	564	187

Description

6500725834 teta:tetb na+/h+ and multifunctional antiporter:teta:teta:l:tet:tetracycline resistance protein (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) tetB tetB Bacillus subtilis 1423 -11529692 219694 tetb:tet (de:tetracycline resistance protein) (db:swissprot) TCRB_BACSU P23054 BACILLUS SUBTILIS 1423 -11529692 131193 tetb tetracycline resistance protein tetb:tetracycline-resistance determinant (cl:tetracycline resistance protein) (db:pir1.dat) YTBSY8 JT0427 Bacillus subtilis 1423 -11529692 214962 tetb tetracycline resistance protein (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:35677) (re:37053) (di:complement) BAC180K D26185 g467362 Bacillus subtilis 1423 -11529692 5000689047 tet protein (db:genpept-bct1) (de:bacillus subtilis gsy908 tet gene for tetracycline-resistance.) (le:188) (re:1564) (di:direct) BSTET X08034 g580940 Bacillus subtilis 1423 -11529692 7500892848 tetb na+/h+ and multifunctional antiporter (fn:tetracycline resistance) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (nt:alternate gene name: teta, teta(l)) (le:187609) (re:188985) (di:complement) BSUB0021 Z99124 g2636624 Bacillus subtilis 1423 -11529692 100913 tetb:tet (de:tetracycline resistance protein) (db:swissprot) TCRB_BACSU P23054 BACILLUS SUBTILIS 1423 -11529692

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761952	2256	24412	678	225

Description

5000689048 tetracycline resistance leader peptide (gtcfc:13.3) (keggfc:14.2) (bsorffc:7.4.1) (db:gtc-bacillus subtilis) tetL tetL Bacillus subtilis 1423 -11529693 219693 tetl (de:tetracycline resistance leader peptide) (db:swissprot) LPTR_BACSU P23053 BACILLUS SUBTILIS 1423 -11529693 131582 tetl tet leader peptide:tetracycline resistance leader peptide tetl (cl:tet leader peptide) (db:pir1.dat) LFBSTT S04802 Bacillus subtilis 1423 -11529693 219361 (db:genpept-bct1) (de:b.subtilis is1k transposable element dna in the region beforetetbs908.) (nt:leader sequence) (le:971) (re:1033) (di:direct) BSIS1K X58999 g39965 Bacillus subtilis 1423 -11529693 7500885140 leader peptide (db:genpept-bct1) (de:bacillus subtilis gsy908 tet gene for tetracycline-resistance.) (le:92) (re:154) (di:direct) BSTET X08034 g40208 Bacillus subtilis 1423 -11529693 6500725835 tetl tetracycline resistance leader peptide (db:genpept-bct1) (de:bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.) (le:189019) (re:189081) (di:complement) BSUB0021 Z99124 g2636625 Bacillus subtilis 1423 -11529693 82439 tetl (de:tetracycline resistance leader peptide) (db:swissprot) LPTR_BACSU P23053 BACILLUS SUBTILIS 1423 -11529693

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761977	2257	24413	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761978	2258	24414	876	291

Description

6500725836 yole:uvrx uv-damage repair protein (gtcfc:13.4) (keggfc:14.2) (bsorffc:7.6.1) (db:gtc-bacillus subtilis) uvrX uvrX Bacillus subtilis 1423 -11529694 7000694898 uvrx uv-damage repair protein uvrx (cl:umuc protein) (db:pir2.dat) A69730 A69730 Bacillus subtilis 1423 -11529694 7000694899 uvrx uv-damage repair protein (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: yole) (le:74108) (re:75358) (di:complement) BSUB0012 Z99115 g2634570 Bacillus subtilis 1423 -11529694 7500955487 yole impb/mucb/samb family protein (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:14792) (re:16042) (di:direct) AF020713 AF020713 g3025495 Bacteriophage SPBc2 66797 -11529694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761982	2259	24415	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761984	2260	24416	750	249

Description

GTC ORF with score 385 to: (db:genpept-bct1) (de:bradyrhizobium japonicum electron transfer flavoprotein smallsubunit (etfs) nd large subunit (etfl) genes, complete cds.) (nt:electron transfer flavoprotein small subunit; beta) (le:76) (re:825) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761987	2261	24417	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761988	2262	24418	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501761998	2263	24419	558	185

Description

6500725837 ywtf:bsu_3579 an in-frame tga stop codon is found after leu-225:readthrough or pseudogene (gtcfc:14.1) (keggfc:14.2) (db:gtc-bacillus subtilis) BSU_3579 BSU_3579 Bacillus subtilis 1423 -11529695 6000691730 ywtf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.) (nt:an in-frame tga stop codon is found after leu-225) (le:96206) (re:97174) (di:direct) BSUB0019 Z99122 e1184490 Bacillus subtilis 1423 -11529695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762000	2264	24420	783	261

Description

5000689472 hypothetical protein:hypothetical 7.9 kd protein in dnan-recf intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaA yaaA Bacillus subtilis 1423 -11529696 214993 yaaa (de:hypothetical 7.9 kd protein in dnan-recf intergenic region) (db:swissprot) YAAA_BACSU P05650 BACILLUS SUBTILIS 1423 -11529696 7000687102 yaaa conserved hypothetical protein yaaa:hypothetical 8k protein oric region (db:pir2.dat) (mp:0) C22930 C22930 Bacillus subtilis 1423 -11529696 7500895957 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:66808) (re:67023) (di:direct) BAC180K D26185 g467393 Bacillus subtilis 1423 -11529696 219453 (db:genpept-bct1) (de:bacillus subtilis oric region.) (nt:orf 71 (aa 1-71)) (le:3982) (re:4197) (di:direct) BSORIC X02369 g40016 Bacillus subtilis 1423 -11529696 7502851636 yaaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:3206) (re:3421) (di:direct) BSUB0001 Z99104 g2632270 Bacillus subtilis 1423 -11529696 109483 yaaa (de:hypothetical 7.9 kd protein in dnan-recf intergenic region) (db:swissprot) YAAA_BACSU P05650 BACILLUS SUBTILIS 1423 -11529696 170051 yaaa conserved hypothetical protein yaaa:hypothetical 8k protein oric region (db:pir) (mp:0) C22930 C22930 Bacillus subtilis 1423 -11529696 6500725838 hypothetical protein:hypothetical 7.9 kd protein in dnan-recf intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaA yaaA Bacillus subtilis 1423 -11529696

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762001	2265	24421	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762009	2266	24422	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762010	2267	24423	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762022	2268	24424	1194	398

Description

5000689473 hypothetical protein:hypothetical 5.9 kd protein in recf-gyrb intergeni region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaB yaaB Bacillus subtilis 1423 -11529697 109487 yaab (de:hypothetical 5.9 kd protein in recf-gyrb intergeni region) (db:swissprot) YAAB_BACSU P37525 BACILLUS SUBTILIS 1423 -11529697 7000687103 yaab hypothetical protein yaab (db:pir2.dat) S66035 S66035 Bacillus subtilis 1423 -11529697 7500895960 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:68169) (re:68327) (di:direct) BAC180K D26185 g467395 Bacillus subtilis 1423 -11529697 214995 yaab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:4567) (re:4725) (di:direct) BSUB0001 Z99104 g2632272 Bacillus subtilis 1423 -11529697 206215 yaab hypothetical protein yaab (db:pir) S66035 S66035 Bacillus subtilis 1423 -11529697 6500725839 hypothetical protein:hypothetical 5.9 kd protein in recf-gyrb intergeni region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaB yaaB Bacillus subtilis 1423 -11529697

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762034	2269	24425	1131	376

Description

5000689474 hypothetical protein:hypothetical 38.0 kd protein in gira-guab intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaC yaaC Bacillus subtilis 1423 -11529698 109489 yaac (de:hypothetical 38.0 kd protein in gira-guab intergenic region) (db:swissprot) YAAC_BACSU P37526 BACILLUS SUBTILIS 1423 -11529698 7000687104 yaac hypothetical protein yaac (db:pir2.dat) S66038 S66038 Bacillus subtilis 1423 -11529698 7500895961 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:78447) (re:79394) (di:complement) BAC180K D26185 g467398 Bacillus subtilis 1423 -11529698 214998 yaac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:14845) (re:15792) (di:complement) BSUB0001 Z99104 g2632275 Bacillus subtilis 1423 -11529698 206216 yaac hypothetical protein yaac (db:pir) S66038 S66038 Bacillus subtilis 1423 -11529698 6500725840 hypothetical protein:hypothetical 38.0 kd protein in gira-guab intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaC yaaC Bacillus subtilis 1423 -11529698

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762044	2270	24426	444	147

Description

5000689475 hypothetical protein:31.6 kd guanylylated protein in daca-sers intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaD yaaD Bacillus subtilis 1423 -11529699 7000687105 yaad conserved hypothetical protein yaad (db:pir2.dat) S66041 S66041 Bacillus subtilis 1423 -11529699 215001 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:82662) (re:83546) (di:direct) BAC180K D26185 g467401 Bacillus subtilis 1423 -11529699 7500963546 yaad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:19060) (re:19944) (di:direct) BSUB0001 Z99104 g2632278 Bacillus subtilis 1423 -11529699 6500725841 hypothetical protein:31.6 kd guanylylated protein in daca-sers intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaD yaaD Bacillus subtilis 1423 -11529699 109493 yaad_bacsu (de:31.6 kd guanylylated protein in daca-sers intergenic region.) P37527 P37527 Bacillus subtilis 1423 -11529699

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762052	2271	24427	339	112

Description

5000689476 hypothetical protein:hypothetical 21.4 kd protein in daca-sers intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaE yaaE Bacillus subtilis 1423 -11529700 109494 yaae (de:hypothetical 21.4 kd protein in daca-sers intergenic region) (db:swissprot) YAAE_BACSU P37528 BACILLUS SUBTILIS 1423 -11529700 7000687106 yaae conserved hypothetical protein yaae (cl:conserved hypothetical protein hi1648) (db:pir2.dat) S66042 S66042 Bacillus subtilis 1423 -11529700 7500895963 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:83568) (re:84158) (di:direct) BAC180K D26185 g467402 Bacillus subtilis 1423 -11529700 215002 yaae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:19966) (re:20556) (di:direct) BSUB0001 Z99104 g2632279 Bacillus subtilis 1423 -11529700 206218 yaae conserved hypothetical protein yaae (db:pir) S66042 S66042 Bacillus subtilis 1423 -11529700 6500725842 hypothetical protein:hypothetical 21.4 kd protein in daca-sers intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaE yaaE Bacillus subtilis 1423 -11529700

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762059	2272	24428	753	250

Description

5000689477 hypothetical protein:hypothetical 25.4 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaF yaaF Bacillus subtilis 1423 -11529701 109495 yaaf (de:hypothetical 25.4 kd protein in sers-dnaz intergenic region) (db:swissprot) YAAF_BACSU P37529 BACILLUS SUBTILIS 1423 -11529701 7000687107 yaaf deoxypurine kinase subunit homolog yaaf (cl:lactobacillus acidophilus deoxyadenosine kinase) (db:pir2.dat) S66044 S66044 Bacillus subtilis 1423 -11529701 7500895964 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:86096) (re:86749) (di:complement) BAC180K D26185 g467404 Bacillus subtilis 1423 -11529701 215004 yaaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to deoxypurine kinase subunit) (le:22494) (re:23147) (di:complement) BSUB0001 Z99104 g2632281 Bacillus subtilis 1423 -11529701 206219 yaaf deoxypurine kinase subunit homolog yaaf (db:pir) S66044 S66044 Bacillus subtilis 1423 -11529701 6500725843 hypothetical protein:hypothetical 25.4 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaF yaaF Bacillus subtilis 1423 -11529701

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762067	2273	24429	207	69

Description

5000689478 hypothetical protein:hypothetical 24.1 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaG yaaG Bacillus subtilis 1423 -11529702 109497 yaag (de:hypothetical 24.1 kd protein in sers-dnaz intergenic region) (db:swissprot) YAAG_BACSU P37530 BACILLUS SUBTILIS 1423 -11529702 7000687108 yaag deoxypurine kinase subunit homolog yaag (cl:lactobacillus acidophilus deoxyadenosine kinase) (db:pir2.dat) S66045 S66045 Bacillus subtilis 1423 -11529702 7500895966 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:86746) (re:87369) (di:complement) BAC180K D26185 g467405 Bacillus subtilis 1423 -11529702 215005 yaag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to deoxypurine kinase subunit) (le:23144) (re:23767) (di:complement) BSUB0001 Z99104 g2632282 Bacillus subtilis 1423 -11529702 206220 yaag deoxypurine kinase subunit homolog yaag (db:pir) S66045 S66045 Bacillus subtilis 1423 -11529702 6500725844 hypothetical protein:hypothetical 24.1 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaG yaaG Bacillus subtilis 1423 -11529702

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762069	2274	24430	843	281

Description

5000689479 hypothetical protein:hypothetical 48.6 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaH yaaH Bacillus subtilis 1423 -11529703 109498 yaah (de:hypothetical 48.6 kd protein in sers-dnaz intergenic region) (db:swissprot) YAAH_BACSU P37531 BACILLUS SUBTILIS 1423 -11529703 7000687109 yaah conserved hypothetical protein yaah (cl:hypothetical protein yaah) (db:pir2.dat) S66046 S66046 Bacillus subtilis 1423 -11529703 7500895967 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:87468) (re:88751) (di:complement) BAC180K D26185 g467406 Bacillus subtilis 1423 -11529703 215006 yaah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:23866) (re:25149) (di:complement) BSUB0001 Z99104 g2632283 Bacillus subtilis 1423 -11529703 206221 yaah conserved hypothetical protein yaah (db:pir) S66046 S66046 Bacillus subtilis 1423 -11529703 6500725845 hypothetical protein:hypothetical 48.6 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaH yaaH Bacillus subtilis 1423 -11529703

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762070	2275	24431	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762078	2276	24432	462	153

Description

5000689480 hypothetical protein:hypothetical 20.8 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaI yaaI Bacillus subtilis 1423 -11529704 109500 yaai (de:hypothetical 20.8 kd protein in sers-dnaz intergenic region) (db:swissprot) YAAI_BACSU P37532 BACILLUS SUBTILIS 1423 -11529704 7000687110 yaai isochorismatase homolog yaai (cl:hypothetical protein b1011) (db:pir2.dat) S66047 S66047 Bacillus subtilis 1423 -11529704 7500895969 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:88821) (re:89366) (di:complement) BAC180K D26185 g467407 Bacillus subtilis 1423 -11529704 215007 yaai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to isochorismatase) (le:25219) (re:25764) (di:complement) BSUB0001 Z99104 g2632284 Bacillus subtilis 1423 -11529704 206222 yaai isochorismatase homolog yaai (db:pir) S66047 S66047 Bacillus subtilis 1423 -11529704 6500725846 hypothetical protein:hypothetical 20.8 kd protein in sers-dnaz intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaI yaaI Bacillus subtilis 1423 -11529704

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762079	2277	24433	669	222

Description

5000689481 hypothetical protein:hypothetical 17.8 kd protein in sers-dnah intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaJ yaaJ Bacillus subtilis 1423 -11529705 109502 yaaj (de:hypothetical 17.8 kd protein in sers-dnah intergenic region) (db:swissprot) YAAJ_BACSU P21335 BACILLUS SUBTILIS 1423 -11529705 7000687111 yaaj conserved hypothetical protein yaaj (cl:hypothetical protein yaaj) (db:pir2.dat) S11690 S11690 Bacillus subtilis 1423 -11529705 7500895971 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:89452) (re:89937) (di:direct) BAC180K D26185 g467408 Bacillus subtilis 1423 -11529705 215008 (db:genpept-bct1) (de:bacillus subtilis dna for orf17, small cytoplasmic rna and partialdnax gene.) (nt:orf17 (aa 1-161)) (le:129) (re:614) (di:direct) BSORF17 X52144 g40011 Bacillus subtilis 1423 -11529705 219439 yaaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:25850) (re:26335) (di:direct) BSUB0001 Z99104 g2632285 Bacillus subtilis 1423 -11529705 170192 yaaj conserved hypothetical protein yaaj (cl:hypothetical protein yaaj) (db:pir) S11690 S11690 Bacillus subtilis 1423 -11529705 6500725847 hypothetical protein:hypothetical 17.8 kd protein in sers-dnah intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaJ yaaJ Bacillus subtilis 1423 -11529705

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762080	2278	24434	423	140

Description

5000689482 hypothetical protein:hypothetical 11.8 kd protein in dnaz-recr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaK yaaK Bacillus subtilis 1423 -11529706 304135 yaak (de:hypothetical 11.8 kd protein in dnaz-recr intergenic region) (db:swissprot) YAAK_BACSU P24281 BACILLUS SUBTILIS 1423 -11529706 7000687113 yaak conserved hypothetical protein yaak (db:pir2.dat) S13787 S13787 Bacillus subtilis 1423 -11529706 7500895974 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:92129) (re:92452) (di:direct) BAC180K D26185 g467410 Bacillus subtilis 1423 -11529706 219568 (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (nt:orf107) (le:1976) (re:2299) (di:direct) BSRECM X17014 g40073 Bacillus subtilis 1423 -11529706 7502851637 yaak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:28527) (re:28850) (di:direct) BSUB0001 Z99104 g2632287 Bacillus subtilis 1423 -11529706 7502851638 (db:genpept) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (nt:orf107) (le:1976) (re:2299) (di:direct) BSRECM X17014 g40073 Bacillus subtilis 1423 -11529706 109505 yaak (de:hypothetical 11.8 kd protein in dnaz-recr intergenic region) (db:swissprot) YAAK_BACSU P24281 BACILLUS SUBTILIS 1423 -11529706 170188 yaak conserved hypothetical protein yaak (db:pir) S13787 S13787 Bacillus subtilis 1423 -11529706 215010 (db:genpept-bct1) (de:bacillus subtilis dnazx and recr genes and two unidentified readingframes.) (nt:orf107) (le:1976) (re:2299) (di:direct) BSRECM X17014 g40073 Bacillus subtilis 1423 -11529706 6500725848 hypothetical protein:hypothetical 11.8 kd protein in dnaz-recr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaK yaaK Bacillus subtilis 1423 -11529706

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762083	2279	24435	549	182

Description

GTC ORF with score 123 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid zk84.) (nt:final exon in repeat region; similar to long tandem) (le:24170:24288:24411:24654) (re:24234:24357:24597:26737) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762085	2280	24436	297	98

Description

GTC ORF with score 185 to:
(gtcfc:1.1:1.11:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3) (ec:1.1.1.-)
(keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (sgdfc:1.5.1:9.2.0)
(db:gtc-saccharomyces cerevisiae) (gtcfc:carbohydrate ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762088	2281	24437	366	121

Description

5000689483 hypothetical protein:hypothetical 9.2 kd protein in recr-bofa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaL yaaL Bacillus subtilis 1423 -11529707 109506 yaal (de:hypothetical 9.2 kd protein in recr-bofa intergenic region) (db:swissprot) YAAL_BACSU P37533 BACILLUS SUBTILIS 1423 -11529707 169891 yaal hypothetical protein yaal:bofa 5-region hypothetical protein orf74 (db:pir2.dat) A41869 S13790 Bacillus subtilis 1423 -11529707 7500895975 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:93081) (re:93305) (di:direct) BAC180K D26185 g467412 Bacillus subtilis 1423 -11529707 215012 yaal (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:29479) (re:29703) (di:direct) BSUB0001 Z99104 g2632289 Bacillus subtilis 1423 -11529707 7000687114 yaal hypothetical protein yaal:bofa 5-region hypothetical protein orf74 (db:pir) A41869 A41869 Bacillus subtilis 1423 -11529707 6500725849 hypothetical protein:hypothetical 9.2 kd protein in recr-bofa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaL yaaL Bacillus subtilis 1423 -11529707

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762109	2282	24438	1146	381

Description

5000689484 yaam:csfb hypothetical protein:hypothetical 7.4 kd protein in bofa-xpac intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) csfB csfB Bacillus subtilis 1423 -11529708 109507 csfb (de:csfb protein) (db:swissprot) CSFB_BACSU P37534 BACILLUS SUBTILIS 1423 -11529708 7000687115 csfb sigma-f transcribed protein csfb (db:pir2.dat) S27525 S27525 Bacillus subtilis 1423 -11529708 7500879449 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:99131) (re:99325) (di:direct) BAC180K D26185 g467414 Bacillus subtilis 1423 -11529708 215014 (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis orf1 and xpac gene, complete cds's; ssrrna gene,3' end; orf3c 5' end.) (nt:orf1) (le:218) (re:412) (di:direct) BACXPAC M96156 g143829 Bacillus subtilis 1423 -11529708 217058 csfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yaam; sigma-f transcribed) (le:35529) (re:35723) (di:direct) BSUB0001 Z99104 g2632291 Bacillus subtilis 1423 -11529708 170184 csfb sigma-f transcribed protein csfb (db:pir) S27525 S27525 Bacillus subtilis 1423 -11529708 6500725850 yaam hypothetical protein:hypothetical 7.4 kd protein in bofa-xpac intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) csfB csfB Bacillus subtilis 1423 -11529708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762112	2283	24439	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762114	2284	24440	282	93

Description

5000689485 hypothetical protein:hypothetical 43.8 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaN yaaN Bacillus subtilis 1423 -11529709 109508 yaan (de:hypothetical 43.8 kd protein in xpac-abrb intergenic region) (db:swissprot) YAAN_BACSU P37535 BACILLUS SUBTILIS 1423 -11529709 7000687116 yaan toxic cation resistance homolog yaan (cl:tela protein) (db:pir2.dat) S66056 S66056 Bacillus subtilis 1423 -11529709 7500895976 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:100078) (re:101238) (di:direct) BAC180K D26185 g467416 Bacillus subtilis 1423 -11529709 215016 yaan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to toxic cation resistance) (le:36476) (re:37636) (di:direct) BSUB0001 Z99104 g2632293 Bacillus subtilis 1423 -11529709 206223 yaan toxic cation resistance homolog yaan (cl:tela protein) (db:pir) S66056 S66056 Bacillus subtilis 1423 -11529709 6500725851 hypothetical protein:hypothetical 43.8 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaN yaaN Bacillus subtilis 1423 -11529709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762115	2285	24441	360	119

Description

GTC ORF with score 206 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f13c5 (essaiiproject).) (nt:strong similarity to 4-coumarate-coa ligase,) (le:71990:72204:72438) (re:72115:72306:72505) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762278	2286	24442	723	240

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762281	2287	24443	957	318

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762290	2288	24444	1116	372

Description

5000689486 hypothetical protein:hypothetical 53.2 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaO yaaO Bacillus subtilis 1423 -11529710 109509 yaao (de:hypothetical 53.2 kd protein in xpac-abrb intergenic region) (db:swissprot) YAAO_BACSU P37536 BACILLUS SUBTILIS 1423 -11529710 7000687117 yaao lysine decarboxylase homolog yaao (db:pir2.dat) S66057 S66057 Bacillus subtilis 1423 -11529710 7500895977 similar to lysine decarboxylase (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:101320) (re:102762) (di:direct) BAC180K D26185 g467417 Bacillus subtilis 1423 -11529710 215017 yaao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to lysine decarboxylase) (le:37718) (re:39160) (di:direct) BSUB0001 Z99104 g2632294 Bacillus subtilis 1423 -11529710 206264 yaao lysine decarboxylase homolog yaao (db:pir) S66057 S66057 Bacillus subtilis 1423 -11529710 6500725852 hypothetical protein:hypothetical 53.2 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaO yaaO Bacillus subtilis 1423 -11529710

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762295	2289	24445	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762313	2290	24446	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762321	2291	24447	732	243

Description

5000689487 hypothetical protein:hypothetical 12.0 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaQ yaaQ Bacillus subtilis 1423 -11529711 109510 yaaq (de:hypothetical 12.0 kd protein in xpac-abrb intergenic region) (db:swissprot) YAAQ_BACSU P37538 BACILLUS SUBTILIS 1423 -11529711 7000687118 yaaq conserved hypothetical protein yaaq (db:pir2.dat) S66059 S66059 Bacillus subtilis 1423 -11529711 7500895978 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:103471) (re:103800) (di:direct) BAC180K D26185 g467419 Bacillus subtilis 1423 -11529711 215019 yaaq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:39869) (re:40198) (di:direct) BSUB0001 Z99104 g2632296 Bacillus subtilis 1423 -11529711 206225 yaaq conserved hypothetical protein yaaq (db:pir) S66059 S66059 Bacillus subtilis 1423 -11529711 6500725853 hypothetical protein:hypothetical 12.0 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaQ yaaQ Bacillus subtilis 1423 -11529711

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762326	2292	24448	237	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762327	2293	24449	492	163

Description

5000689488 hypothetical protein:hypothetical 16.7 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaR yaaR Bacillus subtilis 1423 -11529712 109511 yaar (de:hypothetical 16.7 kd protein in xpac-abrb intergenic region) (db:swissprot) YAAR_BACSU P37539 BACILLUS SUBTILIS 1423 -11529712 7000687119 yaar hypothetical protein yaar (db:pir2.dat) S66060 S66060 Bacillus subtilis 1423 -11529712 7500895979 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:103813) (re:104253) (di:direct) BAC180K D26185 g467420 Bacillus subtilis 1423 -11529712 215020 yaar (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:40211) (re:40651) (di:direct) BSUB0001 Z99104 g2632297 Bacillus subtilis 1423 -11529712 206226 yaar hypothetical protein yaar (db:pir) S66060 S66060 Bacillus subtilis 1423 -11529712 6500725854 hypothetical protein:hypothetical 16.7 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaR yaaR Bacillus subtilis 1423 -11529712

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762328	2294	24450	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762329	2295	24451	318	105

Description

5000689489 hypothetical protein:hypothetical 31.2 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaT yaaT Bacillus subtilis 1423 -11529713 109513 yaat (de:hypothetical 31.2 kd protein in xpac-abrb intergenic region) (db:swissprot) YAAT_BACSU P37541 BACILLUS SUBTILIS 1423 -11529713 7000687121 yaat signal peptidase ii homolog yaat (db:pir2.dat) S66062 S66062 Bacillus subtilis 1423 -11529713 7500895980 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:105257) (re:106084) (di:direct) BAC180K D26185 g467422 Bacillus subtilis 1423 -11529713 215022 yaat (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to signal peptidase ii) (le:41655) (re:42482) (di:direct) BSUB0001 Z99104 g2632299 Bacillus subtilis 1423 -11529713 206227 yaat signal peptidase ii homolog yaat (db:pir) S66062 S66062 Bacillus subtilis 1423 -11529713 6500725855 hypothetical protein:hypothetical 31.2 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yaaT yaaT Bacillus subtilis 1423 -11529713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762331	2296	24452	783	260

Description

5000689490 hypothetical protein:hypothetical 14.1 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabA yabA Bacillus subtilis 1423 -11529714 109527 yaba (de:hypothetical 14.1 kd protein in xpac-abrb intergenic region) (db:swissprot) YABA_BACSU P37542 BACILLUS SUBTILIS 1423 -11529714 7000687123 yaba hypothetical protein yaba (db:pir2.dat) S66063 S66063 Bacillus subtilis 1423 -11529714 7500895991 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:106099) (re:106458) (di:direct) BAC180K D26185 g467423 Bacillus subtilis 1423 -11529714 215023 yaba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:42497) (re:42856) (di:direct) BSUB0001 Z99104 g2632300 Bacillus subtilis 1423 -11529714 206228 yaba hypothetical protein yaba (db:pir) S66063 S66063 Bacillus subtilis 1423 -11529714 6500725856 hypothetical protein:hypothetical 14.1 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabA yabA Bacillus subtilis 1423 -11529714

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762347	2297	24453	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762362	2298	24454	618	205

Description

5000689491 hypothetical protein:hypothetical 28.3 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabB yabB Bacillus subtilis 1423 -11529715 109529 yabb (de:hypothetical 28.3 kd protein in xpac-abrb intergenic region) (db:swissprot) YABB_BACSU P37543 BACILLUS SUBTILIS 1423 -11529715 7000687124 yabb conserved hypothetical protein yabb (db:pir2.dat) S66064 S66064 Bacillus subtilis 1423 -11529715 7500895992 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:106517) (re:107260) (di:direct) BAC180K D26185 g467424 Bacillus subtilis 1423 -11529715 215024 yabb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:42915) (re:43658) (di:direct) BSUB0001 Z99104 g2632301 Bacillus subtilis 1423 -11529715 206229 yabb conserved hypothetical protein yabb (db:pir) S66064 S66064 Bacillus subtilis 1423 -11529715 6500725857 hypothetical protein:hypothetical 28.3 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabB yabB Bacillus subtilis 1423 -11529715

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762383	2299	24455	1068	355

Description

6500725858 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yazA yazA Bacillus subtilis 1423 -11529716 7000692384 yaza conserved hypothetical protein yaza (cl:hypothetical protein 312) (db:pir2.dat) A69742 A69742 Bacillus subtilis 1423 -11529716 7500963548 yaza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:43645) (re:43944) (di:direct) BSUB0001 Z99104 g2632302 Bacillus subtilis 1423 -11529716

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762397	2300	24456	786	261

Description

5000689492 hypothetical protein:hypothetical 33.0 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabC yabC Bacillus subtilis 1423 -11529717 109532 yabc (de:hypothetical 33.0 kd protein in xpac-abrb intergenic region) (db:swissprot) YABC_BACSU P37544 BACILLUS SUBTILIS 1423 -11529717 7000687125 yabc conserved hypothetical protein yabc (cl:conserved hypothetical protein mg056) (db:pir2.dat) S66065 S66065 Bacillus subtilis 1423 -11529717 7500895994 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:107521) (re:108399) (di:direct) BAC180K D26185 g467425 Bacillus subtilis 1423 -11529717 215025 yabc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:43919) (re:44797) (di:direct) BSUB0001 Z99104 g2632303 Bacillus subtilis 1423 -11529717 206230 yabc conserved hypothetical protein yabc (db:pir) S66065 S66065 Bacillus subtilis 1423 -11529717 6500725859 hypothetical protein:hypothetical 33.0 kd protein in xpac-abrb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabC yabC Bacillus subtilis 1423 -11529717

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762403	2301	24457	198	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762577	2302	24458	549	182

Description

5000689493 hypothetical protein:hypothetical 29.2 kd protein in mets-ksga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabD yabD Bacillus subtilis 1423 -11529718 109536 yabd (de:hypothetical 29.2 kd protein in mets-ksga intergenic region) (db:swissprot) YABD_BACSU P37545 BACILLUS SUBTILIS 1423 -11529718 7000687126 yabd conserved hypothetical protein yabd (cl:hypothetical protein hi0454) (db:pir2.dat) S66068 S66068 Bacillus subtilis 1423 -11529718 7500895996 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:111306) (re:112073) (di:direct) BAC180K D26185 g467428 Bacillus subtilis 1423 -11529718 215028 yabd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:47704) (re:48471) (di:direct) BSUB0001 Z99104 g2632306 Bacillus subtilis 1423 -11529718 206231 yabd conserved hypothetical protein yabd (db:pir) S66068 S66068 Bacillus subtilis 1423 -11529718 6500725860 hypothetical protein:hypothetical 29.2 kd protein in mets-ksga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabD yabD Bacillus subtilis 1423 -11529718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762581	2303	24459	240	79

Description

5000689494 hypothetical protein:hypothetical 47.7 kd protein in mets-ksga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabE yabE Bacillus subtilis 1423 -11529719 109538 yabe (de:hypothetical 47.7 kd protein in mets-ksga intergenic region) (db:swissprot) YABE_BACSU P37546 BACILLUS SUBTILIS 1423 -11529719 7000687127 yabe conserved hypothetical protein yabe (db:pir2.dat) S66069 S66069 Bacillus subtilis 1423 -11529719 7500895997 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:112229) (re:113542) (di:direct) BAC180K D26185 g467429 Bacillus subtilis 1423 -11529719 215029 yabe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:48627) (re:49940) (di:direct) BSUB0001 Z99104 g2632307 Bacillus subtilis 1423 -11529719 206232 yabe conserved hypothetical protein yabe (db:pir) S66069 S66069 Bacillus subtilis 1423 -11529719 6500725861 hypothetical protein:hypothetical 47.7 kd protein in mets-ksga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabE yabE Bacillus subtilis 1423 -11529719

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762582	2304	24460	420	139

Description

GTC ORF with score 417 to: (sr:n.crassa (strain 74a) dna, clones psv50-5:4g) (db:genpept-pln1) (de:n.crassa tryptophan synthetase (trp3) alpha-2 subunit gene,complete cds.) (nt:tryptophan synthetase) (le:483:608:838) (re:530:766:2757) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762583	2305	24461	192	63

Description

5000689495 hypothetical protein:hypothetical 20.7 kd protein in mets-ksga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabF yabF Bacillus subtilis 1423 -11529720 109540 yabf (de:hypothetical 20.7 kd protein in mets-ksga intergenic region) (db:swissprot) YABF_BACSU P37547 BACILLUS SUBTILIS 1423 -11529720 7000687128 yabf conserved hypothetical protein yabf (db:pir2.dat) S66070 S66070 Bacillus subtilis 1423 -11529720 7500895998 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:113687) (re:114247) (di:direct) BAC180K D26185 g467430 Bacillus subtilis 1423 -11529720 215030 yabf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:50085) (re:50645) (di:direct) BSUB0001 Z99104 g2632308 Bacillus subtilis 1423 -11529720 206233 yabf conserved hypothetical protein yabf (db:pir) S66070 S66070 Bacillus subtilis 1423 -11529720 6500725862 hypothetical protein:hypothetical 20.7 kd protein in mets-ksga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabF yabF Bacillus subtilis 1423 -11529720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762585	2306	24462	660	220

Description

5000689496 hypothetical protein:hypothetical 33.3 kd protein in ksga-veg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabG yabG Bacillus subtilis 1423 -11529721 109543 yabg (de:hypothetical 33.3 kd protein in ksga-veg intergenic region) (db:swissprot) YABG_BACSU P37548 BACILLUS SUBTILIS 1423 -11529721 7000687130 yabg hypothetical protein yabg (db:pir2.dat) S66072 S66072 Bacillus subtilis 1423 -11529721 7500896000 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:115280) (re:116152) (di:direct) BAC180K D26185 g467432 Bacillus subtilis 1423 -11529721 215032 yabg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:51678) (re:52550) (di:direct) BSUB0001 Z99104 g2632310 Bacillus subtilis 1423 -11529721 206234 yabg hypothetical protein yabg (db:pir) S66072 S66072 Bacillus subtilis 1423 -11529721 6500725863 hypothetical protein:hypothetical 33.3 kd protein in ksga-veg intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabG yabG Bacillus subtilis 1423 -11529721

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762588	2307	24463	336	111

Description

5000689471 hypothetical protein:veg protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) veg veg Bacillus subtilis 1423 -11529722 105142 veg (de:veg protein) (db:swissprot) VEG_BACSU P37466 BACILLUS SUBTILIS 1423 -11529722 7000686948 veg hypothetical protein veg (db:pir2.dat) S66073 S66073 Bacillus subtilis 1423 -11529722 7500894132 veg unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:116363) (re:116623) (di:direct) BAC180K D26185 g467433 Bacillus subtilis 1423 -11529722 215033 veg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:52761) (re:53021) (di:direct) BSUB0001 Z99104 g2632311 Bacillus subtilis 1423 -11529722 206297 veg hypothetical protein veg (db:pir) S66073 S66073 Bacillus subtilis 1423 -11529722 6500725864 hypothetical protein:veg protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) veg veg Bacillus subtilis 1423 -11529722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762590	2308	24464	681	226

Description

5000689497 hypothetical protein:hypothetical 31.7 kd protein in sspf-purr intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabH yabH Bacillus subtilis 1423 -11529723 109544 yabh (de:hypothetical 31.7 kd protein in sspf-purr intergenic region (orf1)) (db:swissprot) YABH_BACSU P37550 BACILLUS SUBTILIS 1423 -11529723 7000687131 yabh conserved hypothetical protein yabh (db:pir2.dat) S66075 S66075 Bacillus subtilis 1423 -11529723 7500896001 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:117116) (re:117985) (di:direct) BAC180K D26185 g467435 Bacillus subtilis 1423 -11529723 215035 yabh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:53514) (re:54383) (di:direct) BSUB0001 Z99104 g2632313 Bacillus subtilis 1423 -11529723 206235 yabh conserved hypothetical protein yabh (db:pir) S66075 S66075 Bacillus subtilis 1423 -11529723 6500725865 hypothetical protein:hypothetical 31.7 kd protein in sspf-purr intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabH yabH Bacillus subtilis 1423 -11529723

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762595	2309	24465	546	181

Description

5000689498 hypothetical protein:hypothetical 13.7 kd protein in purr-spovg intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabJ yabJ Bacillus subtilis 1423 -11529724 109548 yabj (de:hypothetical 13.7 kd protein in purr-spovg intergenic region (orf2)) (db:swissprot) YABJ_BACSU P37552 BACILLUS SUBTILIS 1423 -11529724 7000687133 yabj conserved hypothetical protein yabj (cl:hypothetical protein hi0719) (db:pir2.dat) S66077 S66077 Bacillus subtilis 1423 -11529724 7500896003 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:118895) (re:119272) (di:direct) BAC180K D26185 g467437 Bacillus subtilis 1423 -11529724 215037 yabj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:55293) (re:55670) (di:direct) BSUB0001 Z99104 g2632315 Bacillus subtilis 1423 -11529724 206237 yabj conserved hypothetical protein yabj (cl:hypothetical protein hi0719) (db:pir) S66077 S66077 Bacillus subtilis 1423 -11529724 6500725866 hypothetical protein:hypothetical 13.7 kd protein in purr-spovg intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabJ yabJ Bacillus subtilis 1423 -11529724

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762610	2310	24466	567	188

Description

5000689499 hypothetical protein:hypothetical 8.8 kd protein in spovc-mfd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabK yabK Bacillus subtilis 1423 -11529725 109551 yabk (de:hypothetical 8.8 kd protein in spovc-mfd intergenic region) (db:swissprot) YABK_BACSU P37553 BACILLUS SUBTILIS 1423 -11529725 7000687135 yabk hypothetical protein yabk (db:pir2.dat) S66084 S66084 Bacillus subtilis 1423 -11529725 7500896005 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:123730) (re:123960) (di:direct) BAC180K D26185 g467443 Bacillus subtilis 1423 -11529725 215043 yabk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:60128) (re:60358) (di:direct) BSUB0001 Z99104 g2632321 Bacillus subtilis 1423 -11529725 206238 yabk hypothetical protein yabk (db:pir) S66084 S66084 Bacillus subtilis 1423 -11529725 6500725867 hypothetical protein:hypothetical 8.8 kd protein in spovc-mfd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabK yabK Bacillus subtilis 1423 -11529725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762616	2311	24467	747	248

Description

GTC ORF with score 662 to: (fn:presumably involved in translation termination) (sr:human) (db:genpept) (de:human eukaryotic release factor 3b mrna, complete cds.) (nt:erf3b; similar to ricinus communis erf3 and) (le:195) (re:2249) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762626	2312	24468	483	160

Description

5000689500 hypothetical protein:hypothetical 57.4 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabM yabM Bacillus subtilis 1423 -11529726 109554 yabm (de:hypothetical 57.4 kd protein in mfd-divic intergenic region) (db:swissprot) YABM_BACSU P37555 BACILLUS SUBTILIS 1423 -11529726 7000687137 yabm amino acid transporter homolog yabm:spovb protein (db:pir2.dat) S66087 S66087 Bacillus subtilis 1423 -11529726 7500896008 similar to spovb (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:128417) (re:130015) (di:direct) BAC180K D26185 g467446 Bacillus subtilis 1423 -11529726 215046 yabm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to amino acid transporter) (le:64815) (re:66413) (di:direct) BSUB0001 Z99104 g2632324 Bacillus subtilis 1423 -11529726 206284 yabm amino acid transporter homolog yabm:spovb protein (db:pir) S66087 S66087 Bacillus subtilis 1423 -11529726 6500725868 hypothetical protein:hypothetical 57.4 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabM yabM Bacillus subtilis 1423 -11529726

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762627	2313	24469	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762645	2314	24470	831	276

Description

5000689501 hypothetical protein:hypothetical 56.1 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabN yabN Bacillus subtilis 1423 -11529727 109556 yabn (de:hypothetical 56.1 kd protein in mfd-divic intergenic region) (db:swissprot) YABN_BACSU P37556 BACILLUS SUBTILIS 1423 -11529727 7000687139 yabn conserved hypothetical protein yabn:beta-lactamase regulatory protein homolog yabn (cl:beta-lactamase regulatory protein homolog:beta-lactamase regulatory protein homology) (db:pir2.dat) S66088 S66088 Bacillus subtilis 1423 -11529727 7500896010 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:130005) (re:131474) (di:direct) BAC180K D26185 g467447 Bacillus subtilis 1423 -11529727 215047 yabn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:66403) (re:67872) (di:direct) BSUB0001 Z99104 g2632325 Bacillus subtilis 1423 -11529727 206239 yabn conserved hypothetical protein yabn:beta-lactamase regulatory protein homolog yabn (cl:beta-lactamase regulatory protein homolog:beta-lactamase regulatory protein homology) (db:pir) S66088 S66088 Bacillus subtilis 1423 -11529727 6500725869 hypothetical protein:hypothetical 56.1 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabN yabN Bacillus subtilis 1423 -11529727

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762648	2315	24471	267	88

Description

5000689502 hypothetical protein:hypothetical 9.7 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabO yabO Bacillus subtilis 1423 -11529728 109558 yabo (de:hypothetical 9.7 kd protein in mfd-divic intergenic region) (db:swissprot) YABO_BACSU P37557 BACILLUS SUBTILIS 1423 -11529728 7000687140 yabo conserved hypothetical protein yabo (db:pir2.dat) S66089 S66089 Bacillus subtilis 1423 -11529728 7500896011 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:131477) (re:131737) (di:direct) BAC180K D26185 g467448 Bacillus subtilis 1423 -11529728 215048 yabo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:67875) (re:68135) (di:direct) BSUB0001 Z99104 g2632326 Bacillus subtilis 1423 -11529728 206240 yabo conserved hypothetical protein yabo (db:pir) S66089 S66089 Bacillus subtilis 1423 -11529728 6500725870 hypothetical protein:hypothetical 9.7 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabO yabO Bacillus subtilis 1423 -11529728

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762650	2316	24472	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762683	2317	24473	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762698	2318	24474	540	179

Description

5000689503 hypothetical protein:hypothetical 11.4 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabP yabP Bacillus subtilis 1423 -11529729 109561 yabp (de:hypothetical 11.4 kd protein in mfd-divic intergenic region) (db:swissprot) YABP_BACSU P37558 BACILLUS SUBTILIS 1423 -11529729 7000687142 yabp hypothetical protein yabp (db:pir2.dat) S66090 S66090 Bacillus subtilis 1423 -11529729 7500896014 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:131816) (re:132118) (di:direct) BAC180K D26185 g467449 Bacillus subtilis 1423 -11529729 215049 yabp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:68214) (re:68516) (di:direct) BSUB0001 Z99104 g2632327 Bacillus subtilis 1423 -11529729 206241 yabp hypothetical protein yabp (db:pir) S66090 S66090 Bacillus subtilis 1423 -11529729 6500725871 hypothetical protein:hypothetical 11.4 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabP yabP Bacillus subtilis 1423 -11529729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762703	2319	24475	288	95

Description

5000689504 hypothetical protein:hypothetical 25.1 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabQ yabQ Bacillus subtilis 1423 -11529730 109563 yabq (de:hypothetical 25.1 kd protein in mfd-divic intergenic region) (db:swissprot) YABQ_BACSU P37559 BACILLUS SUBTILIS 1423 -11529730 7000687144 yabq divic 5-region hypothetical protein yabq (db:pir2.dat) S66091 S66091 Bacillus subtilis 1423 -11529730 7500896016 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:132115) (re:132750) (di:direct) BAC180K D26185 g467450 Bacillus subtilis 1423 -11529730 215050 yabq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:68513) (re:69148) (di:direct) BSUB0001 Z99104 g2632328 Bacillus subtilis 1423 -11529730 206242 yabq divic 5-region hypothetical protein yabq (db:pir) S66091 S66091 Bacillus subtilis 1423 -11529730 6500725872 hypothetical protein:hypothetical 25.1 kd protein in mfd-divic intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabQ yabQ Bacillus subtilis 1423 -11529730

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762705	2320	24476	207	68

Description

5000689505 hypothetical protein:hypothetical 14.2 kd protein in divic-spoiie intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabR yabR Bacillus subtilis 1423 -11529731 109565 yabr (de:hypothetical 14.2 kd protein in divic-spoiie intergenic region) (db:swissprot) YABR_BACSU P37560 BACILLUS SUBTILIS 1423 -11529731 7000687146 yabr polyribonucleotide nucleotidyltransferase homolog yabr:divic 3-region hypothetical protein (cl:polyribonucleotide nucleotidyltransferase homolog yabr) (db:pir2.dat) C53380 C53380 Bacillus subtilis 1423 -11529731 7500896018 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:133226) (re:133612) (di:direct) BAC180K D26185 g467452 Bacillus subtilis 1423 -11529731 215052 unknown (db:genpept-bct1) (de:bacillus subtilis cell division protein (divic) gene, complete cds,transfer rna genes, complete sequence and sporulation protein(spoiie) gene, 5' end of cds.) (nt:orf128; homologous to rna binding domain of e. coli) (le:914) (re:1... BACDIVIC L23497 g385178 Bacillus subtilis 1423 -11529731 215538 yabr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to polyribonucleotide) (le:69624) (re:70010) (di:direct) BSUB0001 Z99104 g2632330 Bacillus subtilis 1423 -11529731 169963 yabr polyribonucleotide nucleotidyltransferase homolog yabr:divic 3-region hypothetical protein (db:pir) C53380 C53380 Bacillus subtilis 1423 -11529731 6500725873 hypothetical protein:hypothetical 14.2 kd protein in divic-spoiie intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabR yabR Bacillus subtilis 1423 -11529731

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762706	2321	24477	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762711	2322	24478	435	144

Description

5000689506 hypothetical protein:hypothetical 26.8 kd protein in spoiie-hpt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabS yabS Bacillus subtilis 1423 -11529732 109566 yabs (de:hypothetical 26.8 kd protein in spoiie-hpt intergenic region) (db:swissprot) YABS_BACSU P37561 BACILLUS SUBTILIS 1423 -11529732 7000687147 yabs conserved hypothetical protein yabs (db:pir2.dat) S66095 S66095 Bacillus subtilis 1423 -11529732 7500896019 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:136706) (re:137443) (di:direct) BAC180K D26185 g467454 Bacillus subtilis 1423 -11529732 215054 yabs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:73104) (re:73841) (di:direct) BSUB0001 Z99104 g2632332 Bacillus subtilis 1423 -11529732 206243 yabs conserved hypothetical protein yabs (db:pir) S66095 S66095 Bacillus subtilis 1423 -11529732 6500725874 hypothetical protein:hypothetical 26.8 kd protein in spoiie-hpt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabS yabS Bacillus subtilis 1423 -11529732

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762721	2323	24479	636	212

Description

6500725875 hypothetical protein:probable serine/threonine-protein kinase in spoiie-hpt intergenic region (gtcfc:14.1) (ec:2.7.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yabT yabT Bacillus subtilis 1423 -11529733 7000693120 yabt hypothetical protein yabt (db:pir2.dat) S66096 S66096 Bacillus subtilis 1423 -11529733 7500964073 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:137532) (re:138425) (di:direct) BAC180K D26185 g467455 Bacillus subtilis 1423 -11529733 215055 yabt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:73930) (re:74823) (di:direct) BSUB0001 Z99104 g2632333 Bacillus subtilis 1423 -11529733 206244 yabt hypothetical protein yabt (db:pir) S66096 S66096 Bacillus subtilis 1423 -11529733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762898	2324	24480	1146	382

Description

6500725876 hypothetical protein:hypothetical 55.1 kd protein in spoiie-hpt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacA yacA Bacillus subtilis 1423 -11529734 7500963509 yaca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to cell-cycle protein) (le:74927) (re:76345) (di:direct) BSUB0001 Z99104 g2632334 Bacillus subtilis 1423 -11529734 7000692341 yaca cell-cycle protein homolog yaca (db:pir) D69740 D69740 Bacillus subtilis 1423 -11529734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762899	2325	24481	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762913	2326	24482	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762914	2327	24483	435	144

Description

5000689508 hypothetical protein:hypothetical 26.2 kd protein in ftsh-cysk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacB yacB Bacillus subtilis 1423 -11529735 109589 yacb (de:hypothetical 26.2 kd protein in ftsh-cysk intergenic region) (db:swissprot) YACB_BACSU P37564 BACILLUS SUBTILIS 1423 -11529735 7000687148 yacb conserved hypothetical protein yacb (db:pir2.dat) S66100 S66100 Bacillus subtilis 1423 -11529735 7500896027 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:142692) (re:143393) (di:direct) BAC180K D26185 g467459 Bacillus subtilis 1423 -11529735 215059 yacb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:79090) (re:79791) (di:direct) BSUB0001 Z99104 g2632337 Bacillus subtilis 1423 -11529735 206246 yacb conserved hypothetical protein yacb (db:pir) S66100 S66100 Bacillus subtilis 1423 -11529735 6500725877 hypothetical protein:hypothetical 26.2 kd protein in ftsh-cysk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacB yacB Bacillus subtilis 1423 -11529735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762933	2328	24484	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762934	2329	24485	513	170

Description

5000689509 hypothetical protein:hypothetical 31.8 kd protein in ftsh-cysk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacC yacC Bacillus subtilis 1423 -11529736 109590 yacc (de:hypothetical 31.8 kd protein in ftsh-cysk intergenic region) (db:swissprot) YACC_BACSU P37565 BACILLUS SUBTILIS 1423 -11529736 7000687149 yacc conserved hypothetical protein yacc (cl:conserved hypothetical protein sll1988) (db:pir2.dat) S66101 S66101 Bacillus subtilis 1423 -11529736 7500896028 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:143479) (re:144354) (di:direct) BAC180K D26185 g467460 Bacillus subtilis 1423 -11529736 215060 yacc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:79877) (re:80752) (di:direct) BSUB0001 Z99104 g2632338 Bacillus subtilis 1423 -11529736 206247 yacc conserved hypothetical protein yacc (db:pir) S66101 S66101 Bacillus subtilis 1423 -11529736 6500725878 hypothetical protein:hypothetical 31.8 kd protein in ftsh-cysk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacC yacC Bacillus subtilis 1423 -11529736

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762944	2330	24486	1065	354

Description

5000689510 hypothetical protein:hypothetical 34.1 kd protein in ftsh-cysk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacD yacD Bacillus subtilis 1423 -11529737 109592 yacd (de:hypothetical 34.1 kd protein in ftsh-cysk intergenic region) (db:swissprot) YACD_BACSU P37566 BACILLUS SUBTILIS 1423 -11529737 7000687150 yacd protein secretion prsa homolog yacd (db:pir2.dat) S66102 S66102 Bacillus subtilis 1423 -11529737 7500896030 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:144401) (re:145294) (di:direct) BAC180K D26185 g467461 Bacillus subtilis 1423 -11529737 215061 yacd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to protein secretion prsa homolog) (le:80799) (re:81692) (di:direct) BSUB0001 Z99104 g2632339 Bacillus subtilis 1423 -11529737 206248 yacd protein secretion prsa homolog yacd (db:pir) S66102 S66102 Bacillus subtilis 1423 -11529737 6500725879 hypothetical protein:hypothetical 34.1 kd protein in ftsh-cysk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacD yacD Bacillus subtilis 1423 -11529737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762961	2331	24487	717	238

Description

6500725880 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yazB yazB Bacillus subtilis 1423 -11529738 7000693123 yazb hypothetical protein yazb (db:pir2.dat) B69742 B69742 Bacillus subtilis 1423 -11529738 7500964074 yazb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:87398) (re:87607) (di:direct) BSUB0001 Z99104 g2632347 Bacillus subtilis 1423 -11529738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762984	2332	24488	594	197

Description

5000689512 hypothetical protein:hypothetical 37.1 kd protein in folk-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacF yacF Bacillus subtilis 1423 -11529739 109598 yacf (de:hypothetical 37.1 kd protein in folk-lyss intergenic region) (db:swissprot) YACF_BACSU P37567 BACILLUS SUBTILIS 1423 -11529739 7000687153 yacf transcription regulator homolog yacf (db:pir2.dat) S66110 S66110 Bacillus subtilis 1423 -11529739 7500896035 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:151233) (re:152234) (di:direct) BAC180K D26185 g467469 Bacillus subtilis 1423 -11529739 215069 yacf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to transcriptional regulator (nitrogen) (le:87631) (re:88632) (di:direct) BSUB0001 Z99104 g2632348 Bacillus subtilis 1423 -11529739 206249 yacf transcriptional regulator homolog yacf (db:pir) S66110 S66110 Bacillus subtilis 1423 -11529739 6500725881 hypothetical protein:hypothetical 37.1 kd protein in folk-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacF yacF Bacillus subtilis 1423 -11529739

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762993	2333	24489	393	130

Description

5000689514 hypothetical protein:hypothetical 21.0 kd protein in lyss-mecb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacH yacH Bacillus subtilis 1423 -11529740 109603 yach (de:hypothetical 21.0 kd protein in lyss-mecb intergenic region) (db:swissprot) YACH_BACSU P37569 BACILLUS SUBTILIS 1423 -11529740 7000687156 yach conserved hypothetical protein yach (db:pir2.dat) S66113 S66113 Bacillus subtilis 1423 -11529740 7500896038 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:165526) (re:166083) (di:direct) BAC180K D26185 g467472 Bacillus subtilis 1423 -11529740 215072 yach (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:101924) (re:102481) (di:direct) BSUB0001 Z99104 g2632351 Bacillus subtilis 1423 -11529740 206251 yach conserved hypothetical protein yach (db:pir) S66113 S66113 Bacillus subtilis 1423 -11529740 6500725882 hypothetical protein:hypothetical 21.0 kd protein in lyss-mecb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacH yacH Bacillus subtilis 1423 -11529740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501762994	2334	24490	657	219

Description

5000689515 hypothetical protein:hypothetical 41.1 kd protein in lyss-mecb intergenic region:orfx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacI yacI Bacillus subtilis 1423 -11529741 109605 yaci (de:hypothetical 41.1 kd protein in lyss-mecb intergenic region (orfx)) (db:swissprot) YACI_BACSU P37570 BACILLUS SUBTILIS 1423 -11529741 7000687158 yaci creatine kinase homolog yaci (db:pir2.dat) S66114 S66114 Bacillus subtilis 1423 -11529741 7500896040 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:166083) (re:167174) (di:direct) BAC180K D26185 g467473 Bacillus subtilis 1423 -11529741 215073 yaci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to creatine kinase) (le:102481) (re:103572) (di:direct) BSUB0001 Z99104 g2632352 Bacillus subtilis 1423 -11529741 206252 yaci creatine kinase homolog yaci (db:pir) S66114 S66114 Bacillus subtilis 1423 -11529741 6500725883 hypothetical protein:hypothetical 41.1 kd protein in lyss-mecb intergenic region:orfx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacI yacI Bacillus subtilis 1423 -11529741

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763009	2335	24491	666	222

Description

5000689516 hypothetical protein:hypothetical 40.7 kd protein in mecb-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacK yacK Bacillus subtilis 1423 -11529742 109608 yack (de:hypothetical 40.7 kd protein in mecb-gltx intergenic region) (db:swissprot) YACK_BACSU P37573 BACILLUS SUBTILIS 1423 -11529742 7000687159 yack hypothetical protein yack (db:pir2.dat) S66117 S66117 Bacillus subtilis 1423 -11529742 7500896041 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:171075) (re:172157) (di:direct) BAC180K D26185 g467476 Bacillus subtilis 1423 -11529742 215076 yack (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:107473) (re:108555) (di:direct) BSUB0001 Z99104 g2632355 Bacillus subtilis 1423 -11529742 206254 yack hypothetical protein yack (db:pir) S66117 S66117 Bacillus subtilis 1423 -11529742 6500725884 hypothetical protein:hypothetical 40.7 kd protein in mecb-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacK yacK Bacillus subtilis 1423 -11529742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763019	2336	24492	915	305

Description

5000689517 hypothetical protein:hypothetical 40.9 kd protein in mecb-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacL yacL Bacillus subtilis 1423 -11529743 109610 yacl (de:hypothetical 40.9 kd protein in mecb-gltx intergenic region) (db:swissprot) YACL_BACSU Q06754 BACILLUS SUBTILIS 1423 -11529743 7000687161 yacl conserved hypothetical protein yacl (cl:conserved hypothetical protein yacl) (db:pir2.dat) S66118 S66118 Bacillus subtilis 1423 -11529743 7500896043 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:172273) (re:173373) (di:direct) BAC180K D26185 g467477 Bacillus subtilis 1423 -11529743 215077 yacl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:108671) (re:109771) (di:direct) BSUB0001 Z99104 g2632356 Bacillus subtilis 1423 -11529743 206255 yacl conserved hypothetical protein yacl (db:pir) S66118 S66118 Bacillus subtilis 1423 -11529743 6500725885 hypothetical protein:hypothetical 40.9 kd protein in mecb-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacL yacL Bacillus subtilis 1423 -11529743

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763028	2337	24493	756	252

Description

6500725886 hypothetical protein:hypothetical 25.8 kd protein in mecb-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacM yacM Bacillus subtilis 1423 -11529744 7000692383 yacm conserved hypothetical protein yacm (db:pir2.dat) S66119 S66119 Bacillus subtilis 1423 -11529744 7500963547 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:173388) (re:174086) (di:direct) BAC180K D26185 g467478 Bacillus subtilis 1423 -11529744 215078 yacm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:109786) (re:110484) (di:direct) BSUB0001 Z99104 g2632357 Bacillus subtilis 1423 -11529744 206256 yacm conserved hypothetical protein yacm (db:pir) S66119 S66119 Bacillus subtilis 1423 -11529744

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763042	2338	24494	282	93

Description

5000689519 hypothetical protein:hypothetical 17.1 kd protein in mecb-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacN yacN Bacillus subtilis 1423 -11529745 109614 yacn (de:hypothetical 17.1 kd protein in mecb-gltx intergenic region) (db:swissprot) YACN_BACSU Q06756 BACILLUS SUBTILIS 1423 -11529745 7000687162 yacn gltx 5-region conserved hypothetical protein yacn (cl:conserved hypothetical protein hi0671) (db:pir2.dat) F69741 F69741 Bacillus subtilis 1423 -11529745 7500896044 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:174079) (re:174555) (di:direct) BAC180K D26185 g467479 Bacillus subtilis 1423 -11529745 215079 unknown (sr:bacillus subtilis (strain 168t) dna) (db:genpept-bct1) (de:bacillus subtilis glutamyl-trna transferase (gltx), serineacetyltransferase (cyse), and cysteinyl-trna synthetase (cyss)genes, complete cds's.) (le:1139) (re:1615) (di:direct) BACGLUSYN L14580 g289281 Bacillus subtilis 1423 -11529745 215698 yacn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:110477) (re:110953) (di:direct) BSUB0001 Z99104 g2632358 Bacillus subtilis 1423 -11529745 206257 yacn gltx 5-region conserved hypothetical protein yacn (db:pir) F69741 F69741 Bacillus subtilis 1423 -11529745 6500725887 hypothetical protein:hypothetical 17.1 kd protein in mecb-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacN yacN Bacillus subtilis 1423 -11529745

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763049	2339	24495	1098	366

Description

6500725888 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yazC yazC Bacillus subtilis 1423 -11529746 7000692385 yazc conserved hypothetical protein yazc (db:pir2.dat) C69742 C69742 Bacillus subtilis 1423 -11529746 7500963549 yazc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:114851) (re:115282) (di:direct) BSUB0001 Z99104 g2632362 Bacillus subtilis 1423 -11529746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763242	2340	24496	483	160

Description

5000689520 hypothetical protein:hypothetical rrna methylase in cyss 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacO yacO Bacillus subtilis 1423 -11529747 109616 yaco (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase yaco,) (db:swissprot) YACO_BACSU Q06753 BACILLUS SUBTILIS 1423 -11529747 7000687163 yaco conserved hypothetical protein yaco (cl:conserved hypothetical protein hi0860) (db:pir2.dat) S66124 S66124 Bacillus subtilis 1423 -11529747 7500896045 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:178868) (re:179617) (di:direct) BAC180K D26185 g467483 Bacillus subtilis 1423 -11529747 215083 yaco (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:115266) (re:116015) (di:direct) BSUB0001 Z99104 g2632363 Bacillus subtilis 1423 -11529747 206258 yaco conserved hypothetical protein yaco (db:pir) S66124 S66124 Bacillus subtilis 1423 -11529747 6500725889 hypothetical protein:hypothetical rrna methylase in cyss 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacO yacO Bacillus subtilis 1423 -11529747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763245	2341	24497	609	202

Description

5000689521 hypothetical protein:hypothetical 19.7 kd protein in cyss 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacP yacP Bacillus subtilis 1423 -11529748 109617 yacp (de:hypothetical 19.7 kd protein in cyss 3'region) (db:swissprot) YACP_BACSU P37574 BACILLUS SUBTILIS 1423 -11529748 7000687164 yacp conserved hypothetical protein yacp (db:pir2.dat) S66125 S66125 Bacillus subtilis 1423 -11529748 7500896046 unknown (sr:bacillus subtilis (sub_species:marburg, strain:168) dna) (db:genpept-bct1) (de:b. subtilis dna, 180 kilobase region of replication origin.) (le:179624) (re:180136) (di:direct) BAC180K D26185 g467484 Bacillus subtilis 1423 -11529748 215084 yacp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:116022) (re:116534) (di:direct) BSUB0001 Z99104 g2632364 Bacillus subtilis 1423 -11529748 206259 yacp conserved hypothetical protein yacp (db:pir) S66125 S66125 Bacillus subtilis 1423 -11529748 6500725890 hypothetical protein:hypothetical 19.7 kd protein in cyss 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yacP yacP Bacillus subtilis 1423 -11529748

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763248	2342	24498	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763249	2343	24499	549	183

Description

6500725891 ybaa:ybxb hypothetical protein:hypothetical 22.5 kd protein in rpll-rpob intergenic region:p23:orf23 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybxB ybxB Bacillus subtilis 1423 -11529749 110413 ybxb (de:(orf23)) (db:swissprot) YBXB_BACSU P37872 BACILLUS SUBTILIS 1423 -11529749 7000687389 ybxb conserved hypothetical protein ybxb (cl:hypothetical protein mj0882) (db:pir2.dat) F69751 F69751 Bacillus subtilis 1423 -11529749 216611 hypothetical protein (db:genpept-bct1) (de:bacillus subtilis ribosomal protein l7/12 (rpll) gene, beta subunitof rna polymerase (rpobc) gene, 3' end, complete cds, 5' end.) (le:238) (re:843) (di:direct) BACRPLL L24376 g402362 Bacillus subtilis 1423 -11529749 7500896982 ybxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybaa; similar to hypothetical) (le:121065) (re:121670) (di:direct) BSUB0001 Z99104 g2632373 Bacillus subtilis 1423 -11529749 5000689523 (de:(ybxb) (pn:hypothetical 22) (gtcfc:13.07) (ec:) (ybxb_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ybxB ybxB Bacillus subtilis 1423 10052145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763262	2344	24500	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763270	2345	24501	1041	347

Description

6500725892 ybab:ybxf hypothetical protein:probable ribosomal protein in rpoc-rpsl intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybxF ybxF Bacillus subtilis 1423 -11529750 7000694531 ybxf ribosomal protein l7ae family homolog ybxf (cl:rat ribosomal protein l7a) (db:pir2.dat) G69751 G69751 Bacillus subtilis 1423 -11529750 215299 (sr:bacillus subtilis (strain 168 marburg) (clone: 21) dna) (db:genpept-bct1) (de:bacillus subtilis rpob gene, 3' end of cds, rna polymerase beta'subunit (rpoc) gene, complete cds, orf82 gene, complete cds, andribosomal protein s12 gene' 5' end of cds.... BACBPSO L43593 g950304 Bacillus subtilis 1423 -11529750 222749 ybxf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybab; similar to ribosomal) (le:129339) (re:129587) (di:direct) BSUB0001 Z99104 g2632376 Bacillus subtilis 1423 -11529750 7500965158 orf2 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for rna polymerase beta subunit, ribosomalproteins l12 and s7, elongation factors g and tu and ribosomalproteins s10 and l3, partial and complete cds.) (le:2427) (re:... D64127 D64127 g1644220 Bacillus subtilis 1423 -11529750

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763276	2346	24502	720	239

Description

6500725893 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaC ybaC Bacillus subtilis 1423 -11529751 7000693124 ybac hypothetical protein ybac (db:pir2.dat) D69742 D69742 Bacillus subtilis 1423 -11529751 222754 ybac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:134170) (re:135126) (di:direct) BSUB0001 Z99104 g2632381 Bacillus subtilis 1423 -11529751 7500964075 orf3 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for rna polymerase beta subunit, ribosomalproteins l12 and s7, elongation factors g and tu and ribosomalproteins s10 and l3, partial and complete cds.) (le:7258) (re:... D64127 D64127 g1644225 Bacillus subtilis 1423 -11529751

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763280	2347	24503	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763291	2348	24504	309	103

Description

6500725894 ybad:ybxa hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybxA ybxA Bacillus subtilis 1423 -11529752 7502851639 ybxa (de:hypothetical abc transporter atp-binding protein ybxa) (db:swissprot) YBXA_BACSU P40735 BACILLUS SUBTILIS 1423 -11529752 7000692077 ybxa abc transporter atp-binding protein homolog ybxa (cl:atp-binding cassette homology) (db:pir2.dat) E69751 E69751 Bacillus subtilis 1423 -11529752 222732 ybxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybad; similar to abc) (le:150441) (re:151286) (di:direct) BSUB0001 Z99104 g2632412 Bacillus subtilis 1423 -11529752 7500963318 orf4 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:1) (re:846) (di:direct) D64126 D64126 g1644202 Bacillus subtilis 1423 -11529752

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763301	2349	24505	651	216

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763310	2350	24506	453	150

Description

6500725895 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaE ybaE Bacillus subtilis 1423 -11529753 7000692076 ybae abc transporter atp-binding protein homolog ybae (cl:atp-binding cassette homology) (db:pir2.dat) E69742 E69742 Bacillus subtilis 1423 -11529753 222733 ybae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to abc transporter (atp-binding protein)) (le:151301) (re:152131) (di:direct) BSUB0001 Z99104 g2632413 Bacillus subtilis 1423 -11529753 7500963317 orf5 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:861) (re:1691) (di:direct) D64126 D64126 g1644203 Bacillus subtilis 1423 -11529753

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763314	2351	24507	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763318	2352	24508	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763327	2353	24509	771	257

Description

6500725896 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaF ybaF Bacillus subtilis 1423 -11529754 7000693125 ybaf hypothetical protein ybaf (db:pir2.dat) F69742 F69742 Bacillus subtilis 1423 -11529754 7500964076 ybaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:152128) (re:152925) (di:direct) BSUB0001 Z99104 g2632414 Bacillus subtilis 1423 -11529754

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763342	2354	24510	882	294

Description

6500725897 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaJ ybaJ Bacillus subtilis 1423 -11529755 7000693126 ybaj hypothetical protein ybaj (cl:bioc homology) (db:pir2.dat) G69742 G69742 Bacillus subtilis 1423 -11529755 222740 ybaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:155155) (re:155922) (di:direct) BSUB0001 Z99104 g2632418 Bacillus subtilis 1423 -11529755 7500964077 orf10 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:4716) (re:5483) (di:direct) D64126 D64126 g1644210 Bacillus subtilis 1423 -11529755

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763352	2355	24511	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763355	2356	24512	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763357	2357	24513	228	75

Description

6500725898 ybxh:ybak hypothetical protein:hypothetical 17.6 kd protein in cwld 5region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaK ybaK Bacillus subtilis 1423 -11529756 219115 ybak (de:hypothetical 17.6 kd protein in cwld 5'region (orf1)) (db:swissprot) YBAK_BACSU P50862 BACILLUS SUBTILIS 1423 -11529756 7000687263 ybak hypothetical protein ybak (db:pir2.dat) H69742 H69742 Bacillus subtilis 1423 -11529756 5000689140 (db:genpept-bct1) (de:b.subtilis cwld, rec223 and gerd genes.) (nt:orf1) (le:64) (re:507) (di:direct) BSCWLD X74737 g1177248 Bacillus subtilis 1423 -11529756 222741 ybak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybxh) (le:156108) (re:156551) (di:direct) BSUB0001 Z99104 g2632419 Bacillus subtilis 1423 -11529756 7500896535 orf11 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:5669) (re:6112) (di:direct) D64126 D64126 g1644211 Bacillus subtilis 1423 -11529756 7502851640 (db:genpept) (de:b.subtilis cwld, rec223 and gerd genes.) (nt:orf1) (le:64) (re:507) (di:direct) BSCWLD X74737 g1177248 Bacillus subtilis 1423 -11529756 110176 ybak (de:hypothetical 17.6 kd protein in cwld 5'region (orf1)) (db:swissprot) YBAK_BACSU P50862 BACILLUS SUBTILIS 1423 -11529756

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763386	2358	24514	303	101

Description

6500725899 ybxi:rec233:ybal hypothetical protein:hypothetical 38.6 kd protein in cwld-gerd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaL ybaL Bacillus subtilis 1423 -11529757 219117 ybal:rec233 (de:hypothetical 38.6 kd protein in cwld-gerd intergenic region) (db:swissprot) YBAL_BACSU P50863 BACILLUS SUBTILIS 1423 -11529757 7000687265 ybal atp-binding mrp-like protein homolog ybal (cl:conserved probable membrane protein yil003w) (db:pir2.dat) A69743 A69743 Bacillus subtilis 1423 -11529757 5000689141 rec233 (db:genpept-bct1) (de:b.subtilis cwld, rec223 and gerd genes.) (le:1376) (re:2434) (di:direct) BSCWLD X74737 g1177249 Bacillus subtilis 1423 -11529757 222743 ybal (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybxi; similar to atp-binding) (le:157420) (re:158478) (di:direct) BSUB0001 Z99104 g2632421 Bacillus subtilis 1423 -11529757 7500896538 orf14 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:6981) (re:8039) (di:direct) D64126 D64126 g1644213 Bacillus subtilis 1423 -11529757 7502851641 rec233 (db:genpept) (de:b.subtilis cwld, rec223 and gerd genes.) (le:1376) (re:2434) (di:direct) BSCWLD X74737 g1177249 Bacillus subtilis 1423 -11529757 110180 ybal:rec233 (de:hypothetical 38.6 kd protein in cwld-gerd intergenic region) (db:swissprot) YBAL_BACSU P50863 BACILLUS SUBTILIS 1423 -11529757

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763588	2359	24515	672	223

Description

6500725900 ybxc:ybam:kbaa hypothetical protein:kinb signaling pathway activation protein (gtcfc:12.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) kbaA kbaA Bacillus subtilis 1423 -11529758 80448 kbaa (de:kinb signaling pathway activation protein) (db:swissprot) KBAA_BACSU P16449 BACILLUS SUBTILIS 1423 -11529758 7000685663 kbaa kinb sporulation signaling pathway activator kbaa:integral membrane protein kbaa (db:pir2.dat) JC6024 JC6024 Bacillus subtilis 1423 -11529758 7500884483 kbaa (fn:activation of the kinb signaling pathway to) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybxc, ybam) (le:159181) (re:159777) (di:direct) BSUB0001 Z99104 g2632423 Bacillus subtilis 1423 -11529758 219873 orf15 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:8742) (re:9338) (di:direct) D64126 D64126 g1644215 Bacillus subtilis 1423 -11529758 222745 kbaa kbaa (fn:involved in activation of the kinb signaling) (db:genpept-bct2) (de:bacillus subtilis germination protein (gerd) gene, partial cds,kinb signaling pathway activation protein (kbaa) gene, completecds, and nodb homolog (orfx) gene, partial cds.) (nt:p... BSU23797 U23797 g1143817 Bacillus subtilis 1423 -11529758 170293 kbaa kinb sporulation signaling pathway activator kbaa:integral membrane protein kbaa (db:pir) JC6024 JC6024 Bacillus subtilis 1423 -11529758 5000689089 (de:(kbaa) (pn:kinb signaling pathway activation protein) (gtcfc:13.07) (ec:) (kbaa_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) kbaA kbaA Bacillus subtilis 1423 10022696

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763590	2360	24516	357	118

Description

6500725901 ybxg:yban hypothetical protein:similar to polysaccharide deacetylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaN ybaN Bacillus subtilis 1423 -11529759 7000694435 yban polysaccharide deacetylase homolog yban (cl:nodb homology) (db:pir2.dat) B69743 B69743 Bacillus subtilis 1423 -11529759 222746 yban (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybxg; similar to) (le:159778) (re:160542) (di:complement) BSUB0001 Z99104 g2632424 Bacillus subtilis 1423 -11529759 7500965091 orf16 unknown (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genes for ribosomal proteins l13 and s9, putativecell wall hydrolase cwld, gerd protein, 16s ribosomal rna and 23sribosomal rna.) (le:9339) (re:10103) (di:complement) D64126 D64126 g1644216 Bacillus subtilis 1423 -11529759

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763591	2361	24517	222	73

Description

6500725902 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaR ybaR Bacillus subtilis 1423 -11529760 7000692386 ybar conserved hypothetical protein ybar (cl:integral membrane protein hp0228) (db:pir2.dat) C69743 C69743 Bacillus subtilis 1423 -11529760 7500955222 ybar (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:177082) (re:178518) (di:direct) BSUB0001 Z99104 g2632425 Bacillus subtilis 1423 -11529760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763604	2362	24518	384	128

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763614	2363	24519	447	148

Description

6500725903 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybaS ybaS Bacillus subtilis 1423 -11529761 7000693127 ybas hypothetical protein ybas (db:pir2.dat) D69743 D69743 Bacillus subtilis 1423 -11529761 7500964078 ybas (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:178733) (re:179584) (di:direct) BSUB0001 Z99104 g2632426 Bacillus subtilis 1423 -11529761

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763616	2364	24520	480	159

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763624	2365	24521	1200	399

Description

6500725904 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbA ybbA Bacillus subtilis 1423 -11529762 7000693128 ybba hypothetical protein ybba (db:pir2.dat) E69743 E69743 Bacillus subtilis 1423 -11529762 7500964079 ybba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:179594) (re:180163) (di:complement) BSUB0001 Z99104 g2632427 Bacillus subtilis 1423 -11529762

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763631	2366	24522	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763640	2367	24523	312	104

Description

6500725905 yzbc:ybbb hypothetical protein:hypothetical transcriptional regulator in feua 5region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbB ybbB Bacillus subtilis 1423 -11529763 110200 ybbb (de:(orf3)) (db:swissprot) YBBB_BACSU P40408 BACILLUS SUBTILIS 1423 -11529763 7000687279 ybbb transcription regulator arac/xyls family homolog ybbb (db:pir2.dat) I39841 I39841 Bacillus subtilis 1423 -11529763 7500896562 ybbb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:2068) (re:3657) (di:complement) AB002150 AB002150 g1944004 Bacillus subtilis 1423 -11529763 215587 (sr:bacillus subtilis (individual_isolate ms94, strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis feua, b, and c genes, 3 orfs, 2 complete cds'sand 5'end.) (nt:putative initiation codon gug. homology with) (le:3532) (re:5121) (di:direct) BACFEUABC L19954 g438457 Bacillus subtilis 1423 -11529763 1500685646 ybbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yzbc; similar to) (le:183412) (re:185001) (di:complement) BSUB0001 Z99104 g2632431 Bacillus subtilis 1423 -11529763 170639 ybbb transcriptional regulator arac/xyls family homolog ybbb (db:pir) I39841 I39841 Bacillus subtilis 1423 -11529763 5000689149 (de:(ybbb) (pn:hypothetical transcriptional regulator in feua 5"region:orf3) (gtcfc:13.07) (ec:) (ybbb_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) ybbB ybbB Bacillus subtilis 1423 10051932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763641	2368	24524	717	238

Description

GTC ORF with score 278 to: (fn:membrane bound cation transporter) (db:genpept-pln1) (de:neurospora crassa calcium/proton exchanger (cax) mrna, completecds.) (nt:similar to the vacuolar ca+2/h+ exchanger of) (le:449) (re:1780) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763652	2369	24525	648	216

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763657	2370	24526	765	254

Description

6500725906 yzbb:ybbc hypothetical protein:hypothetical 46.0 kd protein in feua 5region precursor:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbC ybbC Bacillus subtilis 1423 -11529764 110202 ybbc (de:hypothetical 46.0 kd protein in feua 5'region precursor (orf2)) (db:swissprot) YBBC_BACSU P40407 BACILLUS SUBTILIS 1423 -11529764 7000687281 ybbc hypothetical protein ybbc (db:pir2.dat) I39840 I39840 Bacillus subtilis 1423 -11529764 7500896564 ybbc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:3848) (re:5092) (di:complement) AB002150 AB002150 g1944005 Bacillus subtilis 1423 -11529764 215586 (sr:bacillus subtilis (individual_isolate ms94, strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis feua, b, and c genes, 3 orfs, 2 complete cds'sand 5'end.) (nt:19/20 residue stretch (32-51) identical to) (le:2097) (re:3341) (di:direct) BACFEUABC L19954 g438456 Bacillus subtilis 1423 -11529764 1500685647 ybbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: yzbb) (le:185192) (re:186436) (di:complement) BSUB0001 Z99104 g2632432 Bacillus subtilis 1423 -11529764 170094 ybbc hypothetical protein ybbc (db:pir) I39840 I39840 Bacillus subtilis 1423 -11529764 5000689150 (de:(ybbc) (pn:hypothetical 46) (gtcfc:13.07) (ec:) (ybbc_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) ybbC ybbC Bacillus subtilis 1423 10051934

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763664	2371	24527	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763684	2372	24528	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763697	2373	24529	864	288

Description

GTC ORF with score 208 to: (sr:schizosaccharomyces pombe cdna to mrna, clone_lib:pgad gh) (db:genpept-pln2) (de:schizosaccharomyces pombe mrna, partial cds, similar to human ga17protein.) (nt:unknown: similar to human ga17 protein) (le:<1) (re:1246) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763703	2374	24530	843	280

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763716	2375	24531	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763718	2376	24532	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763982	2377	24533	975	325

Description

6500725907 hypothetical protein:similar to beta-lactamase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbE ybbE Bacillus subtilis 1423 -11529765 7000692264 ybbe beta-lactamase homolog ybbe (db:pir2.dat) A69744 A69744 Bacillus subtilis 1423 -11529765 7500963446 ybbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to beta-lactamase) (le:188406) (re:189731) (di:complement) BSUB0001 Z99104 g2632434 Bacillus subtilis 1423 -11529765

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763989	2378	24534	285	94

Description

6500725908 hypothetical protein:similar to sucrose phosphotransferase enzyme ii (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbF ybbF Bacillus subtilis 1423 -11529766 7000694645 ybbf sucrose phosphotransferase enzyme ii homolog ybbf (cl:phosphotransferase system sucrose-specific enzyme ii, factor ii) (db:pir2.dat) B69744 B69744 Bacillus subtilis 1423 -11529766 215704 ybbf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:8473) (re:9813) (di:complement) AB002150 AB002150 g1256135 Bacillus subtilis 1423 -11529766 3500684454 ybbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to sucrose phosphotransferase enzyme ii) (le:189816) (re:191156) (di:complement) BSUB0001 Z99104 g2632435 Bacillus subtilis 1423 -11529766

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763990	2379	24535	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501763991	2380	24536	528	175

Description

6500725909 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbH ybbH Bacillus subtilis 1423 -11529767 7000692387 ybbh conserved hypothetical protein ybbh (cl:hypothetical protein ybbh) (db:pir2.dat) C69744 C69744 Bacillus subtilis 1423 -11529767 7500955861 ybbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:191182) (re:192033) (di:complement) BSUB0001 Z99104 g2632436 Bacillus subtilis 1423 -11529767

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764014	2381	24537	798	265

Description

6500725910 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbI ybbI Bacillus subtilis 1423 -11529768 7000692388 ybbi conserved hypothetical protein ybbi (cl:conserved hypothetical protein b2428) (db:pir2.dat) D69744 D69744 Bacillus subtilis 1423 -11529768 7500963550 ybbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to hypothetical proteins) (le:192050) (re:192964) (di:complement) BSUB0001 Z99104 g2632437 Bacillus subtilis 1423 -11529768

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764017	2382	24538	516	172

Description

6500725911 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbJ ybbJ Bacillus subtilis 1423 -11529769 7000693129 ybbj hypothetical protein ybbj (db:pir2.dat) E69744 E69744 Bacillus subtilis 1423 -11529769 215708 ybbj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:11793) (re:12212) (di:complement) AB002150 AB002150 g1256139 Bacillus subtilis 1423 -11529769 3500684456 ybbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:193135) (re:193554) (di:complement) BSUB0001 Z99104 g2632438 Bacillus subtilis 1423 -11529769

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764020	2383	24539	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764032	2384	24540	945	315

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764035	2385	24541	891	296

Description

6500725912 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbK ybbK Bacillus subtilis 1423 -11529770 7000693130 ybbk hypothetical protein ybbk (db:pir2.dat) F69744 F69744 Bacillus subtilis 1423 -11529770 215709 ybbk (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:12225) (re:12680) (di:complement) AB002150 AB002150 g1256140 Bacillus subtilis 1423 -11529770 3500684457 ybbk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:193567) (re:194022) (di:complement) BSUB0001 Z99104 g2632439 Bacillus subtilis 1423 -11529770

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764045	2386	24542	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764048	2387	24543	246	81

Description

6500725913 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbM ybbM Bacillus subtilis 1423 -11529771 7000693131 ybbm hypothetical protein ybbm (db:pir2.dat) G69744 G69744 Bacillus subtilis 1423 -11529771 6000689998 ybbm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:195415) (re:196041) (di:direct) BSUB0001 Z99104 g2632441 Bacillus subtilis 1423 -11529771 7500964080 ybbm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:765) (re:1391) (di:direct) BSUB0002 Z99105 g2632459 Bacillus subtilis 1423 -11529771

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764059	2388	24544	255	84

Description

6500725914 ybbq:ybbp hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbP ybbP Bacillus subtilis 1423 -11529772 7000692389 ybbp conserved hypothetical protein ybbp (cl:hypothetical protein ybbp) (db:pir2.dat) H69744 H69744 Bacillus subtilis 1423 -11529772 1500693167 ybbp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis dna for feub, feua, ybbb, ybbc, ybbd, ybza, ybbe,ybbf, ybbh, ybbi, ybbj, ybbk, ybbl, ybbm, ybbp, complete cds.) (le:14863) (re:15684) (di:direct) AB002150 AB002150 g1944009 Bacillus subtilis 1423 -11529772 6000686401 ybbp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:alternate gene name: ybbq; similar to hypothetical) (le:196202) (re:197023) (di:direct) BSUB0001 Z99104 g2632442 Bacillus subtilis 1423 -11529772 7500955957 ybbp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ybbq; similar to hypothetical) (le:1552) (re:2373) (di:direct) BSUB0002 Z99105 g2632460 Bacillus subtilis 1423 -11529772

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764060	2389	24545	693	230

Description

6500725915 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbR ybbR Bacillus subtilis 1423 -11529773 7000693132 ybbr hypothetical protein ybbr (db:pir2.dat) A69745 A69745 Bacillus subtilis 1423 -11529773 6000690000 ybbr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:197016) (re:198467) (di:direct) BSUB0001 Z99104 g2632443 Bacillus subtilis 1423 -11529773 7500964081 ybbr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:2366) (re:3817) (di:direct) BSUB0002 Z99105 g2632461 Bacillus subtilis 1423 -11529773

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764068	2390	24546	261	86

Description

GTC ORF with score 133 to: (or:Pneumocystis carinii) (cl:fasb-fasc-fasd multifunctional enzyme:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase homology:dihydroneopterin aldolase homology:dihydropteroate synthase homology) (db:pir2.dat)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764072	2391	24547	387	128

Description

6500725916 hypothetical protein:similar to phosphoglucomutase:glycolysis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbT ybbT Bacillus subtilis 1423 -11529774 7000694408 ybbt phosphoglucomutase glycolysis homolog ybbt (cl:probable phosphorylating protein urec) (db:pir2.dat) B69745 B69745 Bacillus subtilis 1423 -11529774 6000690002 ybbt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to phosphoglucomutase (glycolysis)) (le:198486) (re:199832) (di:direct) BSUB0001 Z99104 g2632444 Bacillus subtilis 1423 -11529774 7500965069 ybbt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to phosphoglucomutase (glycolysis)) (le:3836) (re:5182) (di:direct) BSUB0002 Z99105 g2632462 Bacillus subtilis 1423 -11529774

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764082	2392	24548	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764083	2393	24549	1185	395

Description

6500725917 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybbU ybbU Bacillus subtilis 1423 -11529775 7000693133 ybbu hypothetical protein ybbu (db:pir2.dat) C69745 C69745 Bacillus subtilis 1423 -11529775 6000690004 ybbu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:202112) (re:202252) (di:direct) BSUB0001 Z99104 g2632446 Bacillus subtilis 1423 -11529775 7500964082 ybbu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:7462) (re:7602) (di:direct) BSUB0002 Z99105 g2632464 Bacillus subtilis 1423 -11529775 7500964083 ybzd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:5095) (re:5235) (di:direct) AB006424 AB006424 g3599597 Bacillus subtilis 1423 -11529775

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764093	2394	24550	696	231

Description

6500725918 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcC ybcC Bacillus subtilis 1423 -11529776 7000693134 ybcc hypothetical protein ybcc (db:pir2.dat) D69745 D69745 Bacillus subtilis 1423 -11529776 6000690006 ybcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:206927) (re:207169) (di:direct) BSUB0001 Z99104 g2632451 Bacillus subtilis 1423 -11529776 7500964084 ybcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:12277) (re:12519) (di:direct) BSUB0002 Z99105 g2632469 Bacillus subtilis 1423 -11529776

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764097	2395	24551	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764114	2396	24552	609	202

Description

6500725919 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcD ybcD Bacillus subtilis 1423 -11529777 7000693135 ybcd hypothetical protein ybcd (db:pir2.dat) E69745 E69745 Bacillus subtilis 1423 -11529777 6000690008 ybcd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:207166) (re:209430) (di:direct) BSUB0001 Z99104 g2632452 Bacillus subtilis 1423 -11529777 7500964085 ybcd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:12516) (re:14780) (di:direct) BSUB0002 Z99105 g2632470 Bacillus subtilis 1423 -11529777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764123	2397	24553	357	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764126	2398	24554	456	151

Description

6500725920 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcF ybcF Bacillus subtilis 1423 -11529778 7000693136 ybcf hypothetical protein ybcf (cl:methanobacterium thermoautotrophicum carbonic anhydrase) (db:pir2.dat) F69745 F69745 Bacillus subtilis 1423 -11529778 6000690010 ybcf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:209619) (re:210146) (di:direct) BSUB0001 Z99104 g2632453 Bacillus subtilis 1423 -11529778 7500964086 ybcf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:14969) (re:15496) (di:direct) BSUB0002 Z99105 g2632471 Bacillus subtilis 1423 -11529778

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764127	2399	24555	744	247

Description

6500725921 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcH ybcH Bacillus subtilis 1423 -11529779 7000693137 ybch hypothetical protein ybch (db:pir2.dat) G69745 G69745 Bacillus subtilis 1423 -11529779 6000690012 ybch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:210210) (re:210500) (di:direct) BSUB0001 Z99104 g2632454 Bacillus subtilis 1423 -11529779 7500964087 ybch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:15560) (re:15850) (di:direct) BSUB0002 Z99105 g2632472 Bacillus subtilis 1423 -11529779 7500964088 ybch (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:13201) (re:13491) (di:direct) AB006424 AB006424 g3599605 Bacillus subtilis 1423 -11529779

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764128	2400	24556	345	114

Description

6500725922 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcI ybcI Bacillus subtilis 1423 -11529780 7000693138 ybci hypothetical protein ybci (db:pir2.dat) H69745 H69745 Bacillus subtilis 1423 -11529780 6000690014 ybci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (le:210558) (re:210932) (di:direct) BSUB0001 Z99104 g2632455 Bacillus subtilis 1423 -11529780 7500964089 ybci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:15908) (re:16282) (di:direct) BSUB0002 Z99105 g2632473 Bacillus subtilis 1423 -11529780 7500964090 ybci (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:13549) (re:13923) (di:direct) AB006424 AB006424 g3599606 Bacillus subtilis 1423 -11529780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764131	2401	24557	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764135	2402	24558	939	312

Description

6500725923 hypothetical protein:similar to chloramphenicol resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcL ybcL Bacillus subtilis 1423 -11529781 7000692363 ybcl chloramphenicol resistance protein homolog ybcl (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) A69746 A69746 Bacillus subtilis 1423 -11529781 6000690016 ybcl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 1 of 21): from 1 to213080.) (nt:similar to chloramphenicol resistance protein) (le:211845) (re:213017) (di:direct) BSUB0001 Z99104 g2632456 Bacillus subtilis 1423 -11529781 7500963525 ybcl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to chloramphenicol resistance protein) (le:17195) (re:18367) (di:direct) BSUB0002 Z99105 g2632474 Bacillus subtilis 1423 -11529781 7500963526 ybcl (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:14840) (re:16012) (di:direct) AB006424 AB006424 g3599609 Bacillus subtilis 1423 -11529781

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764136	2403	24559	201	66

Description

6500725924 hypothetical protein:similar to glucosamine-fructose-6-phosphate aminotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcM ybcM Bacillus subtilis 1423 -11529782 7000693030 ybcm glucosamine-fructose-6-phosphate aminotran homolog ybcm (db:pir2.dat) B69746 B69746 Bacillus subtilis 1423 -11529782 7500964011 ybcm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glucosamine-fructose-6-phosphate) (le:18491) (re:18805) (di:direct) BSUB0002 Z99105 g2632475 Bacillus subtilis 1423 -11529782 7500964012 ybcm (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:16136) (re:16450) (di:direct) AB006424 AB006424 g3599610 Bacillus subtilis 1423 -11529782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764144	2404	24560	468	155

Description

6500725925 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcO ybcO Bacillus subtilis 1423 -11529783 7000693139 ybco hypothetical protein ybco (db:pir2.dat) C69746 C69746 Bacillus subtilis 1423 -11529783 7500964091 ybco (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:19276) (re:19443) (di:direct) BSUB0002 Z99105 g2632476 Bacillus subtilis 1423 -11529783 7500964092 ybco (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:16922) (re:17089) (di:direct) AB006424 AB006424 g3599611 Bacillus subtilis 1423 -11529783

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764155	2405	24561	384	127

Description

6500725926 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcP ybcP Bacillus subtilis 1423 -11529784 7000693140 ybcp hypothetical protein ybcp (db:pir2.dat) D69746 D69746 Bacillus subtilis 1423 -11529784 7500964093 ybcp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:19510) (re:19899) (di:direct) BSUB0002 Z99105 g2632477 Bacillus subtilis 1423 -11529784 7500964094 ybcp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:17156) (re:17545) (di:direct) AB006424 AB006424 g3599612 Bacillus subtilis 1423 -11529784

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764158	2406	24562	741	246

Description

GTC ORF with score 622 to: (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (nt:f587; formerly designated yidu) (le:4924) (re:6687) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764172	2407	24563	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764388	2408	24564	726	241

Description

6500725927 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcQ ybcQ Bacillus subtilis 1423 -11529785 7000692390 ybcq conserved hypothetical protein ybcq (db:pir2.dat) E69746 E69746 Bacillus subtilis 1423 -11529785 7500963551 ybcq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:19943) (re:20743) (di:direct) BSUB0002 Z99105 g2632478 Bacillus subtilis 1423 -11529785

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764394	2409	24565	423	140

Description

6500725928 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcS ybcS Bacillus subtilis 1423 -11529786 7000693141 ybcs hypothetical protein ybcs (db:pir2.dat) F69746 F69746 Bacillus subtilis 1423 -11529786 7500964095 ybcs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:20740) (re:21297) (di:direct) BSUB0002 Z99105 g2632479 Bacillus subtilis 1423 -11529786 7500964096 ybcs (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:18387) (re:18944) (di:direct) AB006424 AB006424 g3599615 Bacillus subtilis 1423 -11529786

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764397	2410	24566	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764398	2411	24567	789	263

Description

6500725929 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybcT ybcT Bacillus subtilis 1423 -11529787 7000693142 ybct hypothetical protein ybct (db:pir2.dat) G69746 G69746 Bacillus subtilis 1423 -11529787 7500964097 ybct (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:21294) (re:22229) (di:direct) BSUB0002 Z99105 g2632480 Bacillus subtilis 1423 -11529787 7500964098 ybct (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:18941) (re:19876) (di:direct) AB006424 AB006424 g3599616 Bacillus subtilis 1423 -11529787

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764412	2412	24568	414	137

Description

6500725930 hypothetical protein:similar to abc transporter:binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdA ybdA Bacillus subtilis 1423 -11529788 7000692110 ybda abc transporter binding protein homolog ybda (cl:atp-binding cassette homology) (db:pir2.dat) H69746 H69746 Bacillus subtilis 1423 -11529788 7500963349 ybda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to abc transporter (binding protein)) (le:22248) (re:22967) (di:direct) BSUB0002 Z99105 g2632481 Bacillus subtilis 1423 -11529788 7500963350 ybda (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:19895) (re:20614) (di:direct) AB006424 AB006424 g3599617 Bacillus subtilis 1423 -11529788

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764416	2413	24569	483	161

Description

6500725931 hypothetical protein:similar to abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdB ybdB Bacillus subtilis 1423 -11529789 7000692117 ybdb abc transporter permease homolog ybdb (db:pir2.dat) A69747 A69747 Bacillus subtilis 1423 -11529789 7500963356 ybdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to abc transporter (permease)) (le:23032) (re:24378) (di:direct) BSUB0002 Z99105 g2632482 Bacillus subtilis 1423 -11529789 7500963357 ybdb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:20679) (re:22025) (di:direct) AB006424 AB006424 g3599618 Bacillus subtilis 1423 -11529789

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764439	2414	24570	1302	433

Description

GTC ORF with score 473 to: (db:genpept-bct1) (de:burkholderia pseudomallei putative dihydroorotase (pyrc) gene,partial cds; putative 1-acyl-sn-glycerol-3-phosphateacyltransferase (plsc), putative diadenosine tetraphosphatase(apah), complete cds; type ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764442	2415	24571	537	178

Description

6500725932 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdD ybdD Bacillus subtilis 1423 -11529790 7000693143 ybdd hypothetical protein ybdd (db:pir2.dat) B69747 B69747 Bacillus subtilis 1423 -11529790 7500964099 ybdd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:24425) (re:24838) (di:direct) BSUB0002 Z99105 g2632483 Bacillus subtilis 1423 -11529790 7500964100 ybdd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:22072) (re:22485) (di:direct) AB006424 AB006424 g3599619 Bacillus subtilis 1423 -11529790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764444	2416	24572	204	67

Description

6500725933 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdE ybdE Bacillus subtilis 1423 -11529791 7000692391 ybde conserved hypothetical protein ybde (db:pir2.dat) C69747 C69747 Bacillus subtilis 1423 -11529791 7500963552 ybde (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:24944) (re:25369) (di:direct) BSUB0002 Z99105 g2632484 Bacillus subtilis 1423 -11529791 7500963553 ybde (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:22591) (re:23016) (di:direct) AB006424 AB006424 g3599620 Bacillus subtilis 1423 -11529791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764447	2417	24573	210	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764450	2418	24574	933	311

Description

6500725934 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdG ybdG Bacillus subtilis 1423 -11529792 7000693144 ybdg hypothetical protein ybdg (db:pir2.dat) D69747 D69747 Bacillus subtilis 1423 -11529792 7500964101 ybdg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:25615) (re:26505) (di:direct) BSUB0002 Z99105 g2632485 Bacillus subtilis 1423 -11529792

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764460	2419	24575	1161	386

Description

GTC ORF with score 119 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764485	2420	24576	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764504	2421	24577	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764508	2422	24578	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764522	2423	24579	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764526	2424	24580	996	331

Description

6500725935 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdJ ybdJ Bacillus subtilis 1423 -11529793 7000694839 ybdj two-component response regulator ybdk homolog ybdj) (cl:ompr protein:response regulator homology) (db:pir2.dat) E69747 E69747 Bacillus subtilis 1423 -11529793 7500965387 ybdj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to two-component response regulator (ybdk)) (le:26597) (re:27268) (di:direct) BSUB0002 Z99105 g2632486 Bacillus subtilis 1423 -11529793 7500965388 ybdj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:24248) (re:24919) (di:direct) AB006424 AB006424 g3599623 Bacillus subtilis 1423 -11529793

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764527	2425	24581	345	114

Description

6500725936 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdK ybdK Bacillus subtilis 1423 -11529794 7000694867 ybdk two-component sensor histidine kinase homolog ybdk (db:pir2.dat) F69747 F69747 Bacillus subtilis 1423 -11529794 7500965404 ybdk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to two-component sensor histidine kinase) (le:27289) (re:28251) (di:direct) BSUB0002 Z99105 g2632487 Bacillus subtilis 1423 -11529794 7500965405 ybdk (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:24940) (re:25902) (di:direct) AB006424 AB006424 g3599624 Bacillus subtilis 1423 -11529794

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764541	2426	24582	420	139

Description

6500725937 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdL ybdL Bacillus subtilis 1423 -11529795 7000693145 ybdl hypothetical protein ybdl (db:pir2.dat) G69747 G69747 Bacillus subtilis 1423 -11529795 7500964102 ybdl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:28321) (re:28515) (di:direct) BSUB0002 Z99105 g2632488 Bacillus subtilis 1423 -11529795 7500964103 ybdl (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:25972) (re:26166) (di:direct) AB006424 AB006424 g3599625 Bacillus subtilis 1423 -11529795

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764557	2427	24583	276	92

Description

6500725938 hypothetical protein:similar to protein kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdM ybdM Bacillus subtilis 1423 -11529796 7000694456 ybdm protein kinase homolog ybdm (db:pir2.dat) H69747 H69747 Bacillus subtilis 1423 -11529796 7500965105 ybdm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to protein kinase) (le:28558) (re:29328) (di:complement) BSUB0002 Z99105 g2632489 Bacillus subtilis 1423 -11529796 7500965106 ybdm (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:26209) (re:26979) (di:complement) AB006424 AB006424 g3599626 Bacillus subtilis 1423 -11529796

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764791	2428	24584	759	252

Description

6500725939 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdN ybdN Bacillus subtilis 1423 -11529797 7000693146 ybdn hypothetical protein ybdn (db:pir2.dat) A69748 A69748 Bacillus subtilis 1423 -11529797 7500964104 ybdn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:29414) (re:30271) (di:complement) BSUB0002 Z99105 g2632490 Bacillus subtilis 1423 -11529797 7500964105 ybdn (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:27065) (re:27922) (di:complement) AB006424 AB006424 g3599627 Bacillus subtilis 1423 -11529797

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764798	2429	24585	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764803	2430	24586	336	111

Description

6500725940 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdO ybdO Bacillus subtilis 1423 -11529798 7000693147 ybdo hypothetical protein ybdo (db:pir2.dat) B69748 B69748 Bacillus subtilis 1423 -11529798 7500964106 ybdo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:30403) (re:31587) (di:direct) BSUB0002 Z99105 g2632491 Bacillus subtilis 1423 -11529798 7500964107 ybdo (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:28054) (re:29238) (di:direct) AB006424 AB006424 g3599628 Bacillus subtilis 1423 -11529798

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764807	2431	24587	348	115

Description

6500725941 ybdp:ybxg hypothetical protein:similar to amino acid permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybxG ybxG Bacillus subtilis 1423 -11529799 7500896983 ybxg:ybdp (de:hypothetical transport protein in ndhf-csga intergenic region (orf1)) (db:swissprot) YBXG_BACSU P54425 BACILLUS SUBTILIS 1423 -11529799 7000692195 ybxg amino acid permease homolog ybxg (cl:arginine permease) (db:pir2.dat) H69751 H69751 Bacillus subtilis 1423 -11529799 7500896985 ybxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ybdp; similar to amino acid) (le:31905) (re:33293) (di:direct) BSUB0002 Z99105 g2632492 Bacillus subtilis 1423 -11529799 7500896986 ybdp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:29556) (re:30944) (di:direct) AB006424 AB006424 g3599629 Bacillus subtilis 1423 -11529799

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764811	2432	24588	546	181

Description

5000689153 hypothetical protein:hypothetical 7.5 kd protein in csga 3region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybxH ybxH Bacillus subtilis 1423 -11529800 7500896987 ybxh (de:hypothetical 7.5 kd protein in csga 3'region (orf3)) (db:swissprot) YBXH_BACSU P54426 BACILLUS SUBTILIS 1423 -11529800 7000687390 ybxh:csgac hypothetical protein ybxh:csgac protein (db:pir2.dat) JC6189 JC6189 Bacillus subtilis 1423 -11529800 6500725942 orf3 (db:genpept-bct1) (de:b.subtilis orf1, csga, orf2, orf3, and orf4 genes.) (nt:may be cotranscribed with csga) (le:753) (re:944) (di:direct) BSCSGAORF X92859 g1212790 Bacillus subtilis 1423 -11529800 219101 ybxh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:33670) (re:33861) (di:direct) BSUB0002 Z99105 g2632494 Bacillus subtilis 1423 -11529800 110416 ybxh (de:hypothetical 7.5 kd protein in csga 3'region (orf3)) (db:swissprot) YBXH_BACSU P54426 BACILLUS SUBTILIS 1423 -11529800 4000707429 ybxh:csgac hypothetical protein ybxh:csgac protein (db:pir) JC6189 JC6189 Bacillus subtilis 1423 -11529800

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764814	2433	24589	234	77

Description

6500725943 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybdT ybdT Bacillus subtilis 1423 -11529801 7000693148 ybdt hypothetical protein ybdt (db:pir2.dat) C69748 C69748 Bacillus subtilis 1423 -11529801 7500964108 ybdt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:34864) (re:36117) (di:direct) BSUB0002 Z99105 g2632496 Bacillus subtilis 1423 -11529801 7500964109 ybdt (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:32515) (re:33768) (di:direct) AB006424 AB006424 g3599632 Bacillus subtilis 1423 -11529801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764833	2434	24590	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764840	2435	24591	396	131

Description

6500725944 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybyB ybyB Bacillus subtilis 1423 -11529802 7000693157 ybyb hypothetical protein ybyb (db:pir2.dat) C69752 C69752 Bacillus subtilis 1423 -11529802 7500964125 ybyb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:36158) (re:36418) (di:complement) BSUB0002 Z99105 g2632497 Bacillus subtilis 1423 -11529802

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764853	2436	24592	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764861	2437	24593	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764863	2438	24594	447	148

Description

6500725945 hypothetical protein:similar to amino acid transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybeC ybeC Bacillus subtilis 1423 -11529803 7000692200 ybec amino acid transporter homolog ybec (db:pir2.dat) D69748 D69748 Bacillus subtilis 1423 -11529803 7500963407 ybec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to amino acid transporter) (le:36687) (re:38306) (di:direct) BSUB0002 Z99105 g2632498 Bacillus subtilis 1423 -11529803 7500963408 ybec (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:34338) (re:35957) (di:direct) AB006424 AB006424 g3599634 Bacillus subtilis 1423 -11529803

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764865	2439	24595	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764880	2440	24596	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764894	2441	24597	315	104

Description

6500725946 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybeF ybeF Bacillus subtilis 1423 -11529804 7000693149 ybef hypothetical protein ybef (db:pir2.dat) E69748 E69748 Bacillus subtilis 1423 -11529804 7500964110 ybef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:40964) (re:41212) (di:direct) BSUB0002 Z99105 g2632501 Bacillus subtilis 1423 -11529804 7500964111 ybef (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:38615) (re:38863) (di:direct) AB006424 AB006424 g3599637 Bacillus subtilis 1423 -11529804

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764896	2442	24598	222	73

Description

6500725947 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfA ybfA Bacillus subtilis 1423 -11529805 7000693150 ybfa hypothetical protein ybfa (db:pir2.dat) F69748 F69748 Bacillus subtilis 1423 -11529805 7500964112 ybfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:41304) (re:42221) (di:direct) BSUB0002 Z99105 g2632502 Bacillus subtilis 1423 -11529805 7500964113 ybfa (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:38955) (re:39872) (di:direct) AB006424 AB006424 g3599638 Bacillus subtilis 1423 -11529805

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764903	2443	24599	300	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764909	2444	24600	1086	361

Description

6500725948 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfB ybfB Bacillus subtilis 1423 -11529806 7000692392 ybfb conserved hypothetical protein ybfb (db:pir2.dat) G69748 G69748 Bacillus subtilis 1423 -11529806 7500963554 ybfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:42218) (re:43468) (di:direct) BSUB0002 Z99105 g2632503 Bacillus subtilis 1423 -11529806 7500963555 ybfb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:39869) (re:41119) (di:direct) AB006424 AB006424 g3599639 Bacillus subtilis 1423 -11529806

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764922	2445	24601	513	171

Description

6500725949 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfE ybfE Bacillus subtilis 1423 -11529807 7000693151 ybfe hypothetical protein ybfe (db:pir2.dat) H69748 H69748 Bacillus subtilis 1423 -11529807 7500964114 ybfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:43503) (re:43787) (di:complement) BSUB0002 Z99105 g2632504 Bacillus subtilis 1423 -11529807 7500964115 ybfe (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:41154) (re:41438) (di:complement) AB006424 AB006424 g3599640 Bacillus subtilis 1423 -11529807

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764926	2446	24602	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764927	2447	24603	645	214

Description

6500725950 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfF ybfF Bacillus subtilis 1423 -11529808 7000693152 ybff hypothetical protein ybff (db:pir2.dat) A69749 A69749 Bacillus subtilis 1423 -11529808 7500964116 ybff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:43983) (re:44894) (di:complement) BSUB0002 Z99105 g2632505 Bacillus subtilis 1423 -11529808 7500964117 ybff (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:41634) (re:42545) (di:complement) AB006424 AB006424 g3599641 Bacillus subtilis 1423 -11529808

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764940	2448	24604	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764954	2449	24605	207	69

Description

6500725951 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfG ybfG Bacillus subtilis 1423 -11529809 7000693153 ybfg hypothetical protein ybfg (db:pir2.dat) B69749 B69749 Bacillus subtilis 1423 -11529809 7500964118 ybfg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:44983) (re:47181) (di:complement) BSUB0002 Z99105 g2632506 Bacillus subtilis 1423 -11529809 7500964119 ybfg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:42634) (re:44832) (di:complement) AB006424 AB006424 g3599642 Bacillus subtilis 1423 -11529809

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764955	2450	24606	465	154

Description

6500725952 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfH ybfH Bacillus subtilis 1423 -11529810 7000692393 ybfh conserved hypothetical protein ybfh (db:pir2.dat) C69749 C69749 Bacillus subtilis 1423 -11529810 7500963556 ybfh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:47256) (re:48176) (di:complement) BSUB0002 Z99105 g2632507 Bacillus subtilis 1423 -11529810 7500963557 ybfh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:44907) (re:45827) (di:complement) AB006424 AB006424 g3599643 Bacillus subtilis 1423 -11529810

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501764957	2451	24607	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765125	2452	24608	222	73

Description

6500725953 hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfI ybfI Bacillus subtilis 1423 -11529811 7000694712 ybfi transcription regulator arac/xyls family homolog ybfi (db:pir2.dat) D69749 D69749 Bacillus subtilis 1423 -11529811 7500965286 ybfi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (arac/xyls) (le:48173) (re:49000) (di:complement) BSUB0002 Z99105 g2632508 Bacillus subtilis 1423 -11529811 7500965287 ybfi (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:45824) (re:46651) (di:complement) AB006424 AB006424 g3599644 Bacillus subtilis 1423 -11529811

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765131	2453	24609	408	135

Description

6500725954 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfJ ybfJ Bacillus subtilis 1423 -11529812 7000693154 ybfj hypothetical protein ybfj (db:pir2.dat) E69749 E69749 Bacillus subtilis 1423 -11529812 7500964120 ybfj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:51433) (re:51831) (di:direct) BSUB0002 Z99105 g2632511 Bacillus subtilis 1423 -11529812 7500964121 ybfj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:49084) (re:49482) (di:direct) AB006424 AB006424 g3599647 Bacillus subtilis 1423 -11529812

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765132	2454	24610	222	73

Description

6500725955 hypothetical protein:similar to carboxylesterase (gtcfc:14.1) (ec:3.1.1.1) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfK ybfK Bacillus subtilis 1423 -11529813 7000692323 ybfk carboxylesterase homolog ybfk (db:pir2.dat) F69749 F69749 Bacillus subtilis 1423 -11529813 7500963492 ybfk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to carboxylesterase) (le:51997) (re:52887) (di:direct) BSUB0002 Z99105 g2632512 Bacillus subtilis 1423 -11529813 7500963493 ybfk (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:49648) (re:50538) (di:direct) AB006424 AB006424 g3599648 Bacillus subtilis 1423 -11529813

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765133	2455	24611	195	64

Description

6500725956 hypothetical protein:similar to alkaline phosphatase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfM ybfM Bacillus subtilis 1423 -11529814 7000692172 ybfm alkaline phosphatase homolog ybfm (cl:probable alkaline phosphatase yngc) (db:pir2.dat) G69749 G69749 Bacillus subtilis 1423 -11529814 7500963390 ybfm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to alkaline phosphatase) (le:53607) (re:54095) (di:direct) BSUB0002 Z99105 g2632514 Bacillus subtilis 1423 -11529814 7500963391 ybfm (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:51258) (re:51746) (di:direct) AB006424 AB006424 g3599650 Bacillus subtilis 1423 -11529814

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765147	2456	24612	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765154	2457	24613	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765155	2458	24614	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765169	2459	24615	195	64

Description

GTC ORF with score 96 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid w01a11.) (nt:coded for by c. elegans cdna cm17d4; similar to) (le:26238:26367:27958:28106) (re:26321:26468:28053:28551) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765170	2460	24616	342	113

Description

6500725957 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfN ybfN Bacillus subtilis 1423 -11529815 7000693155 ybfn hypothetical protein ybfn (db:pir2.dat) H69749 H69749 Bacillus subtilis 1423 -11529815 7500964122 ybfn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:54934) (re:55212) (di:direct) BSUB0002 Z99105 g2632516 Bacillus subtilis 1423 -11529815 7500964123 ybfn (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:52585) (re:52863) (di:direct) AB006424 AB006424 g3599652 Bacillus subtilis 1423 -11529815

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765178	2461	24617	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765189	2462	24618	456	152

Description

6500725958 hypothetical protein:similar to erythromycin esterase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfO ybfO Bacillus subtilis 1423 -11529816 7000692970 ybfo erythromycin esterase homolog ybfo (db:pir2.dat) A69750 A69750 Bacillus subtilis 1423 -11529816 7500963973 ybfo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to erythromycin esterase) (le:55318) (re:56658) (di:direct) BSUB0002 Z99105 g2632517 Bacillus subtilis 1423 -11529816 7500963974 ybfo (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:52969) (re:54309) (di:direct) AB006424 AB006424 g3599653 Bacillus subtilis 1423 -11529816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765203	2463	24619	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765211	2464	24620	987	328

Description

6500725959 hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfP ybfP Bacillus subtilis 1423 -11529817 7000694713 ybfp transcription regulator arac/xyls family homolog ybfp (db:pir2.dat) B69750 B69750 Bacillus subtilis 1423 -11529817 7500965288 ybfp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (arac/xyls) (le:56766) (re:57653) (di:direct) BSUB0002 Z99105 g2632518 Bacillus subtilis 1423 -11529817 7500965289 ybfp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:54417) (re:55304) (di:direct) AB006424 AB006424 g3599654 Bacillus subtilis 1423 -11529817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765230	2465	24621	369	123

Description

6500725960 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybfQ ybfQ Bacillus subtilis 1423 -11529818 7000692394 ybfq ycea protein homolog ybfq (cl:escherichia coli ycea protein) (db:pir2.dat) C69750 C69750 Bacillus subtilis 1423 -11529818 7500955863 ybfq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:57853) (re:58821) (di:direct) BSUB0002 Z99105 g2632519 Bacillus subtilis 1423 -11529818 7500955864 ybfq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:55504) (re:56472) (di:direct) AB006424 AB006424 g3599655 Bacillus subtilis 1423 -11529818

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765232	2466	24622	246	81

Description

6500725961 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybgA ybgA Bacillus subtilis 1423 -11529819 7000694735 ybga transcription regulator gntr family homolog ybga (cl:transcription regulator gntr) (db:pir2.dat) F69750 F69750 Bacillus subtilis 1423 -11529819 7500955357 ybga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (gntr family)) (le:63130) (re:63837) (di:direct) BSUB0002 Z99105 g2632523 Bacillus subtilis 1423 -11529819 7500955358 ybga (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:60781) (re:61488) (di:direct) AB006424 AB006424 g3599659 Bacillus subtilis 1423 -11529819

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765241	2467	24623	666	221

Description

6500725962 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybgB ybgB Bacillus subtilis 1423 -11529820 7000693156 ybgb hypothetical protein ybgb (db:pir2.dat) G69750 G69750 Bacillus subtilis 1423 -11529820 7500964124 ybgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:63871) (re:64146) (di:direct) BSUB0002 Z99105 g2632524 Bacillus subtilis 1423 -11529820

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765246	2468	24624	1083	360

Description

6500725963 hypothetical protein:similar to branched-chain amino acid aminotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybgE ybgE Bacillus subtilis 1423 -11529821 7000692290 ybge branched-chain amino acid aminotransferase homolog ybge (cl:branched-chain-amino-acid transaminase bat1) (db:pir2.dat) H69750 H69750 Bacillus subtilis 1423 -11529821 7500963460 ybge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to branched-chain amino acid) (le:64355) (re:65425) (di:direct) BSUB0002 Z99105 g2632525 Bacillus subtilis 1423 -11529821 7500963461 ybge (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:62005) (re:63075) (di:direct) AB006424 AB006424 g3599662 Bacillus subtilis 1423 -11529821

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765253	2469	24625	1125	374

Description

6500725964 hypothetical protein:similar to histidine permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybgF ybgF Bacillus subtilis 1423 -11529822 7000693095 ybgf histidine permease homolog ybgf (cl:arginine permease) (db:pir2.dat) A69751 A69751 Bacillus subtilis 1423 -11529822 7500955180 ybgf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to histidine permease) (le:65462) (re:66874) (di:complement) BSUB0002 Z99105 g2632526 Bacillus subtilis 1423 -11529822 7500955181 ybgf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:63112) (re:64524) (di:complement) AB006424 AB006424 g3599663 Bacillus subtilis 1423 -11529822

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765434	2470	24626	222	73

Description

6500725965 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybgG ybgG Bacillus subtilis 1423 -11529823 7000692395 ybgg conserved hypothetical protein ybgg (db:pir2.dat) B69751 B69751 Bacillus subtilis 1423 -11529823 7500963558 ybgg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:66995) (re:67942) (di:complement) BSUB0002 Z99105 g2632527 Bacillus subtilis 1423 -11529823 7500963559 ybgg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:64645) (re:65592) (di:complement) AB006424 AB006424 g3599664 Bacillus subtilis 1423 -11529823

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765435	2471	24627	237	78

Description

6500725966 hypothetical protein:similar to sodium/proton-dependent alanine transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybgH ybgH Bacillus subtilis 1423 -11529824 7000694597 ybgh sodium/proton-dependent alanine transporte homolog ybgh (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) C69751 C69751 Bacillus subtilis 1423 -11529824 7500965195 ybgh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to sodium/proton-dependent alanine) (le:68071) (re:69462) (di:complement) BSUB0002 Z99105 g2632528 Bacillus subtilis 1423 -11529824 7500965196 ybgh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:65721) (re:67112) (di:complement) AB006424 AB006424 g3599665 Bacillus subtilis 1423 -11529824

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765437	2472	24628	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765439	2473	24629	276	91

Description

6500725967 hypothetical protein:similar to glutaminase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ybgJ ybgJ Bacillus subtilis 1423 -11529825 7000693050 ybgj glutaminase homolog ybgj (cl:hypothetical protein b1524) (db:pir2.dat) D69751 D69751 Bacillus subtilis 1423 -11529825 7500964027 ybgj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glutaminase) (le:69532) (re:70515) (di:complement) BSUB0002 Z99105 g2632529 Bacillus subtilis 1423 -11529825 7500964028 ybgj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct2) (de:bacillus subtilis genomic dna, 70 kb region between 17 and 23degree.) (le:67182) (re:68165) (di:complement) AB006424 AB006424 g3599666 Bacillus subtilis 1423 -11529825

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765450	2474	24630	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765456	2475	24631	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765461	2476	24632	459	152

Description

6500725968 yzga:ycba hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbA ycbA Bacillus subtilis 1423 -11529826 7502851642 ycba (ec:2.7.3.-) (de:hypothetical sensor-like histidine kinase, (orfh)) (db:swissprot) YCBA_BACSU P40758 BACILLUS SUBTILIS 1423 -11529826 7000694868 ycba two-component sensor histidine kinase homolog ycba (db:pir2.dat) D69752 D69752 Bacillus subtilis 1423 -11529826 7500965406 ycba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: yzga; similar to two-component) (le:70887) (re:72050) (di:direct) BSUB0002 Z99105 g2632530 Bacillus subtilis 1423 -11529826

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765464	2477	24633	348	115

Description

6500725969 yzgb:ycbb hypothetical protein:hypothetical 35.7 kd sensory transduction protein:orfj:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbB ycbB Bacillus subtilis 1423 -11529827 110588 ycbb (de:hypothetical 35.7 kd sensory transduction protein (orfj) (orf1)) (db:swissprot) YCBB_BACSU P40759 BACILLUS SUBTILIS 1423 -11529827 7000687400 ycbb two-component response regulator ycba homolog ycbb (cl:response regulator homology) (db:pir2.dat) I39924 I39924 Bacillus subtilis 1423 -11529827 7500921565 (fn:unknown) (sr:bacillus subtilis (strain bd99) dna) (db:genpept-bct1) (de:bacillus subtilis orfh, 3' end and complete orfj.) (nt:putative response regulator of two-component) (le:248) (re:1192) (di:direct) BACORFH L22503 g438470 Bacillus subtilis 1423 -11529827 216416 ycbb homologue of high affinity potassium transport (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:247) (re:1191) (di:direct) BACYCB20 D30808 g709996 Bacillus subtilis 1423 -11529827 217114 ycbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: yzgb; similar to two-component) (le:72061) (re:73005) (di:direct) BSUB0002 Z99105 g2632531 Bacillus subtilis 1423 -11529827 170289 ycbb two-component response regulator ycba homolog ycbb (db:pir) I39924 I39924 Bacillus subtilis 1423 -11529827 5000688858 (de:(ycbb) (pn:hypothetical 35) (gtcfc:12.13) (ec:) (ycbb_bacsu) (keggfc:11.2) (bsorffc:6.1.2) (db:gtc-bacillus subtilis)) ycbB ycbB Bacillus subtilis 1423 10052319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765466	2478	24634	333	110

Description

5000688771 hypothetical protein:probable glucarate transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbE ycbE Bacillus subtilis 1423 -11529828 75016 ycbe (de:probable glucarate transporter) (db:swissprot) GUDT_BACSU P42237 BACILLUS SUBTILIS 1423 -11529828 7000685478 ycbe probalble glucarate transporter (cl:hexuronate transporter) (db:pir2.dat) H69752 H69752 Bacillus subtilis 1423 -11529828 217117 ycbe glucarate dehydratase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:3924) (re:5291) (di:direct) BACYCB20 D30808 g709999 Bacillus subtilis 1423 -11529828 7500882849 ycbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glucarate transporter) (le:75738) (re:77105) (di:direct) BSUB0002 Z99105 g2632534 Bacillus subtilis 1423 -11529828 6500725970 hypothetical protein:probable glucarate transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbE ycbE Bacillus subtilis 1423 -11529828

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765468	2479	24635	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765473	2480	24636	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765481	2481	24637	489	162

Description

5000688923 hypothetical protein:hypothetical transcriptional regulator in pcp 5region:orf6 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbG ycbG Bacillus subtilis 1423 -11529829 110593 ycbg (de:(orf6)) (db:swissprot) YCBG_BACSU P42239 BACILLUS SUBTILIS 1423 -11529829 7000687405 ycbg transcription regulator gntr family homolog ycbg (db:pir2.dat) B69753 B69753 Bacillus subtilis 1423 -11529829 217119 ycbg homologue of protein a which gene locates (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:6765) (re:7466) (di:direct) BACYCB20 D30808 g710001 Bacillus subtilis 1423 -11529829 7500921571 ycbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (gntr family)) (le:78579) (re:79280) (di:direct) BSUB0002 Z99105 g2632536 Bacillus subtilis 1423 -11529829 6500725971 hypothetical protein:hypothetical transcriptional regulator in pcp 5region:orf6 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbG ycbG Bacillus subtilis 1423 -11529829

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765484	2482	24638	633	210

Description

6500725972 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbH ycbH Bacillus subtilis 1423 -11529830 7000692396 ycbh conserved hypothetical protein ycbh (db:pir2.dat) C69753 C69753 Bacillus subtilis 1423 -11529830 7500963560 ycbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:79371) (re:80903) (di:direct) BSUB0002 Z99105 g2632537 Bacillus subtilis 1423 -11529830

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765494	2483	24639	876	291

Description

6500725973 hypothetical protein:similar to viomycin phosphotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbJ ycbJ Bacillus subtilis 1423 -11529831 7000694901 ycbj viomycin phosphotransferase homolog ycbj (db:pir2.dat) D69753 D69753 Bacillus subtilis 1423 -11529831 7500965434 ycbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to viomycin phosphotransferase) (le:81180) (re:82100) (di:direct) BSUB0002 Z99105 g2632538 Bacillus subtilis 1423 -11529831

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765516	2484	24640	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765518	2485	24641	210	69

Description

GTC ORF with score 105 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765519	2486	24642	279	92

Description

6500725974 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczA yczA Bacillus subtilis 1423 -11529832 7000693175 ycza hypothetical protein ycza (db:pir2.dat) H69766 H69766 Bacillus subtilis 1423 -11529832 7500964143 ycza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:82502) (re:82663) (di:direct) BSUB0002 Z99105 g2632539 Bacillus subtilis 1423 -11529832

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765521	2487	24643	354	117

Description

5000689527 hypothetical protein:hypothetical 34.0 kd protein in pcp 5region:orf10 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbK ycbK Bacillus subtilis 1423 -11529833 110601 ycbk (de:hypothetical 34.0 kd protein in pcp 5'region (orf10)) (db:swissprot) YCBK_BACSU P42243 BACILLUS SUBTILIS 1423 -11529833 7000687407 ycbk efflux system homolog ycbk (db:pir2.dat) E69753 E69753 Bacillus subtilis 1423 -11529833 217123 ycbk homologue of glutathione-regulated potassium (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:10870) (re:11808) (di:direct) BACYCB20 D30808 g710005 Bacillus subtilis 1423 -11529833 7500921574 ycbk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to efflux system) (le:82684) (re:83622) (di:direct) BSUB0002 Z99105 g2632540 Bacillus subtilis 1423 -11529833 6500725975 hypothetical protein:hypothetical 34.0 kd protein in pcp 5region:orf10 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbK ycbK Bacillus subtilis 1423 -11529833

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765526	2488	24644	246	81

Description

5000688859 hypothetical protein:hypothetical 25.8 kd sensory transduction protein:orf11 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbL ycbL Bacillus subtilis 1423 -11529834 110602 ycbl (de:hypothetical 25.8 kd sensory transduction protein (orf11)) (db:swissprot) YCBL_BACSU P42244 BACILLUS SUBTILIS 1423 -11529834 7000687409 ycbl two-component response regulator ycbm homolog ycbl) (cl:ompr protein:response regulator homology) (db:pir2.dat) F69753 F69753 Bacillus subtilis 1423 -11529834 217124 ycbl homologue of vancomycin resistance gene product (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:11905) (re:12585) (di:direct) BACYCB20 D30808 g710006 Bacillus subtilis 1423 -11529834 7500921577 ycbl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to two-component response regulator (ycbm)) (le:83719) (re:84399) (di:direct) BSUB0002 Z99105 g2632541 Bacillus subtilis 1423 -11529834 6500725976 hypothetical protein:hypothetical 25.8 kd sensory transduction protein:orf11 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbL ycbL Bacillus subtilis 1423 -11529834

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765537	2489	24645	756	251

Description

5000689528 hypothetical protein:hypothetical 18.0 kd protein in pcp 5region:orf12 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbM ycbM Bacillus subtilis 1423 -11529835 110604 ycbm (de:hypothetical 18.0 kd protein in pcp 5'region (orf12)) (db:swissprot) YCBM_BACSU P42245 BACILLUS SUBTILIS 1423 -11529835 7000687411 ycbm two-component sensor histidine kinase homolog ycbm (db:pir2.dat) G69753 G69753 Bacillus subtilis 1423 -11529835 217125 ycbm homologue of phor of b. subtilis (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:12587) (re:13063) (di:direct) BACYCB20 D30808 g710007 Bacillus subtilis 1423 -11529835 7500921580 ycbm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to two-component sensor histidine kinase) (le:84401) (re:84877) (di:direct) BSUB0002 Z99105 g2632542 Bacillus subtilis 1423 -11529835 6500725977 hypothetical protein:hypothetical 18.0 kd protein in pcp 5region:orf12 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbM ycbM Bacillus subtilis 1423 -11529835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765539	2490	24646	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765557	2491	24647	714	237

Description

6500725978 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbN ycbN Bacillus subtilis 1423 -11529836 7500921582 ycbn (de:hypothetical 31.7 kd protein in gltp-cwlj intergenic region (orf13)) (db:swissprot) YCBN_BACSU P42246 BACILLUS SUBTILIS 1423 -11529836 7000692078 ycbn abc transporter atp-binding protein homolog ycbn (cl:atp-binding cassette homology) (db:pir2.dat) H69753 H69753 Bacillus subtilis 1423 -11529836 7500921584 ycbn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to abc transporter (atp-binding protein)) (le:85033) (re:85872) (di:direct) BSUB0002 Z99105 g2632543 Bacillus subtilis 1423 -11529836

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765563	2492	24648	843	280

Description

6500725979 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbO ycbO Bacillus subtilis 1423 -11529837 7000693158 ycbo hypothetical protein ycbo (db:pir2.dat) A69754 A69754 Bacillus subtilis 1423 -11529837 7500964126 ycbo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:85991) (re:86434) (di:direct) BSUB0002 Z99105 g2632544 Bacillus subtilis 1423 -11529837

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765568	2493	24649	468	155

Description

5000689531 hypothetical protein:hypothetical 14.1 kd protein in pcp 5region:orf15 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbP ycbP Bacillus subtilis 1423 -11529838 110607 ycbp (de:hypothetical 14.1 kd protein in pcp 5'region (orf15)) (db:swissprot) YCBP_BACSU P42248 BACILLUS SUBTILIS 1423 -11529838 7000687413 ycbp conserved hypothetical protein ycbp (cl:hypothetical protein ycbp) (db:pir2.dat) B69754 B69754 Bacillus subtilis 1423 -11529838 217128 ycbp homologue of nadh-ubiquinone oxidoreductase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:14847) (re:15233) (di:complement) BACYCB20 D30808 g710010 Bacillus subtilis 1423 -11529838 7500921588 ycbp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins from b. subtilis) (le:86661) (re:87047) (di:complement) BSUB0002 Z99105 g2632545 Bacillus subtilis 1423 -11529838 6500725980 hypothetical protein:hypothetical 14.1 kd protein in pcp 5region:orf15 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbP ycbP Bacillus subtilis 1423 -11529838

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765570	2494	24650	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765579	2495	24651	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765764	2496	24652	459	152

Description

5000689532 ycbq:cwlj hypothetical protein:hypothetical 16.4 kd protein in pcp 5region:orf16 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cwlJ cwlJ Bacillus subtilis 1423 -11529839 110608 cwlj (de:cell wall hydrolase cwlj) (db:swissprot) CWLJ_BACSU P42249 BACILLUS SUBTILIS 1423 -11529839 7000687414 cwlj cell wall hydrolase sporulation cwlj (db:pir2.dat) H69610 H69610 Bacillus subtilis 1423 -11529839 217129 ycbq unknown (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:15547) (re:15975) (di:direct) BACYCB20 D30808 g710011 Bacillus subtilis 1423 -11529839 7500879598 cwlj (fn:cell wall hydrolase) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: ycbq) (le:87361) (re:87789) (di:direct) BSUB0002 Z99105 g2632546 Bacillus subtilis 1423 -11529839 6500725981 ycbq hypothetical protein:hypothetical 16.4 kd protein in pcp 5region:orf16 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cwlJ cwlJ Bacillus subtilis 1423 -11529839

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765765	2497	24653	288	95

Description

5000689533 hypothetical protein:hypothetical 28.0 kd protein in pcp 5region:orf17 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbR ycbR Bacillus subtilis 1423 -11529840 110609 ycbr (de:hypothetical 28.0 kd protein in pcp 5'region (orf17)) (db:swissprot) YCBR_BACSU P42250 BACILLUS SUBTILIS 1423 -11529840 7000687415 ycbr toxic cation resistance protein homolog ycbr (db:pir2.dat) C69754 C69754 Bacillus subtilis 1423 -11529840 217130 ycbr unknown (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna around 20 degrees region of chromosomecontaining ycka-t genes.) (le:16081) (re:16812) (di:direct) BACYCB20 D30808 g710012 Bacillus subtilis 1423 -11529840 7500921592 ycbr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to toxic cation resistance protein) (le:87895) (re:88626) (di:direct) BSUB0002 Z99105 g2632547 Bacillus subtilis 1423 -11529840 6500725982 hypothetical protein:hypothetical 28.0 kd protein in pcp 5region:orf17 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbR ycbR Bacillus subtilis 1423 -11529840

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765783	2498	24654	750	250

Description

GTC ORF with score 440 to: (sr:thale cress) (db:genpept-pln1) (de:sequence of bac f5i14 from arabidopsis thaliana chromosome 1,complete sequence.) (nt:ests gb|t45673,gb|n37512 come from this gene.) (le:94242:95089:95364) (re:95006:95191:95410) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765810	2499	24655	207	68

Description

6500725983 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczB yczB Bacillus subtilis 1423 -11529841 7000692409 yczb conserved hypothetical protein yczb (cl:conserved hypothetical secreted protein hp0320) (db:pir2.dat) A69767 A69767 Bacillus subtilis 1423 -11529841 7500963571 yczb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:90670) (re:90882) (di:direct) BSUB0002 Z99105 g2632549 Bacillus subtilis 1423 -11529841

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765819	2500	24656	222	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765830	2501	24657	534	178

Description

6500725984 hypothetical protein:hypothetical 28.2 kd protein in pcp 5region:orf19 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbT ycbT Bacillus subtilis 1423 -11529842 7500921597 ycbt (de:hypothetical 28.1 kd protein in phod-pcp intergenic region (orf19)) (db:swissprot) YCBT_BACSU P42252 BACILLUS SUBTILIS 1423 -11529842 7000692397 ycbt conserved hypothetical protein ycbt (cl:conserved hypothetical protein hi0188) (db:pir2.dat) D69754 D69754 Bacillus subtilis 1423 -11529842 7500921599 ycbt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:90943) (re:91680) (di:direct) BSUB0002 Z99105 g2632550 Bacillus subtilis 1423 -11529842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765838	2502	24658	402	133

Description

6500725985 hypothetical protein:similar to nifs protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycbU ycbU Bacillus subtilis 1423 -11529843 7500921600 ycbu (de:(orf21)) (db:swissprot) YCBU_BACSU P42253 BACILLUS SUBTILIS 1423 -11529843 7000694317 ycbu nifs protein homolog homolog ycbu (db:pir2.dat) E69754 E69754 Bacillus subtilis 1423 -11529843 5500687006 ycbu ycbu (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of class-v proteins of) (le:592) (re:1704) (di:direct) AB000617 AB000617 g2415717 Bacillus subtilis 1423 -11529843 7500921603 ycbu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to nifs protein homolog) (le:92403) (re:93515) (di:direct) BSUB0002 Z99105 g2632552 Bacillus subtilis 1423 -11529843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765852	2503	24659	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765863	2504	24660	474	157

Description

6500725986 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczC yczC Bacillus subtilis 1423 -11529844 7000692410 yczc conserved hypothetical protein yczc (db:pir2.dat) B69767 B69767 Bacillus subtilis 1423 -11529844 7500963572 yczc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:97785) (re:98168) (di:complement) BSUB0002 Z99105 g2632557 Bacillus subtilis 1423 -11529844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765868	2505	24661	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765875	2506	24662	216	71

Description

6500725987 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yccF yccF Bacillus subtilis 1423 -11529845 7000693159 yccf hypothetical protein yccf (db:pir2.dat) G69754 G69754 Bacillus subtilis 1423 -11529845 5500687012 yccf yccf (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (le:6592) (re:7668) (di:direct) AB000617 AB000617 g2415723 Bacillus subtilis 1423 -11529845 7500964127 yccf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:98403) (re:99479) (di:direct) BSUB0002 Z99105 g2632558 Bacillus subtilis 1423 -11529845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765892	2507	24663	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765893	2508	24664	636	211

Description

GTC ORF with score 114 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid k08h10, complete sequence.) (nt:cdna est yk370a12.5 comes from this gene; cdna est) (le:36653:37946:z73975:1373) (re:37891:38011:1480) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501765899	2509	24665	768	255

Description

6500725988 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yccG yccG Bacillus subtilis 1423 -11529846 7000694869 yccg two-component sensor histidine kinase homolog yccg (db:pir2.dat) H69754 H69754 Bacillus subtilis 1423 -11529846 5500687013 yccg yccg (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (le:7708) (re:8664) (di:complement) AB000617 AB000617 g2415724 Bacillus subtilis 1423 -11529846 7500965407 yccg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to two-component sensor histidine kinase) (le:99519) (re:100475) (di:complement) BSUB0002 Z99105 g2632559 Bacillus subtilis 1423 -11529846

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766113	2510	24666	426	141

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766125	2511	24667	327	108

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766127	2512	24668	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766131	2513	24669	687	228

Description

6500725989 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yccH yccH Bacillus subtilis 1423 -11529847 7000694840 ycch two-component response regulator yccg homolog ycch) (db:pir2.dat) A69755 A69755 Bacillus subtilis 1423 -11529847 219919 ycch ycch (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of sensor/response regulator protein of) (le:8677) (re:9378) (di:complement) AB000617 AB000617 g2415725 Bacillus subtilis 1423 -11529847 5500687014 (db:genpept-bct1) (de:bacillus subtilis nata (nata) and natb (natb) genes, complete cds.) (nt:orfr) (le:1407) (re:2108) (di:complement) BSU30873 U30873 g1663527 Bacillus subtilis 1423 -11529847 7500965389 ycch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to two-component response regulator (yccg)) (le:100488) (re:101189) (di:complement) BSUB0002 Z99105 g2632560 Bacillus subtilis 1423 -11529847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766151	2514	24670	1740	580

Description

6500725990 yzae:ycck hypothetical protein:similar to ion channel (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yccK yccK Bacillus subtilis 1423 -11529848 7500921622 ycck (de:hypothetical oxidoreductase in natb-rapj intergenic region (orfc)) (db:swissprot) YCCK_BACSU P46905 BACILLUS SUBTILIS 1423 -11529848 7000694120 ycck ion channel homolog ycck (cl:conserved hypothetical protein ypl088w) (db:pir2.dat) B69755 B69755 Bacillus subtilis 1423 -11529848 5500687015 ycck ycck (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:hypothetical yzae protein (function unknown) in the) (le:11555) (re:12487) (di:direct) AB000617 AB000617 g2415728 Bacillus subtilis 1423 -11529848 7500921625 ycck (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: yzae; similar to ion channel) (le:103370) (re:104302) (di:direct) BSUB0002 Z99105 g2632563 Bacillus subtilis 1423 -11529848

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766183	2515	24671	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766188	2516	24672	477	158

Description

6500725991 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdA ycdA Bacillus subtilis 1423 -11529849 7000693160 ycda hypothetical protein ycda (db:pir2.dat) C69755 C69755 Bacillus subtilis 1423 -11529849 5500687016 ycda ycda (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (le:12527) (re:13591) (di:complement) AB000617 AB000617 g2415729 Bacillus subtilis 1423 -11529849 7500964128 ycda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:104342) (re:105406) (di:complement) BSUB0002 Z99105 g2632564 Bacillus subtilis 1423 -11529849

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766203	2517	24673	489	162

Description

6500725992 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdB ycdB Bacillus subtilis 1423 -11529850 7000693161 ycdb hypothetical protein ycdb (db:pir2.dat) D69755 D69755 Bacillus subtilis 1423 -11529850 5500687017 ycdb ycdb (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:similar to ycdc) (le:13919) (re:15337) (di:direct) AB000617 AB000617 g2415730 Bacillus subtilis 1423 -11529850 7500964129 ycdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:105734) (re:107152) (di:direct) BSUB0002 Z99105 g2632565 Bacillus subtilis 1423 -11529850

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766204	2518	24674	318	106

Description

6500725993 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdC ycdC Bacillus subtilis 1423 -11529851 7000693162 ycdc hypothetical protein ycdc (db:pir2.dat) E69755 E69755 Bacillus subtilis 1423 -11529851 5500687018 ycdc ycdc (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:similar to ycdb) (le:15524) (re:16885) (di:direct) AB000617 AB000617 g2415731 Bacillus subtilis 1423 -11529851 7500964130 ycdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:107339) (re:108700) (di:direct) BSUB0002 Z99105 g2632566 Bacillus subtilis 1423 -11529851

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766205	2519	24675	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766207	2520	24676	279	92

Description

6500725994 hypothetical protein:similar to 1-alanoyl-d-glutamate peptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdD ycdD Bacillus subtilis 1423 -11529852 7000694139 ycdd 1-alanoyl-d-glutamate peptidase homolog ycdd (db:pir2.dat) F69755 F69755 Bacillus subtilis 1423 -11529852 5500687019 ycdd ycdd (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of ply gene product (phage lysin) of) (le:16893) (re:17396) (di:complement) AB000617 AB000617 g2415732 Bacillus subtilis 1423 -11529852 7500964879 ycdd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to 1-alanoyl-d-glutamate peptidase) (le:108708) (re:109211) (di:complement) BSUB0002 Z99105 g2632567 Bacillus subtilis 1423 -11529852

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766209	2521	24677	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766215	2522	24678	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766242	2523	24679	723	241

Description

6500725995 hypothetical protein:similar to glucose 1-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdF ycdF Bacillus subtilis 1423 -11529853 7000693032 ycdf glucose 1-dehydrogenase homolog ycdf (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) G69755 G69755 Bacillus subtilis 1423 -11529853 5500687021 ycdf ycdf (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of glucose-1-dehydrogenase of bacillus) (le:18747) (re:19523) (di:direct) AB000617 AB000617 g2415734 Bacillus subtilis 1423 -11529853 7500964014 ycdf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to glucose 1-dehydrogenase) (le:110562) (re:111338) (di:direct) BSUB0002 Z99105 g2632569 Bacillus subtilis 1423 -11529853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766251	2524	24680	1179	393

Description

6500725996 hypothetical protein:similar to adhesion protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdH ycdH Bacillus subtilis 1423 -11529854 7000692160 ycdh adhesion protein homolog ycdh (cl:adhesin b) (db:pir2.dat) A69756 A69756 Bacillus subtilis 1423 -11529854 5500687023 ycdh ycdh (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of adhesion protein precursor of) (le:21421) (re:22380) (di:direct) AB000617 AB000617 g2415736 Bacillus subtilis 1423 -11529854 7500963384 ycdh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to adhesion protein) (le:113236) (re:114195) (di:direct) BSUB0002 Z99105 g2632571 Bacillus subtilis 1423 -11529854

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766270	2525	24681	1185	395

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766529	2526	24682	591	196

Description

6500725997 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycdI ycdI Bacillus subtilis 1423 -11529855 7000692079 ycdi abc transporter atp-binding protein homolog ycdi (cl:atp-binding cassette homology) (db:pir2.dat) B69756 B69756 Bacillus subtilis 1423 -11529855 5500687024 ycdi ycdi (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of streptococcus parasanguis adhesion) (le:22436) (re:23131) (di:direct) AB000617 AB000617 g2415737 Bacillus subtilis 1423 -11529855 7500963319 ycdi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to abc transporter (atp-binding protein)) (le:114251) (re:114946) (di:direct) BSUB0002 Z99105 g2632572 Bacillus subtilis 1423 -11529855

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766530	2527	24683	270	90

Description

6500725998 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceA yceA Bacillus subtilis 1423 -11529856 7000692398 ycea conserved hypothetical protein ycea (cl:conserved hypothetical protein hi0360) (db:pir2.dat) C69756 C69756 Bacillus subtilis 1423 -11529856 5500687025 ycea ycea (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of a hypothetical 32.8 kda protein in) (le:23089) (re:23931) (di:direct) AB000617 AB000617 g2415738 Bacillus subtilis 1423 -11529856 7500963561 ycea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:114904) (re:115746) (di:direct) BSUB0002 Z99105 g2632573 Bacillus subtilis 1423 -11529856

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766533	2528	24684	420	139

Description

6500725999 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceB yceB Bacillus subtilis 1423 -11529857 7000692399 yceb conserved hypothetical protein yceb (cl:ynbw protein) (db:pir2.dat) D69756 D69756 Bacillus subtilis 1423 -11529857 5500687026 yceb yceb (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of a hypothetical 36.6 kda protein in) (le:23969) (re:24910) (di:complement) AB000617 AB000617 g2415739 Bacillus subtilis 1423 -11529857 7500963562 yceb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:115784) (re:116725) (di:complement) BSUB0002 Z99105 g2632574 Bacillus subtilis 1423 -11529857

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766537	2529	24685	1110	370

Description

6500726000 hypothetical protein:similar to tellurium resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceC yceC Bacillus subtilis 1423 -11529858 7000694667 ycec tellurium resistance protein homolog ycec (db:pir2.dat) E69756 E69756 Bacillus subtilis 1423 -11529858 5500687027 ycec ycec (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable tellurite-resistance relating protein;) (le:25248) (re:25847) (di:direct) AB000617 AB000617 g2415740 Bacillus subtilis 1423 -11529858 7500965252 ycec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to tellurium resistance protein) (le:117063) (re:117662) (di:direct) BSUB0002 Z99105 g2632575 Bacillus subtilis 1423 -11529858

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766538	2530	24686	828	276

Description

6500726001 hypothetical protein:similar to tellurium resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceD yceD Bacillus subtilis 1423 -11529859 7000694668 yced tellurium resistance protein homolog yced (db:pir2.dat) F69756 F69756 Bacillus subtilis 1423 -11529859 5500687028 yced yced (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable tellurite-resistance relating protein;) (le:25869) (re:26450) (di:direct) AB000617 AB000617 g2415741 Bacillus subtilis 1423 -11529859 7500965253 yced (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to tellurium resistance protein) (le:117684) (re:118265) (di:direct) BSUB0002 Z99105 g2632576 Bacillus subtilis 1423 -11529859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766547	2531	24687	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766549	2532	24688	213	70

Description

6500726002 hypothetical protein:similar to tellurium resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceE yceE Bacillus subtilis 1423 -11529860 7000694669 ycee tellurium resistance protein homolog ycee (db:pir2.dat) G69756 G69756 Bacillus subtilis 1423 -11529860 5500687029 ycee ycee (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable tellurite-resistance relating protein;) (le:26485) (re:27063) (di:direct) AB000617 AB000617 g2415742 Bacillus subtilis 1423 -11529860 7500965254 ycee (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to tellurium resistance protein) (le:118300) (re:118878) (di:direct) BSUB0002 Z99105 g2632577 Bacillus subtilis 1423 -11529860

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766550	2533	24689	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766552	2534	24690	657	218

Description

6500726003 hypothetical protein:similar to tellurium resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceF yceF Bacillus subtilis 1423 -11529861 7000694670 ycef tellurium resistance protein homolog ycef (cl:hypothetical protein sll1022) (db:pir2.dat) H69756 H69756 Bacillus subtilis 1423 -11529861 5500687030 ycef ycef (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable tellurite-resistance relating protein;) (le:27114) (re:27887) (di:direct) AB000617 AB000617 g2415743 Bacillus subtilis 1423 -11529861 7500955959 ycef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to tellurium resistance protein) (le:118929) (re:119702) (di:direct) BSUB0002 Z99105 g2632578 Bacillus subtilis 1423 -11529861

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766566	2535	24691	417	138

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766567	2536	24692	570	189

Description

6500726004 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceG yceG Bacillus subtilis 1423 -11529862 7000693163 yceg hypothetical protein yceg (db:pir2.dat) A69757 A69757 Bacillus subtilis 1423 -11529862 5500687031 yceg yceg (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable tellurite-resistance relating protein) (le:27972) (re:29585) (di:direct) AB000617 AB000617 g2415744 Bacillus subtilis 1423 -11529862 7500964131 yceg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:119787) (re:121400) (di:direct) BSUB0002 Z99105 g2632579 Bacillus subtilis 1423 -11529862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766571	2537	24693	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766574	2538	24694	453	150

Description

6500726005 hypothetical protein:similar to toxic anion resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceH yceH Bacillus subtilis 1423 -11529863 7000694694 yceh toxic anion resistance protein homolog yceh (cl:tela protein) (db:pir2.dat) B69757 B69757 Bacillus subtilis 1423 -11529863 5500687032 yceh yceh (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable tellurite-resistance relating protein;) (le:29601) (re:30692) (di:direct) AB000617 AB000617 g2415745 Bacillus subtilis 1423 -11529863 7500955838 yceh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to toxic anion resistance protein) (le:121416) (re:122507) (di:direct) BSUB0002 Z99105 g2632580 Bacillus subtilis 1423 -11529863

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766580	2539	24695	1068	355

Description

6500726006 hypothetical protein:similar to transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceI yceI Bacillus subtilis 1423 -11529864 7000694814 ycei transporter homolog ycei (db:pir2.dat) C69757 C69757 Bacillus subtilis 1423 -11529864 5500687033 ycei ycei (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:probable tellurite-resistance relating protein;) (le:30814) (re:32016) (di:direct) AB000617 AB000617 g2415746 Bacillus subtilis 1423 -11529864 7500965368 ycei (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transporter) (le:122629) (re:123831) (di:direct) BSUB0002 Z99105 g2632581 Bacillus subtilis 1423 -11529864

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766581	2540	24696	582	193

Description

6500726007 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceJ yceJ Bacillus subtilis 1423 -11529865 7000694250 ycej multidrug-efflux transporter homolog ycej (db:pir2.dat) D69757 D69757 Bacillus subtilis 1423 -11529865 5500687034 ycej ycej (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (nt:homologue of multidrug-resistance protein bmr of) (le:32269) (re:33441) (di:complement) AB000617 AB000617 g2415747 Bacillus subtilis 1423 -11529865 7500964974 ycej (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to multidrug-efflux transporter) (le:124084) (re:125256) (di:complement) BSUB0002 Z99105 g2632582 Bacillus subtilis 1423 -11529865

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766625	2541	24697	225	74

Description

6500726008 hypothetical protein:similar to transcriptional regulator:arsr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yceK yceK Bacillus subtilis 1423 -11529866 7000694720 ycek transcription regulator arsr family homolog ycek (cl:arsenical resistance operon repressor) (db:pir2.dat) E69757 E69757 Bacillus subtilis 1423 -11529866 5500687035 ycek ycek (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 22 to 25 degree region, completecds.) (le:33510) (re:33812) (di:complement) AB000617 AB000617 g2415748 Bacillus subtilis 1423 -11529866 7500965295 ycek (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (arsr family)) (le:125325) (re:125627) (di:complement) BSUB0002 Z99105 g2632583 Bacillus subtilis 1423 -11529866

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766626	2542	24698	237	78

Description

6500726009 hypothetical protein:hypothetical 41.5 kd protein in amhx-amye intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgA ycgA Bacillus subtilis 1423 -11529867 1500686233 ycga (de:hypothetical 41.5 kd protein in amhx-amye intergenic region) (db:swissprot) YCGA_BACSU P55908 BACILLUS SUBTILIS 1423 -11529867 7000687458 ycga conserved hypothetical protein ycga (cl:haemophilus influenzae conserved hypothetical protein hi0594) (db:pir2.dat) F69757 F69757 Bacillus subtilis 1423 -11529867 222568 ycga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:130485) (re:131675) (di:direct) BSUB0002 Z99105 g2632588 Bacillus subtilis 1423 -11529867 7500921774 ycga homologue of hypothetical protein hi10594 of h. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:4787) (re:5977) (di:direct) D50453 D50453 g1805374 Bacillus subtilis 1423 -11529867

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766632	2543	24699	765	255

Description

6500726010 hypothetical protein:hypothetical 22.3 kd protein in amhx-amye intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgB ycgB Bacillus subtilis 1423 -11529868 1500686234 ycgb (de:hypothetical 22.3 kd protein in amhx-amye intergenic region) (db:swissprot) YCGB_BACSU P55909 BACILLUS SUBTILIS 1423 -11529868 7000687459 ycgb hypothetical protein ycgb (db:pir2.dat) G69757 G69757 Bacillus subtilis 1423 -11529868 222569 ycgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:131791) (re:132372) (di:direct) BSUB0002 Z99105 g2632589 Bacillus subtilis 1423 -11529868 7500921775 ycgb (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:6093) (re:6674) (di:direct) D50453 D50453 g1805375 Bacillus subtilis 1423 -11529868

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766640	2544	24700	840	280

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766656	2545	24701	423	140

Description

6500726011 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgE ycgE Bacillus subtilis 1423 -11529869 7000693164 ycge hypothetical protein ycge (db:pir2.dat) H69757 H69757 Bacillus subtilis 1423 -11529869 7500964132 ycge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:139003) (re:139470) (di:direct) BSUB0002 Z99105 g2632594 Bacillus subtilis 1423 -11529869

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766658	2546	24702	609	203

Description

6500726012 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgF ycgF Bacillus subtilis 1423 -11529870 7000693165 ycgf hypothetical protein ycgf (db:pir2.dat) A69758 A69758 Bacillus subtilis 1423 -11529870 7500964133 ycgf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:139544) (re:140173) (di:direct) BSUB0002 Z99105 g2632595 Bacillus subtilis 1423 -11529870

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766666	2547	24703	372	123

Description

6500726013 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgG ycgG Bacillus subtilis 1423 -11529871 7000692400 ycgg conserved hypothetical protein ycgg (db:pir2.dat) B69758 B69758 Bacillus subtilis 1423 -11529871 222576 ycgg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins from b. subtilis) (le:140243) (re:141004) (di:direct) BSUB0002 Z99105 g2632596 Bacillus subtilis 1423 -11529871 7500963563 ycgg (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:14546) (re:15307) (di:direct) D50453 D50453 g1805382 Bacillus subtilis 1423 -11529871

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766685	2548	24704	645	215

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766696	2549	24705	792	264

Description

6500726014 hypothetical protein:similar to amino acid transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgH ycgH Bacillus subtilis 1423 -11529872 7000692201 ycgh amino acid transporter homolog ycgh (db:pir2.dat) C69758 C69758 Bacillus subtilis 1423 -11529872 222577 ycgh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to amino acid transporter) (le:141036) (re:142169) (di:complement) BSUB0002 Z99105 g2632597 Bacillus subtilis 1423 -11529872 7500963409 ycgh homologue of aromatic amino acids transport (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:15339) (re:16472) (di:complement) D50453 D50453 g1805383 Bacillus subtilis 1423 -11529872

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766700	2550	24706	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766711	2551	24707	846	282

Description

GTC ORF with score 119 to: (db:genpept-pln1) (de:aspergillus niger atcc 46951 acid phosphatase (apha) gene, partialcds.) (nt:phosphate-repressible; gene previously called paca) (le:<1:84:829:1323) (re:35:779:1269:1674) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766723	2552	24708	594	198

Description

6500726015 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgI ycgI Bacillus subtilis 1423 -11529873 7000693166 ycgi hypothetical protein ycgi (db:pir2.dat) D69758 D69758 Bacillus subtilis 1423 -11529873 7500964134 ycgi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:142336) (re:143070) (di:direct) BSUB0002 Z99105 g2632598 Bacillus subtilis 1423 -11529873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766724	2553	24709	522	173

Description

6500726016 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgJ ycgJ Bacillus subtilis 1423 -11529874 7000693167 ycgj hypothetical protein ycgj (cl:escherichia coli yafe protein:bioc homology) (db:pir2.dat) E69758 E69758 Bacillus subtilis 1423 -11529874 7500964135 ycgj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:145535) (re:146221) (di:complement) BSUB0002 Z99105 g2632602 Bacillus subtilis 1423 -11529874

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766727	2554	24710	270	89

Description

6500726017 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgK ycgK Bacillus subtilis 1423 -11529875 7000694752 ycgk transcription regulator lysr family homolog ycgk (db:pir2.dat) F69758 F69758 Bacillus subtilis 1423 -11529875 222583 ycgk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (lysr family)) (le:146414) (re:147388) (di:direct) BSUB0002 Z99105 g2632603 Bacillus subtilis 1423 -11529875 7500965322 ycgk homologue of regulatory protein oxyr of e. coli (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:20715) (re:21689) (di:direct) D50453 D50453 g1805389 Bacillus subtilis 1423 -11529875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766730	2555	24711	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766739	2556	24712	609	202

Description

6500726018 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgL ycgL Bacillus subtilis 1423 -11529876 7000693168 ycgl hypothetical protein ycgl (db:pir2.dat) G69758 G69758 Bacillus subtilis 1423 -11529876 222585 ycgl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:148500) (re:149282) (di:direct) BSUB0002 Z99105 g2632605 Bacillus subtilis 1423 -11529876 7500964136 ycgl (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:22801) (re:23583) (di:direct) D50453 D50453 g1805391 Bacillus subtilis 1423 -11529876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766741	2557	24713	834	278

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766742	2558	24714	873	291

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501766998	2559	24715	378	125

Description

6500726019 hypothetical protein:similar to proline oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgM ycgM Bacillus subtilis 1423 -11529877 7000694446 ycgm proline oxidase homolog ycgm (cl:proline dehydrogenase homolog yusm) (db:pir2.dat) H69758 H69758 Bacillus subtilis 1423 -11529877 222586 ycgm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to proline oxidase) (le:149473) (re:150384) (di:direct) BSUB0002 Z99105 g2632606 Bacillus subtilis 1423 -11529877 7500953855 ycgm (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:23774) (re:24685) (di:direct) D50453 D50453 g1805392 Bacillus subtilis 1423 -11529877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767000	2560	24716	408	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767007	2561	24717	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767009	2562	24718	639	212

Description

6500726020 hypothetical protein:similar to 1-pyrroline-5-carboxylate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgN ycgN Bacillus subtilis 1423 -11529878 7000692033 ycgn 1-pyrroline-5-carboxylate dehydrogenase homolog ycgn (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) A69759 A69759 Bacillus subtilis 1423 -11529878 222587 ycgn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to 1-pyrroline-5-carboxylate dehydrogenase) (le:150401) (re:151948) (di:direct) BSUB0002 Z99105 g2632607 Bacillus subtilis 1423 -11529878 7500963286 ycgn 68% identity protein to (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:24702) (re:26249) (di:direct) D50453 D50453 g1805393 Bacillus subtilis 1423 -11529878

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767048	2563	24719	759	252

Description

6500726021 hypothetical protein:similar to proline permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgO ycgO Bacillus subtilis 1423 -11529879 7000694447 ycgo sodium/proline symporter ycgo:proline permease ycgo (cl:proline carrier protein) (db:pir2.dat) B69759 B69759 Bacillus subtilis 1423 -11529879 222588 ycgo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to proline permease) (le:152144) (re:153493) (di:direct) BSUB0002 Z99105 g2632608 Bacillus subtilis 1423 -11529879 7500955291 ycgo homologue of proline permease of e. coli (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:26445) (re:27794) (di:direct) D50453 D50453 g1805394 Bacillus subtilis 1423 -11529879

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767054	2564	24720	183	60

Description

6500726022 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgP ycgP Bacillus subtilis 1423 -11529880 7000692401 ycgp conserved hypothetical protein ycgp (db:pir2.dat) C69759 C69759 Bacillus subtilis 1423 -11529880 222589 ycgp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:153646) (re:154881) (di:direct) BSUB0002 Z99105 g2632609 Bacillus subtilis 1423 -11529880 7500963564 ycgp homologue of hypothetical protein hi0093 of h. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:27947) (re:29182) (di:direct) D50453 D50453 g1805395 Bacillus subtilis 1423 -11529880

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767058	2565	24721	369	122

Description

6500726023 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgQ ycgQ Bacillus subtilis 1423 -11529881 7000693169 ycgq hypothetical protein ycgq (db:pir2.dat) D69759 D69759 Bacillus subtilis 1423 -11529881 222590 ycgq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:154918) (re:155775) (di:complement) BSUB0002 Z99105 g2632610 Bacillus subtilis 1423 -11529881 7500964137 ycgq (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:29219) (re:30076) (di:complement) D50453 D50453 g1805396 Bacillus subtilis 1423 -11529881

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767060	2566	24722	474	157

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767074	2567	24723	990	330

Description

GTC ORF with score 780 to: (fn:controls phosphorus acquisition) (sr:neurospora crassa strain=74-or23-iva) (db:genpept-pln1) (de:neurospora crassa nuc-2 (nuc-2) gene, complete cds.) (nt:contains six ankyrin repeats; similar to the) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767082	2568	24724	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767088	2569	24725	1131	376

Description

6500726024 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgR ycgR Bacillus subtilis 1423 -11529882 7000693170 ycgr hypothetical protein ycgr (db:pir2.dat) E69759 E69759 Bacillus subtilis 1423 -11529882 222591 ycgr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:155780) (re:156664) (di:complement) BSUB0002 Z99105 g2632611 Bacillus subtilis 1423 -11529882 7500964138 ycgr homologue of unidentified protein of e. coli (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:30081) (re:30965) (di:complement) D50453 D50453 g1805397 Bacillus subtilis 1423 -11529882

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767093	2570	24726	255	84

Description

GTC ORF with score 176 to: (sr:mus sp. balb/c testes) (db:genpept-rod) (de:spot-1=nuclear localization signals (nls)-binding protein (mice,balb/c, testes, mrna, 1320 nt).) (nt:nuclear localization signals (nls)-binding protein;) (le:571) (re:990) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767095	2571	24727	315	104

Description

6500726025 hypothetical protein:similar to aromatic hydrocarbon catabolism (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgS ycgS Bacillus subtilis 1423 -11529883 7000692227 ycgs aromatic hydrocarbon catabolism homolog ycgs (db:pir2.dat) F69759 F69759 Bacillus subtilis 1423 -11529883 7500963428 ycgs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to aromatic hydrocarbon catabolism) (le:156764) (re:157618) (di:complement) BSUB0002 Z99105 g2632612 Bacillus subtilis 1423 -11529883

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767109	2572	24728	978	325

Description

6500726026 hypothetical protein:similar to thioredoxin reductase (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycgT ycgT Bacillus subtilis 1423 -11529884 7000694688 ycgt thioredoxin reductase homolog ycgt (db:pir2.dat) G69759 G69759 Bacillus subtilis 1423 -11529884 7500965271 ycgt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to thioredoxin reductase) (le:157780) (re:158790) (di:direct) BSUB0002 Z99105 g2632613 Bacillus subtilis 1423 -11529884

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767123	2573	24729	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767133	2574	24730	741	246

Description

6500726027 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yciA yciA Bacillus subtilis 1423 -11529885 7000692402 ycia conserved hypothetical protein ycia (db:pir2.dat) H69759 H69759 Bacillus subtilis 1423 -11529885 222600 ycia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:169177) (re:170094) (di:direct) BSUB0002 Z99105 g2632620 Bacillus subtilis 1423 -11529885 7500963565 ycia (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:43480) (re:44397) (di:direct) D50453 D50453 g1805406 Bacillus subtilis 1423 -11529885

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767137	2575	24731	783	261

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767146	2576	24732	459	152

Description

6500726028 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yciB yciB Bacillus subtilis 1423 -11529886 7000692403 ycib conserved hypothetical protein ycib (db:pir2.dat) A69760 A69760 Bacillus subtilis 1423 -11529886 222601 ycib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:170091) (re:170675) (di:direct) BSUB0002 Z99105 g2632621 Bacillus subtilis 1423 -11529886 7500963566 ycib (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:44394) (re:44978) (di:direct) D50453 D50453 g1805407 Bacillus subtilis 1423 -11529886

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767151	2577	24733	216	71

Description

6500726029 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yciC yciC Bacillus subtilis 1423 -11529887 7000692404 ycic conserved hypothetical protein ycic (cl:conserved hypothetical protein ycic) (db:pir2.dat) B69760 B69760 Bacillus subtilis 1423 -11529887 222602 ycic (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:170984) (re:172177) (di:direct) BSUB0002 Z99105 g2632622 Bacillus subtilis 1423 -11529887 7500963567 ycic homologues to nitrile hydratase region (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:45287) (re:46480) (di:direct) D50453 D50453 g1805408 Bacillus subtilis 1423 -11529887

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767155	2578	24734	342	113

Description

5000688772 hypothetical protein:probable amino-acid abc transporter permease protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckA yckA Bacillus subtilis 1423 -11529888 110837 ycka (de:probable amino-acid abc transporter permease protein) (db:swissprot) YCKA_BACSU P42399 BACILLUS SUBTILIS 1423 -11529888 7000687482 ycka amino acid abc transporter permease homolog ycka (cl:histidine permease protein m) (db:pir2.dat) C69760 C69760 Bacillus subtilis 1423 -11529888 217134 ycka homologue of glutamine permease of h. (sr:bacillus subtilis (strain:168trpc2) dna, clone_lib:lambda dashi) (db:genpept-bct1) (de:bacillus subtilis dna around 28 degrees region of chromosomecontaining ycka-h genes.) (le:149) (re:829) (di:complement) BACYCK D30762 g710628 Bacillus subtilis 1423 -11529888 222603 ycka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to amino acid abc transporter (permease)) (le:172226) (re:172906) (di:complement) BSUB0002 Z99105 g2632623 Bacillus subtilis 1423 -11529888 7500921885 ycka homologue of glutamine permease of h. inflenzae (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:46529) (re:47209) (di:complement) D50453 D50453 g1805409 Bacillus subtilis 1423 -11529888 6500726030 hypothetical protein:probable amino-acid abc transporter permease protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckA yckA Bacillus subtilis 1423 -11529888

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767156	2579	24735	366	122

Description

6500726031 hypothetical protein:probable abc transporter binding protein in comj 5region precursor:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckB yckB Bacillus subtilis 1423 -11529889 7000692188 yckb amino acid abc transporter binding protei homolog yckb (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) D69760 D69760 Bacillus subtilis 1423 -11529889 7500963398 yckb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to amino acid abc transporter (binding) (le:172916) (re:173779) (di:complement) BSUB0002 Z99105 g2632624 Bacillus subtilis 1423 -11529889

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767160	2580	24736	1029	343

Description

6500726032 hypothetical protein:hypothetical 17.0 kd protein in comj 5region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckC yckC Bacillus subtilis 1423 -11529890 110839 yckc (de:hypothetical 17.0 kd protein in comj 5'region (orf3)) (db:swissprot) YCKC_BACSU P42401 BACILLUS SUBTILIS 1423 -11529890 7000687483 yckc conserved hypothetical protein yckc (db:pir2.dat) E69760 E69760 Bacillus subtilis 1423 -11529890 222605 yckc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins from b. subtilis) (le:174157) (re:174612) (di:direct) BSUB0002 Z99105 g2632625 Bacillus subtilis 1423 -11529890 7500921886 yckc (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:48461) (re:48916) (di:direct) D50453 D50453 g1805411 Bacillus subtilis 1423 -11529890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767163	2581	24737	858	286

Description

5000689538 hypothetical protein:hypothetical 12.8 kd protein in comj 5region precursor:orf4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckD yckD Bacillus subtilis 1423 -11529891 110840 yckd (de:hypothetical 12.8 kd protein in comj 5'region precursor (orf4)) (db:swissprot) YCKD_BACSU P42402 BACILLUS SUBTILIS 1423 -11529891 7000687484 yckd hypothetical protein yckd (db:pir2.dat) F69760 F69760 Bacillus subtilis 1423 -11529891 217137 yckd unknown (sr:bacillus subtilis (strain:168trpc2) dna, clone_lib:lambda dashi) (db:genpept-bct1) (de:bacillus subtilis dna around 28 degrees region of chromosomecontaining ycka-h genes.) (le:2618) (re:2950) (di:direct) BACYCK D30762 g710631 Bacillus subtilis 1423 -11529891 222606 yckd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:174694) (re:175026) (di:direct) BSUB0002 Z99105 g2632626 Bacillus subtilis 1423 -11529891 7500921887 yckd (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:48998) (re:49330) (di:direct) D50453 D50453 g1805412 Bacillus subtilis 1423 -11529891 6500726033 hypothetical protein:hypothetical 12.8 kd protein in comj 5region precursor:orf4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckD yckD Bacillus subtilis 1423 -11529891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767164	2582	24738	294	97

Description

5000689925 comj:nin hypothetical protein:competence protein j:dna-entry nuclease inhibitor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) nin nin Bacillus subtilis 1423 -11529892 65411 comj:nin (de:competence protein j (dna-entry nuclease inhibitor)) (db:swissprot) COMJ_BACSU P12669 BACILLUS SUBTILIS 1423 -11529892 7000684866 nin competence-specific 18k protein nin:nuca dna degrading activity inhibitor nin (db:pir2.dat) B31100 B31100 Bacillus subtilis 1423 -11529892 7500879079 (sr:b.subtilis (strain 0g1) dna, clone pgv199) (db:genpept-bct1) (de:b.subtilis 14kd and 17kd dna-entry nuclease and competence-specificprotein genes, complete cds.) (nt:18-kd competence-specific protein (ttg start) (le:418) (re:816) (di:direct) BACENCS M21672 g142879 Bacillus subtilis 1423 -11529892 215565 comj competent specific protein (sr:bacillus subtilis (strain:168trpc2) dna, clone_lib:lambda dashi) (db:genpept-bct1) (de:bacillus subtilis dna around 28 degrees region of chromosomecontaining ycka-h genes.) (le:4574) (re:4972) (di:complement) BACYCK D30762 g1438845 Bacillus subtilis 1423 -11529892 217139 nin (fn:inhibition of the dna degrading activity of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:alternate gene name: comj) (le:176650) (re:177048) (di:complement) BSUB0002 Z99105 g2632628 Bacillus subtilis 1423 -11529892 222608 comj competence specific protein (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:50954) (re:51352) (di:complement) D50453 D50453 g1805414 Bacillus subtilis 1423 -11529892 169939 nin competence-specific 18k protein nin:nuca dna degrading activity inhibitor nin (db:pir) B31100 B31100 Bacillus subtilis 1423 -11529892 6500726034 comj hypothetical protein:competence protein j:dna-entry nuclease inhibitor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) nin nin Bacillus subtilis 1423 -11529892

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767166	2583	24739	345	114

Description

5000689539 hypothetical protein:hypothetical 20.0 kd protein in tlpc-srfaa intergenic region:orf9 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckF yckF Bacillus subtilis 1423 -11529893 110841 yckf (de:hypothetical 20.0 kd protein in tlpc-srfaa intergenic region (orf9)) (db:swissprot) YCKF_BACSU P42404 BACILLUS SUBTILIS 1423 -11529893 7000687485 yckf conserved hypothetical protein yckf (cl:conserved hypothetical protein mj1247) (db:pir2.dat) H69760 H69760 Bacillus subtilis 1423 -11529893 217142 yckf unknown (sr:bacillus subtilis (strain:168trpc2) dna, clone_lib:lambda dashi) (db:genpept-bct1) (de:bacillus subtilis dna around 28 degrees region of chromosomecontaining ycka-h genes.) (le:7448) (re:8005) (di:complement) BACYCK D30762 g1438846 Bacillus subtilis 1423 -11529893 222611 yckf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:179524) (re:180081) (di:complement) BSUB0002 Z99105 g2632631 Bacillus subtilis 1423 -11529893 7500921888 yckf (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:53828) (re:54385) (di:complement) D50453 D50453 g1805417 Bacillus subtilis 1423 -11529893 6500726035 hypothetical protein:hypothetical 20.0 kd protein in tlpc-srfaa intergenic region:orf9 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckF yckF Bacillus subtilis 1423 -11529893

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767171	2584	24740	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767184	2585	24741	234	77

Description

6500726036 hypothetical protein:similar to d-arabino 3-hexulose 6-phosphate formaldehyde lyase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckG yckG Bacillus subtilis 1423 -11529894 7500883611 yckg (ec:4.1.2.-) (de:3-hexulose 6-phosphate formaldehyde lyase)) (db:swissprot) HUMS_BACSU P42405 BACILLUS SUBTILIS 1423 -11529894 7000692905 yckg d-arabino 3-hexulose 6-phosphate formaldeh homolog yckg (db:pir2.dat) A69761 A69761 Bacillus subtilis 1423 -11529894 7500883613 yckg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to d-arabino 3-hexulose 6-phosphate) (le:180087) (re:180719) (di:complement) BSUB0002 Z99105 g2632632 Bacillus subtilis 1423 -11529894

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767189	2586	24742	636	211

Description

6500726037 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yckH yckH Bacillus subtilis 1423 -11529895 7000692405 yckh conserved hypothetical protein yckh (cl:conserved hypothetical protein mth1285) (db:pir2.dat) B69761 B69761 Bacillus subtilis 1423 -11529895 7500963568 yckh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:180951) (re:181313) (di:direct) BSUB0002 Z99105 g2632633 Bacillus subtilis 1423 -11529895

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767191	2587	24743	282	94

Description

5000689555 hypothetical protein:hypothetical 44.9 kd protein in srfa4-sfp intergenic region:orf5 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycxA ycxA Bacillus subtilis 1423 -11529896 7500922017 ycxa (de:hypothetical 44.9 kd protein in srfa4-sfp intergenic region (orf5)) (db:swissprot) YCXA_BACSU Q08791 BACILLUS SUBTILIS 1423 -11529896 7000687500 ycxa hypothetical protein ycxa:hypothetical protein 5 srfa operon (db:pir2.dat) I40489 I40489 Bacillus subtilis 1423 -11529896 6500726038 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (nt:orf5) (le:26262) (re:27491) (di:direct) BSSRFAP X70356 g396485 Bacillus subtilis 1423 -11529896 219684 ycxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:208148) (re:209377) (di:direct) BSUB0002 Z99105 g2632639 Bacillus subtilis 1423 -11529896 222619 ycxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:48) (re:1277) (di:direct) BSUB0003 Z99106 g2632654 Bacillus subtilis 1423 -11529896 6000685430 ycxa homologue of ko5b2.5 gene product of c. elegans (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:82451) (re:83680) (di:direct) D50453 D50453 g1805425 Bacillus subtilis 1423 -11529896 111018 ycxa (de:hypothetical 44.9 kd protein in srfa4-sfp intergenic region (orf5)) (db:swissprot) YCXA_BACSU Q08791 BACILLUS SUBTILIS 1423 -11529896 170216 ycxa hypothetical protein ycxa:hypothetical protein 5 srfa operon (db:pir) I40489 I40489 Bacillus subtilis 1423 -11529896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767192	2588	24744	1485	495

Description

5000689556 hypothetical protein:hypothetical 22.0 kd protein in srfa4-sfp intergenic region:orf6 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycxB ycxB Bacillus subtilis 1423 -11529897 7500922020 ycxb (de:hypothetical 22.0 kd protein in srfa4-sfp intergenic region (orf6)) (db:swissprot) YCXB_BACSU Q08793 BACILLUS SUBTILIS 1423 -11529897 7000687501 ycxb hypothetical protein ycxb:hypothetical protein 6 srfa operon (db:pir2.dat) I40490 I40490 Bacillus subtilis 1423 -11529897 6500726039 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (nt:orf6) (le:27506) (re:28063) (di:complement) BSSRFAP X70356 g396487 Bacillus subtilis 1423 -11529897 219685 ycxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:209392) (re:209949) (di:complement) BSUB0002 Z99105 g2632640 Bacillus subtilis 1423 -11529897 222620 ycxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:1292) (re:1849) (di:complement) BSUB0003 Z99106 g2632655 Bacillus subtilis 1423 -11529897 6000685432 ycxb (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:83695) (re:84252) (di:complement) D50453 D50453 g1805426 Bacillus subtilis 1423 -11529897 111024 ycxb (de:hypothetical 22.0 kd protein in srfa4-sfp intergenic region (orf6)) (db:swissprot) YCXB_BACSU Q08793 BACILLUS SUBTILIS 1423 -11529897 170224 ycxb hypothetical protein ycxb:hypothetical protein 6 srfa operon (db:pir) I40490 I40490 Bacillus subtilis 1423 -11529897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767199	2589	24745	462	154

Description

5000689557 hypothetical protein:hypothetical 34.1 kd protein in srfa4-sfp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycxC ycxC Bacillus subtilis 1423 -11529898 7500922023 ycxc (de:hypothetical 34.1 kd protein in srfa4-sfp intergenic region) (db:swissprot) YCXC_BACSU Q08794 BACILLUS SUBTILIS 1423 -11529898 7000687502 ycxc conserved hypothetical protein ycxc:hypothetical protein 7 srfa operon (db:pir2.dat) I40491 I40491 Bacillus subtilis 1423 -11529898 6000685434 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (nt:unnamed protein product) (le:28117) (re:29055) (di:complement) BSSRFAP X70356 g396488 Bacillus subtilis 1423 -11529898 219686 ycxc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins from b. subtilis) (le:210003) (re:210941) (di:complement) BSUB0002 Z99105 g2632641 Bacillus subtilis 1423 -11529898 222621 ycxc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:1903) (re:2841) (di:complement) BSUB0003 Z99106 g2632656 Bacillus subtilis 1423 -11529898 7502851643 ycxc homologue of hypothetical protein of buchnera (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:84306) (re:85244) (di:complement) D50453 D50453 g1805427 Bacillus subtilis 1423 -11529898 111028 ycxc (de:hypothetical 34.1 kd protein in srfa4-sfp intergenic region) (db:swissprot) YCXC_BACSU Q08794 BACILLUS SUBTILIS 1423 -11529898 170226 ycxc conserved hypothetical protein ycxc:hypothetical protein 7 srfa operon (db:pir) I40491 I40491 Bacillus subtilis 1423 -11529898 6500726040 hypothetical protein:hypothetical 34.1 kd protein in srfa4-sfp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycxC ycxC Bacillus subtilis 1423 -11529898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767205	2590	24746	1155	385

Description

5000689558 hypothetical protein:hypothetical 50.8 kd protein in srfa4-sfp intergenic region:orf8 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycxD ycxD Bacillus subtilis 1423 -11529899 7500922026 ycxd (de:hypothetical 50.8 kd protein in srfa4-sfp intergenic region (orf8)) (db:swissprot) YCXD_BACSU Q08792 BACILLUS SUBTILIS 1423 -11529899 7000687503 ycxd gntr-type transcription regulator homolog ycxd:hypothetical protein 8 srfa operon (cl:hypothetical protein b1439) (db:pir2.dat) I40492 I40492 Bacillus subtilis 1423 -11529899 6500726041 (db:genpept-bct1) (de:b.subtilis srfa-sfp gene region for surfactin synthetase.) (nt:orf8) (le:29179) (re:30513) (di:direct) BSSRFAP X70356 g396486 Bacillus subtilis 1423 -11529899 219687 ycxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (gntr family)) (le:211065) (re:212399) (di:direct) BSUB0002 Z99105 g2632642 Bacillus subtilis 1423 -11529899 222622 ycxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (gntr family)) (le:2965) (re:4299) (di:direct) BSUB0003 Z99106 g2632657 Bacillus subtilis 1423 -11529899 6000685436 ycxd homologue of mocr gene product of rhizobium (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:85368) (re:86702) (di:direct) D50453 D50453 g1805428 Bacillus subtilis 1423 -11529899 111032 ycxd (de:hypothetical 50.8 kd protein in srfa4-sfp intergenic region (orf8)) (db:swissprot) YCXD_BACSU Q08792 BACILLUS SUBTILIS 1423 -11529899 170228 ycxd gntr-type transcription regulator homolog ycxd:hypothetical protein 8 srfa operon (cl:hypothetical protein b1439) (db:pir) I40492 I40492 Bacillus subtilis 1423 -11529899

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767398	2591	24747	927	309

Description

6500726042 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczE yczE Bacillus subtilis 1423 -11529900 7000692411 ycze conserved hypothetical protein ycze (db:pir2.dat) C69767 C69767 Bacillus subtilis 1423 -11529900 6000690107 ycze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins from b. subtilis) (le:213174) (re:213821) (di:complement) BSUB0002 Z99105 g2632644 Bacillus subtilis 1423 -11529900 7500963573 ycze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:5074) (re:5721) (di:complement) BSUB0003 Z99106 g2632659 Bacillus subtilis 1423 -11529900

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767423	2592	24748	549	182

Description

6500726043 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclA yclA Bacillus subtilis 1423 -11529901 7000694753 ycla transcription regulator lysr family homolog ycla (db:pir2.dat) F69761 F69761 Bacillus subtilis 1423 -11529901 222627 ycla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to transcriptional regulator (lysr family)) (le:216508) (re:217380) (di:complement) BSUB0002 Z99105 g2632648 Bacillus subtilis 1423 -11529901 6000690113 ycla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (lysr family)) (le:8408) (re:9280) (di:complement) BSUB0003 Z99106 g2632663 Bacillus subtilis 1423 -11529901 7500965323 ycla homologue of als operon regulatory protein alsr (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:90811) (re:91683) (di:complement) D50453 D50453 g1805433 Bacillus subtilis 1423 -11529901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767430	2593	24749	495	164

Description

6500726044 hypothetical protein:similar to phenylacrylic acid decarboxylase (gtcfc:14.1) (ec:4.1.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclB yclB Bacillus subtilis 1423 -11529902 7000694390 yclb phenylacrylic acid decarboxylase homolog yclb (cl:dedf protein) (db:pir2.dat) G69761 G69761 Bacillus subtilis 1423 -11529902 222628 yclb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to phenylacrylic acid decarboxylase) (le:217470) (re:218084) (di:direct) BSUB0002 Z99105 g2632649 Bacillus subtilis 1423 -11529902 6000690115 yclb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to phenylacrylic acid decarboxylase) (le:9370) (re:9984) (di:direct) BSUB0003 Z99106 g2632664 Bacillus subtilis 1423 -11529902 7500955389 yclb homologue of phenylacrylic acid decarboxylase (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:91773) (re:92387) (di:direct) D50453 D50453 g1805434 Bacillus subtilis 1423 -11529902

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767434	2594	24750	258	86

Description

6500726045 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclC yclC Bacillus subtilis 1423 -11529903 7000692406 yclc conserved hypothetical protein yclc (db:pir2.dat) H69761 H69761 Bacillus subtilis 1423 -11529903 222629 yclc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to hypothetical proteins) (le:218087) (re:219508) (di:direct) BSUB0002 Z99105 g2632650 Bacillus subtilis 1423 -11529903 6000690117 yclc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:9987) (re:11408) (di:direct) BSUB0003 Z99106 g2632665 Bacillus subtilis 1423 -11529903 7500963569 yclc homologue of hypothetical protein of e. coli (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:92390) (re:93811) (di:direct) D50453 D50453 g1805435 Bacillus subtilis 1423 -11529903

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767435	2595	24751	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767440	2596	24752	633	210

Description

6500726046 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclD yclD Bacillus subtilis 1423 -11529904 7000693171 ycld hypothetical protein ycld (db:pir2.dat) A69762 A69762 Bacillus subtilis 1423 -11529904 222630 ycld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (le:219525) (re:220214) (di:direct) BSUB0002 Z99105 g2632651 Bacillus subtilis 1423 -11529904 6000690119 ycld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:11425) (re:12114) (di:direct) BSUB0003 Z99106 g2632666 Bacillus subtilis 1423 -11529904 7500964139 ycld (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:93828) (re:94517) (di:direct) D50453 D50453 g1805436 Bacillus subtilis 1423 -11529904

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767444	2597	24753	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767452	2598	24754	567	189

Description

6500726047 hypothetical protein:similar to prolyl aminopeptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclE yclE Bacillus subtilis 1423 -11529905 7000694452 ycle prolyl aminopeptidase homolog ycle (db:pir2.dat) B69762 B69762 Bacillus subtilis 1423 -11529905 222631 ycle (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.) (nt:similar to prolyl aminopeptidase) (le:220280) (re:221125) (di:direct) BSUB0002 Z99105 g2632652 Bacillus subtilis 1423 -11529905 6000690121 ycle (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to prolyl aminopeptidase) (le:12180) (re:13025) (di:direct) BSUB0003 Z99106 g2632667 Bacillus subtilis 1423 -11529905 7500965103 ycle (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:94583) (re:95428) (di:direct) D50453 D50453 g1805437 Bacillus subtilis 1423 -11529905

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767465	2599	24755	891	296

Description

6500726048 hypothetical protein:similar to di-tripeptide abc transporter:membrane protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclF yclF Bacillus subtilis 1423 -11529906 7000687487 yclf (de:hypothetical 53.3 kd protein in sfp-gerka intergenic region) (db:swissprot) YCLF_BACSU P94408 BACILLUS SUBTILIS 1423 -11529906 7000687488 yclf di-tripeptide abc transporter membrane pr homolog yclf (cl:peptide transporter protein) (db:pir2.dat) C69762 C69762 Bacillus subtilis 1423 -11529906 222632 yclf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to di-tripeptide abc transporter (membrane) (le:13065) (re:14543) (di:complement) BSUB0003 Z99106 g2632668 Bacillus subtilis 1423 -11529906 7500921894 yclf homologue of di-tripeptide transporter dtp of l. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:95468) (re:96946) (di:complement) D50453 D50453 g1805438 Bacillus subtilis 1423 -11529906

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767466	2600	24756	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767490	2601	24757	408	135

Description

6500726049 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclG yclG Bacillus subtilis 1423 -11529907 7000693172 yclg hypothetical protein yclg (db:pir2.dat) D69762 D69762 Bacillus subtilis 1423 -11529907 222633 yclg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:14823) (re:16577) (di:direct) BSUB0003 Z99106 g2632669 Bacillus subtilis 1423 -11529907 7500964140 yclg (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:97226) (re:98980) (di:direct) D50453 D50453 g1805439 Bacillus subtilis 1423 -11529907

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767497	2602	24758	804	267

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767498	2603	24759	978	325

Description

6500726050 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczF yczF Bacillus subtilis 1423 -11529908 7000693176 yczf hypothetical protein yczf (db:pir2.dat) D69767 D69767 Bacillus subtilis 1423 -11529908 7500964144 yczf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:16593) (re:16814) (di:complement) BSUB0003 Z99106 g2632670 Bacillus subtilis 1423 -11529908

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767502	2604	24760	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767519	2605	24761	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767536	2606	24762	576	191

Description

6500726051 hypothetical protein:spore germination protein ka (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) gerKA gerKA Bacillus subtilis 1423 -11529909 222634 gerka (fn:germination response to the combination of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:16940) (re:18574) (di:direct) BSUB0003 Z99106 g2632671 Bacillus subtilis 1423 -11529909 7500964007 gerka spore germination protein gerka (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:99343) (re:100977) (di:direct) D50453 D50453 g1805440 Bacillus subtilis 1423 -11529909 7000693025 gerka germination response to the combination of glucose:fructose:gerka (db:pir) H69630 H69630 Bacillus subtilis 1423 -11529909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767537	2607	24763	318	106

Description

GTC ORF with score 136 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid b0304.) (nt:similar to cytochrome p450) (le:10559:10704:10969:11223) (re:10645:10833:11057:11316) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767546	2608	24764	906	302

Description

5000689085 hypothetical protein:spore germination protein kc precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) gerKC gerKC Bacillus subtilis 1423 -11529910 74508 gerkc (de:spore germination protein kc precursor) (db:swissprot) GRKC_BACSU P49941 BACILLUS SUBTILIS 1423 -11529910 7000685454 gerkc germination response protein gerkc (db:pir2.dat) I39859 I39859 Bacillus subtilis 1423 -11529910 303341 gerk gerkc (fn:possible spore germination apparatus protein) (sr:bacillus subtilis (strain:168tt) dna) (db:genpept-bct1) (de:bacillus subtilis dna for gerka, gerkc and gerkb, complete cds.) (le:1945) (re:3168) (di:direct) BACGERK D78187 g1063255 Bacillus subtilis 1423 -11529910 215660 gerkc (fn:germination response to the combination of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:18564) (re:19787) (di:direct) BSUB0003 Z99106 g2632672 Bacillus subtilis 1423 -11529910 222635 gerkc spore germination protein gerkc (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:100967) (re:102190) (di:direct) D50453 D50453 g1805441 Bacillus subtilis 1423 -11529910 170012 gerkc germination response protein gerkc (db:pir) I39859 I39859 Bacillus subtilis 1423 -11529910 6500726052 hypothetical protein:spore germination protein kc precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) gerKC gerKC Bacillus subtilis 1423 -11529910

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767550	2609	24765	1527	508

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767559	2610	24766	222	74

Description

5000689084 hypothetical protein:spore germination protein kb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) gerKB gerKB Bacillus subtilis 1423 -11529911 74507 gerkb (de:spore germination protein kb) (db:swissprot) GRKB_BACSU P49940 BACILLUS SUBTILIS 1423 -11529911 7000685453 gerkb germination response protein gerkb (cl:spore germination protein) (db:pir2.dat) I39860 I39860 Bacillus subtilis 1423 -11529911 303342 gerk gerkb (fn:possible spore germination apparatus protein) (sr:bacillus subtilis (strain:168tt) dna) (db:genpept-bct1) (de:bacillus subtilis dna for gerka, gerkc and gerkb, complete cds.) (le:3193) (re:4314) (di:direct) BACGERK D78187 g1063256 Bacillus subtilis 1423 -11529911 215661 gerkb (fn:germination response to the combination of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:19812) (re:20933) (di:direct) BSUB0003 Z99106 g2632673 Bacillus subtilis 1423 -11529911 222636 gerkb spore germination protein gerkb (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:102215) (re:103336) (di:direct) D50453 D50453 g1805442 Bacillus subtilis 1423 -11529911 170011 gerkb germination response protein gerkb (cl:spore germination protein) (db:pir) I39860 I39860 Bacillus subtilis 1423 -11529911 6500726053 hypothetical protein:spore germination protein kb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) gerKB gerKB Bacillus subtilis 1423 -11529911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767560	2611	24767	690	229

Description

6500726054 hypothetical protein:similar to abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclH yclH Bacillus subtilis 1423 -11529912 7000692118 yclh abc transporter permease homolog yclh (cl:atp-binding cassette homology) (db:pir2.dat) E69762 E69762 Bacillus subtilis 1423 -11529912 222637 yclh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to abc transporter (permease)) (le:21038) (re:21718) (di:complement) BSUB0003 Z99106 g2632674 Bacillus subtilis 1423 -11529912 7500963358 yclh homologue of hypothetical protein in a rapamycin (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:103441) (re:104121) (di:complement) D50453 D50453 g1805443 Bacillus subtilis 1423 -11529912

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767785	2612	24768	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767799	2613	24769	495	164

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767800	2614	24770	492	163

Description

6500726055 hypothetical protein:similar to transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclI yclI Bacillus subtilis 1423 -11529913 7000694815 ycli transporter homolog ycli (db:pir2.dat) F69762 F69762 Bacillus subtilis 1423 -11529913 222638 ycli (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transporter) (le:21734) (re:23194) (di:complement) BSUB0003 Z99106 g2632675 Bacillus subtilis 1423 -11529913 7500965369 ycli homologue of hypothetical protein in a rapamycin (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:104137) (re:105597) (di:complement) D50453 D50453 g1805444 Bacillus subtilis 1423 -11529913

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767803	2615	24771	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767807	2616	24772	234	77

Description

6500726056 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclJ yclJ Bacillus subtilis 1423 -11529914 7000694841 yclj two-component response regulator yclk homolog yclj) (cl:ompr protein:response regulator homology) (db:pir2.dat) G69762 G69762 Bacillus subtilis 1423 -11529914 222639 yclj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to two-component response regulator (yclk)) (le:23407) (re:24090) (di:direct) BSUB0003 Z99106 g2632676 Bacillus subtilis 1423 -11529914 7500965390 yclj homologue of alkaline phosphatase synthesis (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:105810) (re:106493) (di:direct) D50453 D50453 g1805445 Bacillus subtilis 1423 -11529914

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767811	2617	24773	198	66

Description

6500726057 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclK yclK Bacillus subtilis 1423 -11529915 7000694870 yclk two-component sensor histidine kinase homolog yclk (db:pir2.dat) H69762 H69762 Bacillus subtilis 1423 -11529915 222640 yclk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to two-component sensor histidine kinase) (le:24077) (re:25498) (di:direct) BSUB0003 Z99106 g2632677 Bacillus subtilis 1423 -11529915 7500965408 yclk homologue of alkaline phosphatase synthesis (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:106480) (re:107901) (di:direct) D50453 D50453 g1805446 Bacillus subtilis 1423 -11529915

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767813	2618	24774	465	154

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767824	2619	24775	972	323

Description

6500726058 hypothetical protein:similar to homoserine dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yclM yclM Bacillus subtilis 1423 -11529916 7000693109 yclm homoserine dehydrogenase homolog yclm (cl:aspartate kinase homology) (db:pir2.dat) A69763 A69763 Bacillus subtilis 1423 -11529916 222643 yclm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to homoserine dehydrogenase) (le:27453) (re:28817) (di:complement) BSUB0003 Z99106 g2632680 Bacillus subtilis 1423 -11529916 7500964056 yclm homologue of aspartokinase 2 alpha and beta (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:109856) (re:111220) (di:complement) D50453 D50453 g1805449 Bacillus subtilis 1423 -11529916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767825	2620	24776	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767842	2621	24777	417	138

Description

6500726059 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnB ycnB Bacillus subtilis 1423 -11529917 7000694240 ycnb multidrug resistance protein homolog ycnb (db:pir2.dat) F69763 F69763 Bacillus subtilis 1423 -11529917 222648 ycnb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to multidrug resistance protein) (le:32866) (re:34284) (di:complement) BSUB0003 Z99106 g2632685 Bacillus subtilis 1423 -11529917 7500964967 ycnb homologue of multidrug resistance protein b (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:115269) (re:116687) (di:complement) D50453 D50453 g1805454 Bacillus subtilis 1423 -11529917

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767843	2622	24778	354	117

Description

6500726060 hypothetical protein:similar to transcriptional regulator:tetr/acrr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnC ycnC Bacillus subtilis 1423 -11529918 7000694782 ycnc transcription regulator tetr/acrr family homolog ycnc (db:pir2.dat) G69763 G69763 Bacillus subtilis 1423 -11529918 222649 ycnc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (tetr/acrr) (le:34304) (re:35182) (di:complement) BSUB0003 Z99106 g2632686 Bacillus subtilis 1423 -11529918 7500965344 ycnc (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:116707) (re:117585) (di:complement) D50453 D50453 g1805455 Bacillus subtilis 1423 -11529918

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767858	2623	24779	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767859	2624	24780	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767865	2625	24781	492	163

Description

6500726061 hypothetical protein:similar to nadph-flavin oxidoreductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnD ycnD Bacillus subtilis 1423 -11529919 7500921895 ycnd (de:hypothetical 27.9 kd protein in phrc-gdh intergenic region) (db:swissprot) YCND_BACSU P94424 BACILLUS SUBTILIS 1423 -11529919 7000694311 ycnd nadph-flavin oxidoreductase homolog ycnd (cl:nadph-flavin oxidoreductase homolog) (db:pir2.dat) H69763 H69763 Bacillus subtilis 1423 -11529919 7500921897 ycnd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to nadph-flavin oxidoreductase) (le:35346) (re:36095) (di:complement) BSUB0003 Z99106 g2632687 Bacillus subtilis 1423 -11529919 222650 ycnd homologue of nadph-flavin oxidoreductase frp of (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:117749) (re:118498) (di:complement) D50453 D50453 g1805456 Bacillus subtilis 1423 -11529919

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767875	2626	24782	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767879	2627	24783	486	162

Description

GTC ORF with score 184 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid y54e2a, complete sequence.) (nt:cdna est yk330e11.3 comes from this gene; cdna est) (le:60394:60545:60703:61187) (re:60495:60650:61131:61646) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767889	2628	24784	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767894	2629	24785	279	92

Description

6500726062 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnE ycnE Bacillus subtilis 1423 -11529920 7500921899 ycne (de:hypothetical 10.9 kd protein in phrc-gdh intergenic region) (db:swissprot) YCNE_BACSU P94425 BACILLUS SUBTILIS 1423 -11529920 7000692407 ycne conserved hypothetical protein ycne (db:pir2.dat) A69764 A69764 Bacillus subtilis 1423 -11529920 7500921901 ycne (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:36112) (re:36399) (di:complement) BSUB0003 Z99106 g2632688 Bacillus subtilis 1423 -11529920 222651 ycne (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:118515) (re:118802) (di:complement) D50453 D50453 g1805457 Bacillus subtilis 1423 -11529920

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767895	2630	24786	528	175

Description

6500726063 hypothetical protein:similar to transcriptional regulator:arsr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczG yczG Bacillus subtilis 1423 -11529921 7000694721 yczg transcription regulator arsr family homolog yczg (cl:arsenical resistance operon repressor) (db:pir2.dat) E69767 E69767 Bacillus subtilis 1423 -11529921 7500965296 yczg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (arsr family)) (le:36539) (re:36853) (di:direct) BSUB0003 Z99106 g2632689 Bacillus subtilis 1423 -11529921

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767899	2631	24787	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767927	2632	24788	288	95

Description

6500726064 hypothetical protein:similar to transcriptional regulator:gntr family / aminotransferase:mocr-like (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnF ycnF Bacillus subtilis 1423 -11529922 7000694729 ycnf transcription regulator gntr family homolog ycnf (cl:hypothetical protein b1439) (db:pir2.dat) B69764 B69764 Bacillus subtilis 1423 -11529922 222652 ycnf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (gntr family)) (le:36855) (re:38294) (di:complement) BSUB0003 Z99106 g2632690 Bacillus subtilis 1423 -11529922 7500965303 ycnf homologue of regulatory protein mocr of r. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:119258) (re:120697) (di:complement) D50453 D50453 g1805458 Bacillus subtilis 1423 -11529922

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767929	2633	24789	240	79

Description

6500726065 hypothetical protein:similar to succinate-semialdehyde dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnH ycnH Bacillus subtilis 1423 -11529923 7000694642 ycnh succinate-semialdehyde dehydrogenase homolog ycnh (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) D69764 D69764 Bacillus subtilis 1423 -11529923 222654 ycnh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to succinate-semialdehyde dehydrogenase) (le:39780) (re:41168) (di:direct) BSUB0003 Z99106 g2632692 Bacillus subtilis 1423 -11529923 7500965229 ycnh homologue of succinate semialdehyde (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:122183) (re:123571) (di:direct) D50453 D50453 g1805460 Bacillus subtilis 1423 -11529923

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767930	2634	24790	480	159

Description

6500726066 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycxE ycxE Bacillus subtilis 1423 -11529924 7000692408 ycxe conserved hypothetical protein ycxe (db:pir2.dat) G69766 G69766 Bacillus subtilis 1423 -11529924 222655 ycxe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:41291) (re:42154) (di:direct) BSUB0003 Z99106 g2632693 Bacillus subtilis 1423 -11529924 7500963570 ycxe homologues to hypothetical 30.5 kda protein gdh1 (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:123694) (re:124557) (di:direct) D50453 D50453 g1805461 Bacillus subtilis 1423 -11529924

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767939	2635	24791	336	111

Description

6500726067 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnI ycnI Bacillus subtilis 1423 -11529925 7000693173 ycni hypothetical protein ycni (db:pir2.dat) E69764 E69764 Bacillus subtilis 1423 -11529925 222657 ycni (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:43004) (re:43618) (di:complement) BSUB0003 Z99106 g2632695 Bacillus subtilis 1423 -11529925 7500964141 ycni (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:125407) (re:126021) (di:complement) D50453 D50453 g1805463 Bacillus subtilis 1423 -11529925

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767940	2636	24792	474	157

Description

6500726068 hypothetical protein:similar to copper export protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnJ ycnJ Bacillus subtilis 1423 -11529926 7000692879 ycnj copper export protein homolog ycnj (db:pir2.dat) F69764 F69764 Bacillus subtilis 1423 -11529926 222658 ycnj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to copper export protein) (le:43631) (re:45256) (di:complement) BSUB0003 Z99106 g2632696 Bacillus subtilis 1423 -11529926 7500963910 ycnj homologue of copper export protein pcod of e. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:126034) (re:127659) (di:complement) D50453 D50453 g1805464 Bacillus subtilis 1423 -11529926

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767945	2637	24793	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767950	2638	24794	486	161

Description

6500726069 hypothetical protein:similar to transcriptional regulator:deor family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnK ycnK Bacillus subtilis 1423 -11529927 7000694725 ycnk transcription regulator deor family homolog ycnk (db:pir2.dat) G69764 G69764 Bacillus subtilis 1423 -11529927 222659 ycnk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (deor family)) (le:45291) (re:45863) (di:complement) BSUB0003 Z99106 g2632697 Bacillus subtilis 1423 -11529927 7500965300 ycnk (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:127694) (re:128266) (di:complement) D50453 D50453 g1805465 Bacillus subtilis 1423 -11529927

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767951	2639	24795	759	252

Description

6500726070 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycnL ycnL Bacillus subtilis 1423 -11529928 7000693174 ycnl hypothetical protein ycnl (db:pir2.dat) H69764 H69764 Bacillus subtilis 1423 -11529928 222660 ycnl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:46028) (re:46381) (di:direct) BSUB0003 Z99106 g2632698 Bacillus subtilis 1423 -11529928 7500964142 ycnl (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:128431) (re:128784) (di:direct) D50453 D50453 g1805466 Bacillus subtilis 1423 -11529928

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501767954	2640	24796	354	117

Description

6500726071 hypothetical protein:similar to 3-isopropylmalate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsA ycsA Bacillus subtilis 1423 -11529929 7502851644 ycsa (de:hypothetical 33.1 kd protein in mtld-sipu intergenic region) (db:swissprot) YCSA_BACSU P42958 BACILLUS SUBTILIS 1423 -11529929 7000692049 ycsa tartrate dehydrogenase (cl:3-isopropylmalate dehydrogenase) (ec:1.1.1.93) (db:pir2.dat) A69765 A69765 Bacillus subtilis 1423 -11529929 7500953809 ycsa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to 3-isopropylmalate dehydrogenase) (le:49647) (re:50552) (di:direct) BSUB0003 Z99106 g2632701 Bacillus subtilis 1423 -11529929

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768173	2641	24797	228	75

Description

6500726072 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczH yczH Bacillus subtilis 1423 -11529930 7000693177 yczh hypothetical protein yczh (db:pir2.dat) F69767 F69767 Bacillus subtilis 1423 -11529930 7500964145 yczh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:51515) (re:52072) (di:complement) BSUB0003 Z99106 g2632703 Bacillus subtilis 1423 -11529930

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768177	2642	24798	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768181	2643	24799	486	161

Description

5000689544 hypothetical protein:hypothetical 19.6 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsD ycsD Bacillus subtilis 1423 -11529931 110900 ycsd (de:hypothetical 19.6 kd protein in sipu-pbpc intergenic region) (db:swissprot) YCSD_BACSU P42961 BACILLUS SUBTILIS 1423 -11529931 7000687489 ycsd conserved hypothetical protein ycsd (db:pir2.dat) I39892 I39892 Bacillus subtilis 1423 -11529931 7500921937 unknown protein (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:5847) (re:6359) (di:direct) BAC39R D38161 g707081 Bacillus subtilis 1423 -11529931 215096 ycsd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:52158) (re:52670) (di:direct) BSUB0003 Z99106 g2632704 Bacillus subtilis 1423 -11529931 222666 ycsd (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:134555) (re:135067) (di:direct) D50453 D50453 g1805472 Bacillus subtilis 1423 -11529931 170235 ycsd conserved hypothetical protein ycsd (db:pir) I39892 I39892 Bacillus subtilis 1423 -11529931 6500726073 hypothetical protein:hypothetical 19.6 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsD ycsD Bacillus subtilis 1423 -11529931

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768195	2644	24800	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768197	2645	24801	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768207	2646	24802	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768212	2647	24803	495	164

Description

GTC ORF with score 156 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0554.) (nt:similar to saccharomyces cerevisiae hypothetical) (le:86) (re:814) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768219	2648	24804	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768226	2649	24805	477	158

Description

5000689545 hypothetical protein:hypothetical 28.1 kd protein in sipu 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsE ycsE Bacillus subtilis 1423 -11529932 110901 ycse (de:hypothetical 28.1 kd protein in sipu 3'region) (db:swissprot) YCSE_BACSU P42962 BACILLUS SUBTILIS 1423 -11529932 7000687490 ycse conserved hypothetical protein ycse (db:pir2.dat) I39893 I39893 Bacillus subtilis 1423 -11529932 7500921938 similar to hypothetical 29:7 kda e. coli (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:6562) (re:7311) (di:direct) BAC39R D38161 g707082 Bacillus subtilis 1423 -11529932 215097 ycse (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:52873) (re:53622) (di:direct) BSUB0003 Z99106 g2632705 Bacillus subtilis 1423 -11529932 222667 ycse homologue to hypothetical 29.7 kda protein in (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:135270) (re:136019) (di:direct) D50453 D50453 g1805473 Bacillus subtilis 1423 -11529932 170236 ycse conserved hypothetical protein ycse (db:pir) I39893 I39893 Bacillus subtilis 1423 -11529932 6500726074 hypothetical protein:hypothetical 28.1 kd protein in sipu 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsE ycsE Bacillus subtilis 1423 -11529932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768240	2650	24806	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768242	2651	24807	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768249	2652	24808	252	83

Description

6500726075 hypothetical protein:similar to lactam utilization protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsF ycsF Bacillus subtilis 1423 -11529933 110902 ycsf (de:hypothetical 22.7 kd protein in sipu 3'region) (db:swissprot) YCSF_BACSU P42963 BACILLUS SUBTILIS 1423 -11529933 7000687491 ycsf lactam utilization protein ycsf (cl:bacillus subtilis lactam utilization protein ycsf) (db:pir2.dat) D69765 D69765 Bacillus subtilis 1423 -11529933 222668 ycsf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to lactam utilization protein) (le:53827) (re:54462) (di:direct) BSUB0003 Z99106 g2632706 Bacillus subtilis 1423 -11529933 7500921939 ycsf lactam utilization protein lamb homologue of h. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:136224) (re:136859) (di:direct) D50453 D50453 g1805474 Bacillus subtilis 1423 -11529933

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768262	2653	24809	831	276

Description

6500726076 ycsh:ycsg hypothetical protein:similar to branched chain amino acids transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsG ycsG Bacillus subtilis 1423 -11529934 7000692289 ycsg branched chain amino acids transporter homolog ycsg (db:pir2.dat) E69765 E69765 Bacillus subtilis 1423 -11529934 7500963459 ycsg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ycsh; similar to branched) (le:54666) (re:55826) (di:direct) BSUB0003 Z99106 g2632707 Bacillus subtilis 1423 -11529934

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768265	2654	24810	1464	488

Description

5000689549 hypothetical protein:hypothetical 28.1 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsI ycsI Bacillus subtilis 1423 -11529935 110905 ycsi (de:hypothetical 28.1 kd protein in sipu-pbpc intergenic region) (db:swissprot) YCSI_BACSU P42966 BACILLUS SUBTILIS 1423 -11529935 7000687492 ycsi conserved hypothetical protein ycsi (db:pir2.dat) I39897 I39897 Bacillus subtilis 1423 -11529935 7500921941 unknown protein (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:9541) (re:10314) (di:direct) BAC39R D38161 g707086 Bacillus subtilis 1423 -11529935 215101 ycsi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:55850) (re:56623) (di:direct) BSUB0003 Z99106 g2632708 Bacillus subtilis 1423 -11529935 222670 ycsi homologues to unidentified protein of (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:138248) (re:139021) (di:direct) D50453 D50453 g1805476 Bacillus subtilis 1423 -11529935 170240 ycsi conserved hypothetical protein ycsi (db:pir) I39897 I39897 Bacillus subtilis 1423 -11529935 6500726077 hypothetical protein:hypothetical 28.1 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsI ycsI Bacillus subtilis 1423 -11529935

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768267	2655	24811	792	263

Description

5000689550 hypothetical protein:hypothetical 63.8 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsJ ycsJ Bacillus subtilis 1423 -11529936 110906 ycsj (de:hypothetical 63.8 kd protein in sipu-pbpc intergenic region) (db:swissprot) YCSJ_BACSU P42967 BACILLUS SUBTILIS 1423 -11529936 7000687493 ycsj allophanate hydrolase homolog ycsj:probable urea amidolyase (db:pir2.dat) G69765 G69765 Bacillus subtilis 1423 -11529936 7500921942 urea amidolyase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:10358) (re:12094) (di:direct) BAC39R D38161 g790943 Bacillus subtilis 1423 -11529936 215102 ycsj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to allophanate hydrolase) (le:56667) (re:58403) (di:direct) BSUB0003 Z99106 g2632709 Bacillus subtilis 1423 -11529936 222671 ycsj homologues to hypothetical protein hi1731 of h. (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:139065) (re:140801) (di:direct) D50453 D50453 g1805477 Bacillus subtilis 1423 -11529936 170660 ycsj allophanate hydrolase homolog ycsj:probable urea amidolyase (db:pir) G69765 G69765 Bacillus subtilis 1423 -11529936 6500726078 hypothetical protein:hypothetical 63.8 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsJ ycsJ Bacillus subtilis 1423 -11529936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768272	2656	24812	879	292

Description

6500726079 hypothetical protein:hypothetical transcriptional regulator in mtld 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsO ycsO Bacillus subtilis 1423 -11529937 7000694744 ycso transcription regulator iclr homolog ycso:regulatory protein for aceab (cl:acetate operon repressor) (db:pir2.dat) B69766 B69766 Bacillus subtilis 1423 -11529937 222672 ycso (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (iclr family)) (le:58419) (re:59159) (di:direct) BSUB0003 Z99106 g2632710 Bacillus subtilis 1423 -11529937 7500965316 ycso homologue of pectin degradation repressor kdgr (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:140817) (re:141557) (di:direct) D50453 D50453 g1805478 Bacillus subtilis 1423 -11529937

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768309	2657	24813	228	75

Description

5000689551 hypothetical protein:hypothetical 23.6 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsK ycsK Bacillus subtilis 1423 -11529938 110907 ycsk (de:hypothetical 23.6 kd protein in sipu-pbpc intergenic region) (db:swissprot) YCSK_BACSU P42969 BACILLUS SUBTILIS 1423 -11529938 7000687494 ycsk conserved hypothetical protein ycsk (db:pir2.dat) I39900 I39900 Bacillus subtilis 1423 -11529938 7500921943 unknown protein (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:12925) (re:13566) (di:direct) BAC39R D38161 g707089 Bacillus subtilis 1423 -11529938 215104 ycsk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:59234) (re:59875) (di:direct) BSUB0003 Z99106 g2632711 Bacillus subtilis 1423 -11529938 222673 ycsk (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:141632) (re:142273) (di:direct) D50453 D50453 g1805479 Bacillus subtilis 1423 -11529938 170244 ycsk conserved hypothetical protein ycsk (db:pir) I39900 I39900 Bacillus subtilis 1423 -11529938 6500726080 hypothetical protein:hypothetical 23.6 kd protein in sipu-pbpc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsK ycsK Bacillus subtilis 1423 -11529938

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768333	2658	24814	504	167

Description

6500726081 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczI yczI Bacillus subtilis 1423 -11529939 7000693178 yczi hypothetical protein yczi (db:pir2.dat) G69767 G69767 Bacillus subtilis 1423 -11529939 7500964146 yczi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:60048) (re:60293) (di:direct) BSUB0003 Z99106 g2632712 Bacillus subtilis 1423 -11529939

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768334	2659	24815	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768337	2660	24816	279	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768564	2661	24817	726	242

Description

6500726082 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yczJ yczJ Bacillus subtilis 1423 -11529940 7000693179 yczj hypothetical protein yczj (db:pir2.dat) H69767 H69767 Bacillus subtilis 1423 -11529940 7500964147 yczj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:60299) (re:60586) (di:complement) BSUB0003 Z99106 g2632713 Bacillus subtilis 1423 -11529940

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768572	2662	24818	393	130

Description

5000689554 hypothetical protein:hypothetical 34.1 kd protein in pbpc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsN ycsN Bacillus subtilis 1423 -11529941 110910 ycsn (de:hypothetical oxidoreductase in pbpc-lrpc intergenic region) (db:swissprot) YCSN_BACSU P42972 BACILLUS SUBTILIS 1423 -11529941 7000687495 ycsn aryl-alcohol dehydrogenase homolog ycsn (db:pir2.dat) I39903 I39903 Bacillus subtilis 1423 -11529941 7500921944 aryl-alcohol dehydrogenase (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis genome around 39 degrees region encoding 17 orfs,complete cds.) (le:16533) (re:17435) (di:direct) BAC39R D38161 g790945 Bacillus subtilis 1423 -11529941 215107 ycsn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to aryl-alcohol dehydrogenase) (le:62845) (re:63747) (di:direct) BSUB0003 Z99106 g2632715 Bacillus subtilis 1423 -11529941 222676 ycsn homologue of aryl-alcohol dehydrogenase of (sr:bacillus subtilis (strain:168 trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 25-36 degree region containing theamye-srfa region, complete cds.) (le:145240) (re:146142) (di:direct) D50453 D50453 g1805482 Bacillus subtilis 1423 -11529941 169873 ycsn aryl-alcohol dehydrogenase homolog ycsn (db:pir) I39903 I39903 Bacillus subtilis 1423 -11529941 6500726083 hypothetical protein:hypothetical 34.1 kd protein in pbpc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ycsN ycsN Bacillus subtilis 1423 -11529941

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768573	2663	24819	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768582	2664	24820	774	257

Description

6500726084 hypothetical protein:similar to transcriptional antiterminator:bglg family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaA ydaA Bacillus subtilis 1423 -11529942 7000694706 ydaa transcription antiterminator bglg family homolog ydaa (db:pir2.dat) A69768 A69768 Bacillus subtilis 1423 -11529942 302672 ydaa (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable hth_lysr_family transcriptional) (le:189) (re:2273) (di:direct) AB001488 AB001488 g1881227 Bacillus subtilis 1423 -11529942 7500965279 ydaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional antiterminator (bglg) (le:63933) (re:66017) (di:direct) BSUB0003 Z99106 g2632716 Bacillus subtilis 1423 -11529942

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768594	2665	24821	462	153

Description

6500726085 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaB ydaB Bacillus subtilis 1423 -11529943 7000692412 ydab conserved hypothetical protein ydab (cl:acetate--coa ligase homology) (db:pir2.dat) B69768 B69768 Bacillus subtilis 1423 -11529943 302673 ydab (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to enzymes which act via an atp-dependent) (le:2484) (re:3881) (di:direct) AB001488 AB001488 g1881228 Bacillus subtilis 1423 -11529943 7500963574 ydab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:66228) (re:67625) (di:direct) BSUB0003 Z99106 g2632717 Bacillus subtilis 1423 -11529943

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768597	2666	24822	732	243

Description

6500726086 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaC ydaC Bacillus subtilis 1423 -11529944 7000692413 ydac conserved hypothetical protein ydac (cl:bioc homology) (db:pir2.dat) C69768 C69768 Bacillus subtilis 1423 -11529944 302674 ydac (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in several) (le:4016) (re:4561) (di:complement) AB001488 AB001488 g1881229 Bacillus subtilis 1423 -11529944 7500963575 ydac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:67760) (re:68305) (di:complement) BSUB0003 Z99106 g2632718 Bacillus subtilis 1423 -11529944

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768603	2667	24823	300	99

Description

6500726087 hypothetical protein:similar to alcohol dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaD ydaD Bacillus subtilis 1423 -11529945 7000692166 ydad alcohol dehydrogenase homolog ydad (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D69768 D69768 Bacillus subtilis 1423 -11529945 302675 ydad (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:belongs to the insect-type alcohol dehydrogenase /) (le:4769) (re:5629) (di:direct) AB001488 AB001488 g1881230 Bacillus subtilis 1423 -11529945 7500963388 ydad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to alcohol dehydrogenase) (le:68513) (re:69373) (di:direct) BSUB0003 Z99106 g2632719 Bacillus subtilis 1423 -11529945

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768611	2668	24824	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768627	2669	24825	327	109

Description

6500726088 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaE ydaE Bacillus subtilis 1423 -11529946 7000693180 ydae hypothetical protein ydae (db:pir2.dat) E69768 E69768 Bacillus subtilis 1423 -11529946 302676 ydae (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:5645) (re:6148) (di:direct) AB001488 AB001488 g1881231 Bacillus subtilis 1423 -11529946 7500964148 ydae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:69389) (re:69892) (di:direct) BSUB0003 Z99106 g2632720 Bacillus subtilis 1423 -11529946

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768632	2670	24826	603	200

Description

6500726089 hypothetical protein:similar to acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaF ydaF Bacillus subtilis 1423 -11529947 7000692144 ydaf acetyltransferase homolog ydaf (db:pir2.dat) F69768 F69768 Bacillus subtilis 1423 -11529947 302677 ydaf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable acetyltransferase.) (le:6233) (re:6784) (di:direct) AB001488 AB001488 g1881232 Bacillus subtilis 1423 -11529947 7500963373 ydaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to acetyltransferase) (le:69977) (re:70528) (di:direct) BSUB0003 Z99106 g2632721 Bacillus subtilis 1423 -11529947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768638	2671	24827	207	69

Description

6500726090 yzza:ydag hypothetical protein:general stress protein 26 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaG ydaG Bacillus subtilis 1423 -11529948 74591 ydag (de:general stress protein 26 (gsp26)) (db:swissprot) GS26_BACSU P80238 BACILLUS SUBTILIS 1423 -11529948 7000685456 ydag general stress protein homolog ydag (db:pir2.dat) G69768 G69768 Bacillus subtilis 1423 -11529948 302678 ydag (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:6862) (re:7284) (di:direct) AB001488 AB001488 g1881233 Bacillus subtilis 1423 -11529948 7500882774 ydag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: yzza; similar to general) (le:70606) (re:71028) (di:direct) BSUB0003 Z99106 g2632722 Bacillus subtilis 1423 -11529948

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768643	2672	24828	180	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768647	2673	24829	495	165

Description

6500726091 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaH ydaH Bacillus subtilis 1423 -11529949 7000692414 ydah conserved hypothetical protein ydah (db:pir2.dat) H69768 H69768 Bacillus subtilis 1423 -11529949 302679 ydah (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:7790) (re:8599) (di:direct) AB001488 AB001488 g1881234 Bacillus subtilis 1423 -11529949 7500963576 ydah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:71534) (re:72343) (di:direct) BSUB0003 Z99106 g2632723 Bacillus subtilis 1423 -11529949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768652	2674	24830	375	124

Description

6500726092 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydzA ydzA Bacillus subtilis 1423 -11529950 7000693235 ydza hypothetical protein ydza (db:pir2.dat) E69790 E69790 Bacillus subtilis 1423 -11529950 7500964203 ydza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:72387) (re:72677) (di:complement) BSUB0003 Z99106 g2632724 Bacillus subtilis 1423 -11529950

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768680	2675	24831	900	300

Description

GTC ORF with score 200 to: (sr:pyrococcus horikoshii (strain:ot3) dna) (db:genpept-bct1) (de:pyrococcus horikoshii ot3 genomic dna, 1-287000 nt. position (1/7).) (nt:similar to owl:bmu17283 percent identity: 37.634 in) (le:267332) (re:268474) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768686	2676	24832	954	317

Description

6500726093 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaJ ydaJ Bacillus subtilis 1423 -11529951 7000693181 ydaj hypothetical protein ydaj (db:pir2.dat) A69769 A69769 Bacillus subtilis 1423 -11529951 7500964149 ydaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:75747) (re:76835) (di:direct) BSUB0003 Z99106 g2632727 Bacillus subtilis 1423 -11529951

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768687	2677	24833	729	242

Description

6500726094 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaK ydaK Bacillus subtilis 1423 -11529952 7000693182 ydak hypothetical protein ydak (db:pir2.dat) B69769 B69769 Bacillus subtilis 1423 -11529952 302683 ydak (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:13072) (re:13923) (di:direct) AB001488 AB001488 g1881238 Bacillus subtilis 1423 -11529952 7500964150 ydak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:76816) (re:77667) (di:direct) BSUB0003 Z99106 g2632728 Bacillus subtilis 1423 -11529952

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768690	2678	24834	405	134

Description

6500726095 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaL ydaL Bacillus subtilis 1423 -11529953 7000693183 ydal hypothetical protein ydal (db:pir2.dat) C69769 C69769 Bacillus subtilis 1423 -11529953 7500964151 ydal (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:77678) (re:79387) (di:direct) BSUB0003 Z99106 g2632729 Bacillus subtilis 1423 -11529953

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768698	2679	24835	741	247

Description

6500726096 hypothetical protein:similar to cellulose synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaM ydaM Bacillus subtilis 1423 -11529954 7000692354 ydam cellulose synthase homolog ydam (db:pir2.dat) D69769 D69769 Bacillus subtilis 1423 -11529954 302685 ydam (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in many) (le:15636) (re:16898) (di:direct) AB001488 AB001488 g1881240 Bacillus subtilis 1423 -11529954 7500963518 ydam (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to cellulose synthase) (le:79380) (re:80642) (di:direct) BSUB0003 Z99106 g2632730 Bacillus subtilis 1423 -11529954

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768705	2680	24836	1431	476

Description

6500726097 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaN ydaN Bacillus subtilis 1423 -11529955 7000693184 ydan hypothetical protein ydan (db:pir2.dat) E69769 E69769 Bacillus subtilis 1423 -11529955 7500964152 ydan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:80648) (re:82759) (di:direct) BSUB0003 Z99106 g2632731 Bacillus subtilis 1423 -11529955

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768709	2681	24837	645	214

Description

6500726098 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaO ydaO Bacillus subtilis 1423 -11529956 7000692415 ydao conserved hypothetical protein ydao (db:pir2.dat) F69769 F69769 Bacillus subtilis 1423 -11529956 302687 ydao (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, weak similarity to yeef_ecoli.) (le:19491) (re:21314) (di:direct) AB001488 AB001488 g1881242 Bacillus subtilis 1423 -11529956 7500963577 ydao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:83235) (re:85058) (di:direct) BSUB0003 Z99106 g2632732 Bacillus subtilis 1423 -11529956

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768721	2682	24838	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768732	2683	24839	1644	547

Description

6500726099 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaQ ydaQ Bacillus subtilis 1423 -11529957 7000693185 ydaq hypothetical protein ydaq (db:pir2.dat) H69769 H69769 Bacillus subtilis 1423 -11529957 302690 ydaq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:23790) (re:24080) (di:direct) AB001488 AB001488 g1881245 Bacillus subtilis 1423 -11529957 7500964153 ydaq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:87534) (re:87824) (di:direct) BSUB0003 Z99106 g2632735 Bacillus subtilis 1423 -11529957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768920	2684	24840	285	95

Description

6500726100 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaR ydaR Bacillus subtilis 1423 -11529958 7500922159 ydar (de:hypothetical 45.7 kd protein in mutt-gsib intergenic region) (db:swissprot) YDAR_BACSU P96593 BACILLUS SUBTILIS 1423 -11529958 7000692416 ydar conserved hypothetical protein ydar (db:pir2.dat) A69770 A69770 Bacillus subtilis 1423 -11529958 302691 ydar (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable integral membrane protein.) (le:24204) (re:25481) (di:complement) AB001488 AB001488 g1881246 Bacillus subtilis 1423 -11529958 7500922162 ydar (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:87948) (re:89225) (di:complement) BSUB0003 Z99106 g2632736 Bacillus subtilis 1423 -11529958

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768921	2685	24841	867	288

Description

6500726101 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaS ydaS Bacillus subtilis 1423 -11529959 7000692417 ydas conserved hypothetical protein ydas (db:pir2.dat) B69770 B69770 Bacillus subtilis 1423 -11529959 302692 ydas (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:25711) (re:25968) (di:complement) AB001488 AB001488 g1881247 Bacillus subtilis 1423 -11529959 7500963578 ydas (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:89455) (re:89712) (di:complement) BSUB0003 Z99106 g2632737 Bacillus subtilis 1423 -11529959

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768926	2686	24842	204	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768942	2687	24843	426	141

Description

6500726102 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydaT ydaT Bacillus subtilis 1423 -11529960 7000693186 ydat hypothetical protein ydat (db:pir2.dat) C69770 C69770 Bacillus subtilis 1423 -11529960 302693 ydat (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:26046) (re:26498) (di:complement) AB001488 AB001488 g1881248 Bacillus subtilis 1423 -11529960 7500964154 ydat (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:89790) (re:90242) (di:complement) BSUB0003 Z99106 g2632738 Bacillus subtilis 1423 -11529960

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768945	2688	24844	726	241

Description

6500726103 hypothetical protein:similar to abc transporter:binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbA ydbA Bacillus subtilis 1423 -11529961 7000692111 ydba abc transporter binding protein homolog ydba (db:pir2.dat) D69770 D69770 Bacillus subtilis 1423 -11529961 302694 ydba (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to b. subtilis atp-binding cassette) (le:26616) (re:27434) (di:direct) AB001488 AB001488 g1881249 Bacillus subtilis 1423 -11529961 7500963351 ydba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to abc transporter (binding protein)) (le:90360) (re:91178) (di:direct) BSUB0003 Z99106 g2632739 Bacillus subtilis 1423 -11529961

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768960	2689	24845	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768979	2690	24846	861	286

Description

6500726104 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbB ydbB Bacillus subtilis 1423 -11529962 7000693187 ydbb hypothetical protein ydbb (db:pir2.dat) E69770 E69770 Bacillus subtilis 1423 -11529962 302696 ydbb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:28066) (re:28407) (di:direct) AB001488 AB001488 g1881251 Bacillus subtilis 1423 -11529962 7500964155 ydbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:91810) (re:92151) (di:direct) BSUB0003 Z99106 g2632741 Bacillus subtilis 1423 -11529962

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768980	2691	24847	354	118

Description

6500726105 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbC ydbC Bacillus subtilis 1423 -11529963 7000693188 ydbc hypothetical protein ydbc (db:pir2.dat) F69770 F69770 Bacillus subtilis 1423 -11529963 302697 ydbc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:28401) (re:28760) (di:direct) AB001488 AB001488 g1881252 Bacillus subtilis 1423 -11529963 7500964156 ydbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:92145) (re:92504) (di:direct) BSUB0003 Z99106 g2632742 Bacillus subtilis 1423 -11529963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768986	2692	24848	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768991	2693	24849	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501768998	2694	24850	867	288

Description

6500726106 hypothetical protein:similar to manganese-containing catalase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbD ydbD Bacillus subtilis 1423 -11529964 1500686245 ydbd (de:general stress protein 80 (gsp80)) (db:swissprot) GS80_BACSU P80878 BACILLUS SUBTILIS 1423 -11529964 7000685457 ydbd manganese-containing catalase homolog ydbd (db:pir2.dat) G69770 G69770 Bacillus subtilis 1423 -11529964 302698 ydbd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to manganese-containing catalase) (le:28797) (re:29618) (di:complement) AB001488 AB001488 g1881253 Bacillus subtilis 1423 -11529964 7500882781 ydbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to manganese-containing catalase) (le:92541) (re:93362) (di:complement) BSUB0003 Z99106 g2632743 Bacillus subtilis 1423 -11529964

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769004	2695	24851	600	199

Description

6500726107 hypothetical protein:similar to c4-dicarboxylate binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbE ydbE Bacillus subtilis 1423 -11529965 7000692299 ydbe c4-dicarboxylate binding protein homolog ydbe (cl:conserved hypothetical protein hi1028) (db:pir2.dat) H69770 H69770 Bacillus subtilis 1423 -11529965 302699 ydbe (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to c4-dicarboxylate-binding periplasmic) (le:29709) (re:30761) (di:complement) AB001488 AB001488 g1881254 Bacillus subtilis 1423 -11529965 7500963469 ydbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to c4-dicarboxylate binding protein) (le:93453) (re:94505) (di:complement) BSUB0003 Z99106 g2632744 Bacillus subtilis 1423 -11529965

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769013	2696	24852	189	62

Description

6500726108 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbF ydbF Bacillus subtilis 1423 -11529966 7000694871 ydbf two-component sensor histidine kinase homolog ydbf (cl:two-component sensor histidine kinase:sensor histidine kinase homology) (db:pir2.dat) A69771 A69771 Bacillus subtilis 1423 -11529966 302700 ydbf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable sensory transduction histidine kinase.) (le:30831) (re:32438) (di:direct) AB001488 AB001488 g1881255 Bacillus subtilis 1423 -11529966 7500955341 ydbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to two-component sensor histidine kinase) (le:94575) (re:96182) (di:direct) BSUB0003 Z99106 g2632745 Bacillus subtilis 1423 -11529966

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769015	2697	24853	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769016	2698	24854	375	124

Description

6500726109 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbG ydbG Bacillus subtilis 1423 -11529967 7000694842 ydbg two-component response regulator ydbf homolog ydbg) (cl:transcription regulator crir:response regulator homology) (db:pir2.dat) B69771 B69771 Bacillus subtilis 1423 -11529967 302701 ydbg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable regulatory component of sensory) (le:32428) (re:33108) (di:direct) AB001488 AB001488 g1881256 Bacillus subtilis 1423 -11529967 7500965391 ydbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to two-component response regulator (ydbf)) (le:96172) (re:96852) (di:direct) BSUB0003 Z99106 g2632746 Bacillus subtilis 1423 -11529967

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769018	2699	24855	198	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769020	2700	24856	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769029	2701	24857	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769041	2702	24858	408	136

Description

6500726110 hypothetical protein:similar to c4-dicarboxylate transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbH ydbH Bacillus subtilis 1423 -11529968 7000692300 ydbh c4-dicarboxylate transport protein homolog ydbh (cl:c4-dicarboxylate carrier protein) (db:pir2.dat) C69771 C69771 Bacillus subtilis 1423 -11529968 302702 ydbh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable c4-dicarboxylate transport protein.) (le:33229) (re:34494) (di:direct) AB001488 AB001488 g1881257 Bacillus subtilis 1423 -11529968 7500955806 ydbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to c4-dicarboxylate transport protein) (le:96973) (re:98238) (di:direct) BSUB0003 Z99106 g2632747 Bacillus subtilis 1423 -11529968

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769042	2703	24859	615	204

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769056	2704	24860	534	178

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769285	2705	24861	1530	510

Description

6500726111 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbI ydbI Bacillus subtilis 1423 -11529969 7000692418 ydbi conserved hypothetical protein ydbi (db:pir2.dat) D69771 D69771 Bacillus subtilis 1423 -11529969 302703 ydbi (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar products in synechocystis) (le:34642) (re:35694) (di:direct) AB001488 AB001488 g1881258 Bacillus subtilis 1423 -11529969 7500963579 ydbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:98386) (re:99438) (di:direct) BSUB0003 Z99106 g2632748 Bacillus subtilis 1423 -11529969

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769293	2706	24862	834	277

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769303	2707	24863	219	72

Description

6500726112 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbJ ydbJ Bacillus subtilis 1423 -11529970 7000692080 ydbj abc transporter atp-binding protein homolog ydbj (cl:atp-binding cassette homology) (db:pir2.dat) E69771 E69771 Bacillus subtilis 1423 -11529970 302704 ydbj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transport atp binding protein.) (le:35971) (re:36897) (di:direct) AB001488 AB001488 g1881259 Bacillus subtilis 1423 -11529970 7500963320 ydbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to abc transporter (atp-binding protein)) (le:99715) (re:100641) (di:direct) BSUB0003 Z99106 g2632749 Bacillus subtilis 1423 -11529970

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769309	2708	24864	579	192

Description

6500726113 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbK ydbK Bacillus subtilis 1423 -11529971 7000692419 ydbk conserved hypothetical protein ydbk (db:pir2.dat) F69771 F69771 Bacillus subtilis 1423 -11529971 302705 ydbk (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable membrane spanning protein.) (le:36917) (re:37657) (di:direct) AB001488 AB001488 g1881260 Bacillus subtilis 1423 -11529971 7500963580 ydbk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:100661) (re:101401) (di:direct) BSUB0003 Z99106 g2632750 Bacillus subtilis 1423 -11529971

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769320	2709	24865	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769325	2710	24866	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769345	2711	24867	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769347	2712	24868	390	129

Description

6500726114 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbL ydbL Bacillus subtilis 1423 -11529972 7000693189 ydbl hypothetical protein ydbl (db:pir2.dat) G69771 G69771 Bacillus subtilis 1423 -11529972 302706 ydbl (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:37752) (re:38087) (di:direct) AB001488 AB001488 g1881261 Bacillus subtilis 1423 -11529972 7500964157 ydbl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:101496) (re:101831) (di:direct) BSUB0003 Z99106 g2632751 Bacillus subtilis 1423 -11529972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769348	2713	24869	450	149

Description

6500726115 hypothetical protein:similar to butyryl-coa dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbM ydbM Bacillus subtilis 1423 -11529973 7000692296 ydbm butyryl-coa dehydrogenase homolog ydbm (db:pir2.dat) H69771 H69771 Bacillus subtilis 1423 -11529973 302707 ydbm (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to acyl-coa dehydrogenase.) (le:38215) (re:39360) (di:direct) AB001488 AB001488 g1881262 Bacillus subtilis 1423 -11529973 7500963467 ydbm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to butyryl-coa dehydrogenase) (le:101959) (re:103104) (di:direct) BSUB0003 Z99106 g2632752 Bacillus subtilis 1423 -11529973

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769349	2714	24870	345	114

Description

6500726116 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbN ydbN Bacillus subtilis 1423 -11529974 7000693190 ydbn hypothetical protein ydbn (db:pir2.dat) A69772 A69772 Bacillus subtilis 1423 -11529974 302708 ydbn (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transcriptional regulatory protein,) (le:39385) (re:39564) (di:complement) AB001488 AB001488 g1881263 Bacillus subtilis 1423 -11529974 7500964158 ydbn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:103129) (re:103308) (di:complement) BSUB0003 Z99106 g2632753 Bacillus subtilis 1423 -11529974

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769351	2715	24871	267	89

Description

6500726117 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbO ydbO Bacillus subtilis 1423 -11529975 7000692420 ydbo conserved hypothetical protein ydbo (cl:conserved hypothetical protein mj0449) (db:pir2.dat) B69772 B69772 Bacillus subtilis 1423 -11529975 302709 ydbo (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in b. subtilis) (le:39929) (re:40801) (di:direct) AB001488 AB001488 g1881264 Bacillus subtilis 1423 -11529975 7500963581 ydbo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:103673) (re:104545) (di:direct) BSUB0003 Z99106 g2632754 Bacillus subtilis 1423 -11529975

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769363	2716	24872	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769365	2717	24873	954	317

Description

6500726118 hypothetical protein:similar to thioredoxin (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbP ydbP Bacillus subtilis 1423 -11529976 7000694680 ydbp thioredoxin homolog ydbp (cl:thioredoxin:thioredoxin homology) (db:pir2.dat) C69772 C69772 Bacillus subtilis 1423 -11529976 302710 ydbp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable thioredoxin.) (le:40816) (re:41136) (di:complement) AB001488 AB001488 g1881265 Bacillus subtilis 1423 -11529976 7500965265 ydbp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to thioredoxin) (le:104560) (re:104880) (di:complement) BSUB0003 Z99106 g2632755 Bacillus subtilis 1423 -11529976

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769371	2718	24874	417	138

Description

6500726119 hypothetical protein:similar to atp-dependent rna helicase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbR ydbR Bacillus subtilis 1423 -11529977 7000692252 ydbr atp-dependent rna helicase homolog ydbr (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) D69772 D69772 Bacillus subtilis 1423 -11529977 302713 ydbr (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:atp-dependent rna helicase dead homolog.) (le:44169) (re:45704) (di:direct) AB001488 AB001488 g1881268 Bacillus subtilis 1423 -11529977 7500954382 ydbr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to atp-dependent rna helicase) (le:107913) (re:109448) (di:direct) BSUB0003 Z99106 g2632758 Bacillus subtilis 1423 -11529977

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769393	2719	24875	609	202

Description

6500726120 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbS ydbS Bacillus subtilis 1423 -11529978 7000693191 ydbs hypothetical protein ydbs (db:pir2.dat) E69772 E69772 Bacillus subtilis 1423 -11529978 302714 ydbs (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:45877) (re:46356) (di:direct) AB001488 AB001488 g1881269 Bacillus subtilis 1423 -11529978 7500964159 ydbs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:109621) (re:110100) (di:direct) BSUB0003 Z99106 g2632759 Bacillus subtilis 1423 -11529978

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769401	2720	24876	882	293

Description

6500726121 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydbT ydbT Bacillus subtilis 1423 -11529979 7000693192 ydbt hypothetical protein ydbt (db:pir2.dat) F69772 F69772 Bacillus subtilis 1423 -11529979 302715 ydbt (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:46346) (re:47827) (di:direct) AB001488 AB001488 g1881270 Bacillus subtilis 1423 -11529979 7500964160 ydbt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:110090) (re:111571) (di:direct) BSUB0003 Z99106 g2632760 Bacillus subtilis 1423 -11529979

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769408	2721	24877	252	83

Description

6500726122 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcA ydcA Bacillus subtilis 1423 -11529980 7000692421 ydca conserved hypothetical protein ydca (db:pir2.dat) G69772 G69772 Bacillus subtilis 1423 -11529980 302716 ydca (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in h. influenzae) (le:48079) (re:48678) (di:complement) AB001488 AB001488 g1881271 Bacillus subtilis 1423 -11529980 7500963582 ydca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:111823) (re:112422) (di:complement) BSUB0003 Z99106 g2632761 Bacillus subtilis 1423 -11529980

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769419	2722	24878	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769452	2723	24879	462	153

Description

6500726123 hypothetical protein:similar to holo-acyl-carrier protein synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcB ydcB Bacillus subtilis 1423 -11529981 7000693107 ydcb holo-acyl-carrier protein synthase homolog ydcb (cl:holo-acp synthase) (db:pir2.dat) H69772 H69772 Bacillus subtilis 1423 -11529981 302717 ydcb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in e. coli and) (le:48773) (re:49138) (di:direct) AB001488 AB001488 g1881272 Bacillus subtilis 1423 -11529981 7500955962 ydcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to holo- acyl-carrier protein synthase) (le:112517) (re:112882) (di:direct) BSUB0003 Z99106 g2632762 Bacillus subtilis 1423 -11529981

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769470	2724	24880	357	118

Description

6500726124 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcC ydcC Bacillus subtilis 1423 -11529982 7000693193 ydcc hypothetical protein ydcc (db:pir2.dat) A69773 A69773 Bacillus subtilis 1423 -11529982 302718 ydcc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:49199) (re:50320) (di:direct) AB001488 AB001488 g1881273 Bacillus subtilis 1423 -11529982 7500964161 ydcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:112943) (re:114064) (di:direct) BSUB0003 Z99106 g2632763 Bacillus subtilis 1423 -11529982

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769471	2725	24881	936	312

Description

6500726125 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcD ydcD Bacillus subtilis 1423 -11529983 7000693194 ydcd hypothetical protein ydcd (db:pir2.dat) B69773 B69773 Bacillus subtilis 1423 -11529983 302720 ydcd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:51720) (re:52001) (di:direct) AB001488 AB001488 g1881275 Bacillus subtilis 1423 -11529983 7500964162 ydcd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:115464) (re:115745) (di:direct) BSUB0003 Z99106 g2632765 Bacillus subtilis 1423 -11529983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769472	2726	24882	342	113

Description

6500726126 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcE ydcE Bacillus subtilis 1423 -11529984 7000692422 ydce conserved hypothetical protein ydce (db:pir2.dat) C69773 C69773 Bacillus subtilis 1423 -11529984 302721 ydce (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in mycobacterium) (le:52006) (re:52356) (di:direct) AB001488 AB001488 g1881276 Bacillus subtilis 1423 -11529984 7500963583 ydce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:115750) (re:116100) (di:direct) BSUB0003 Z99106 g2632766 Bacillus subtilis 1423 -11529984

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769485	2727	24883	285	94

Description

GTC ORF with score 127 to: (fn:sulphur metabolite repression regulation) (db:genpept-pln1) (de:emericella nidulans sulphur metabolite repression regulatory(sconc) gene, complete cds.) (le:710:833:979:1208) (re:764:918:1146:1381) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769488	2728	24884	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769489	2729	24885	237	78

Description

GTC ORF with score 272 to: (fn:sulphur metabolite repression regulation) (db:genpept-pln1) (de:emericella nidulans sulphur metabolite repression regulatory(sconc) gene, complete cds.) (le:710:833:979:1208) (re:764:918:1146:1381) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769490	2730	24886	225	74

Description

GTC ORF with score 275 to: (fn:sulphur metabolite repression regulation) (db:genpept-pln1) (de:emericella nidulans sulphur metabolite repression regulatory(sconc) gene, complete cds.) (le:710:833:979:1208) (re:764:918:1146:1381) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769725	2731	24887	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769726	2732	24888	669	223

Description

5000689560 ycxr:rsbr hypothetical protein:hypothetical 31.1 kd protein in rsbu 5region:orfr (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) rsbR rsbR Bacillus subtilis 1423 -11529985 111053 rsbr (de:rsbr protein) (db:swissprot) RSBR_BACSU P42409 BACILLUS SUBTILIS 1423 -11529985 7000687504 rsbr positive regulator of sigma-b activity rsbr (db:pir2.dat) E69701 E69701 Bacillus subtilis 1423 -11529985 216650 orfr (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:52471) (re:53295) (di:direct) AB001488 AB001488 g1881277 Bacillus subtilis 1423 -11529985 302722 (sr:bacillus subtilis (strain 168 marburg) dna) (db:genpept-bct1) (de:bacillus subtilis (clones paw10, paw50) regulator (rsbu) gene,complete cds, positive regulator (rsbv), 5' end.) (nt:orfr; putative) (le:358) (re:1182) (di:direct) BACRSBU L35574 g642074 Bacillus subtilis 1423 -11529985 7500891132 rsbr (fn:positive regulation of sigma-b activity in) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:alternate gene name: ycxr) (le:116215) (re:117039) (di:direct) BSUB0003 Z99106 g2632767 Bacillus subtilis 1423 -11529985 6500726127 ycxr hypothetical protein:hypothetical 31.1 kd protein in rsbu 5region:orfr (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) rsbR rsbR Bacillus subtilis 1423 -11529985

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769733	2733	24889	531	176

Description

6500726128 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcF ydcF Bacillus subtilis 1423 -11529986 7000693195 ydcf hypothetical protein ydcf (db:pir2.dat) D69773 D69773 Bacillus subtilis 1423 -11529986 302730 ydcf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:57555) (re:57848) (di:direct) AB001488 AB001488 g1881285 Bacillus subtilis 1423 -11529986 7500964163 ydcf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:121299) (re:121592) (di:direct) BSUB0003 Z99106 g2632775 Bacillus subtilis 1423 -11529986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769735	2734	24890	1020	339

Description

6500726129 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcG ydcG Bacillus subtilis 1423 -11529987 7000692423 ydcg conserved hypothetical protein ydcg (cl:bacillus licheniformis oug protein) (db:pir2.dat) E69773 E69773 Bacillus subtilis 1423 -11529987 302731 ydcg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in bacillus) (le:57845) (re:58285) (di:direct) AB001488 AB001488 g1881286 Bacillus subtilis 1423 -11529987 7500963584 ydcg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:121589) (re:122029) (di:direct) BSUB0003 Z99106 g2632776 Bacillus subtilis 1423 -11529987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769743	2735	24891	405	134

Description

6500726130 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcH ydcH Bacillus subtilis 1423 -11529988 7000692424 ydch conserved hypothetical protein ydch (db:pir2.dat) F69773 F69773 Bacillus subtilis 1423 -11529988 302732 ydch (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:58269) (re:58712) (di:direct) AB001488 AB001488 g1881287 Bacillus subtilis 1423 -11529988 7500963585 ydch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:122013) (re:122456) (di:direct) BSUB0003 Z99106 g2632777 Bacillus subtilis 1423 -11529988

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769749	2736	24892	750	249

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769752	2737	24893	555	184

Description

GTC ORF with score 105 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769760	2738	24894	858	286

Description

6500726131 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcI ydcI Bacillus subtilis 1423 -11529989 7000692425 ydci conserved hypothetical protein ydci (cl:hypothetical protein ydci) (db:pir2.dat) G69773 G69773 Bacillus subtilis 1423 -11529989 7500955947 ydci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:122550) (re:124883) (di:direct) BSUB0003 Z99106 g2632778 Bacillus subtilis 1423 -11529989

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769770	2739	24895	219	72

Description

6500726132 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcK ydcK Bacillus subtilis 1423 -11529990 7000692426 ydck conserved hypothetical protein ydck (cl:hypothetical protein hi1173) (db:pir2.dat) H69773 H69773 Bacillus subtilis 1423 -11529990 302735 ydck (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:61365) (re:61817) (di:direct) AB001488 AB001488 g1881290 Bacillus subtilis 1423 -11529990 7500963586 ydck (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:125110) (re:125562) (di:direct) BSUB0003 Z99106 g2632779 Bacillus subtilis 1423 -11529990

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769777	2740	24896	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769779	2741	24897	1338	446

Description

6500726133 hypothetical protein:similar to integrase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcL ydcL Bacillus subtilis 1423 -11529991 7000694111 ydcl integrase homolog ydcl (db:pir2.dat) A69774 A69774 Bacillus subtilis 1423 -11529991 302736 ydcl (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable integrase.) (le:62741) (re:63847) (di:complement) AB001488 AB001488 g1881291 Bacillus subtilis 1423 -11529991 7500964866 ydcl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to integrase) (le:126486) (re:127592) (di:complement) BSUB0003 Z99106 g2632780 Bacillus subtilis 1423 -11529991

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769785	2742	24898	612	203

Description

6500726134 hypothetical protein:similar to immunity region protein in prophage (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcM ydcM Bacillus subtilis 1423 -11529992 7000694101 ydcm immunity region protein in prophage homolog ydcm (db:pir2.dat) B69774 B69774 Bacillus subtilis 1423 -11529992 302737 ydcm (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to immunity region protein in bacteriophage) (le:63860) (re:64369) (di:complement) AB001488 AB001488 g1881292 Bacillus subtilis 1423 -11529992 7500964862 ydcm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to immunity region protein in prophage) (le:127605) (re:128114) (di:complement) BSUB0003 Z99106 g2632781 Bacillus subtilis 1423 -11529992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769787	2743	24899	210	69

Description

6500726135 hypothetical protein:similar to transcriptional regulator:phage-related:xre family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcN ydcN Bacillus subtilis 1423 -11529993 7000694778 ydcn transcription regulator phage-related homolog ydcn (db:pir2.dat) C69774 C69774 Bacillus subtilis 1423 -11529993 302738 ydcn (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable repressor protein.) (le:64366) (re:64749) (di:complement) AB001488 AB001488 g1881293 Bacillus subtilis 1423 -11529993 7500965341 ydcn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator) (le:128111) (re:128494) (di:complement) BSUB0003 Z99106 g2632782 Bacillus subtilis 1423 -11529993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769788	2744	24900	792	263

Description

6500726136 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcO ydcO Bacillus subtilis 1423 -11529994 7000693196 ydco hypothetical protein ydco (db:pir2.dat) D69774 D69774 Bacillus subtilis 1423 -11529994 302739 ydco (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:65528) (re:65788) (di:direct) AB001488 AB001488 g1881294 Bacillus subtilis 1423 -11529994 7500964164 ydco (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:129273) (re:129533) (di:direct) BSUB0003 Z99106 g2632784 Bacillus subtilis 1423 -11529994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769789	2745	24901	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769793	2746	24902	690	230

Description

6500726137 hypothetical protein:similar to transposon protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcP ydcP Bacillus subtilis 1423 -11529995 7000694821 ydcp transposon protein homolog ydcp (db:pir2.dat) E69774 E69774 Bacillus subtilis 1423 -11529995 302740 ydcp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to orf22 and orf23 of enterococcus faecalis) (le:66158) (re:66538) (di:direct) AB001488 AB001488 g1881295 Bacillus subtilis 1423 -11529995 7500965374 ydcp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transposon protein) (le:129903) (re:130283) (di:direct) BSUB0003 Z99106 g2632785 Bacillus subtilis 1423 -11529995

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769800	2747	24903	564	187

Description

6500726138 hypothetical protein:similar to transposon protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcQ ydcQ Bacillus subtilis 1423 -11529996 7000694822 ydcq transposon protein homolog ydcq (db:pir2.dat) F69774 F69774 Bacillus subtilis 1423 -11529996 302741 ydcq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to orf21 of enterococcus faecalis) (le:66574) (re:68016) (di:direct) AB001488 AB001488 g1881296 Bacillus subtilis 1423 -11529996 7500965375 ydcq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transposon protein) (le:130319) (re:131761) (di:direct) BSUB0003 Z99106 g2632786 Bacillus subtilis 1423 -11529996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769809	2748	24904	489	162

Description

6500726139 hypothetical protein:similar to transposon protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcR ydcR Bacillus subtilis 1423 -11529997 7000694823 ydcr transposon protein homolog ydcr (db:pir2.dat) G69774 G69774 Bacillus subtilis 1423 -11529997 302742 ydcr (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to orf20 of enterococcus faecalis) (le:68009) (re:69067) (di:direct) AB001488 AB001488 g1881297 Bacillus subtilis 1423 -11529997 7500965376 ydcr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transposon protein) (le:131754) (re:132812) (di:direct) BSUB0003 Z99106 g2632787 Bacillus subtilis 1423 -11529997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769819	2749	24905	579	192

Description

GTC ORF with score 294 to: (fn:converts p-cumic aldehyde + h20 + nad to) (db:genpept-bct1) (de:pseudomonas putida p-cymene catabolism (cym) and p-cumatecatabolism (cmt) operons and enol-coenzyme a hydratase gene,complete cds.) (nt:cymc) (le:4105) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769839	2750	24906	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769855	2751	24907	513	170

Description

6500726140 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcS ydcS Bacillus subtilis 1423 -11529998 7000692427 ydcs conserved hypothetical protein ydcs (db:pir2.dat) H69774 H69774 Bacillus subtilis 1423 -11529998 302743 ydcs (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to ydct gene product of this entry) (le:69332) (re:69601) (di:direct) AB001488 AB001488 g1881298 Bacillus subtilis 1423 -11529998 7500963587 ydcs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:133077) (re:133346) (di:direct) BSUB0003 Z99106 g2632788 Bacillus subtilis 1423 -11529998

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769861	2752	24908	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769875	2753	24909	276	92

Description

6500726141 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydcT ydcT Bacillus subtilis 1423 -11529999 7000692428 ydct conserved hypothetical protein ydct (db:pir2.dat) A69775 A69775 Bacillus subtilis 1423 -11529999 302744 ydct (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to ydcs gene product of this entry) (le:69640) (re:69906) (di:direct) AB001488 AB001488 g1881299 Bacillus subtilis 1423 -11529999 7500963588 ydct (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:133385) (re:133651) (di:direct) BSUB0003 Z99106 g2632789 Bacillus subtilis 1423 -11529999

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769879	2754	24910	888	295

Description

6500726142 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddA yddA Bacillus subtilis 1423 -11530000 7000693197 ydda hypothetical protein ydda (db:pir2.dat) B69775 B69775 Bacillus subtilis 1423 -11530000 302745 ydda (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:69923) (re:70231) (di:direct) AB001488 AB001488 g1881300 Bacillus subtilis 1423 -11530000 7500964165 ydda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:133668) (re:133976) (di:direct) BSUB0003 Z99106 g2632790 Bacillus subtilis 1423 -11530000

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769891	2755	24911	267	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769894	2756	24912	312	103

Description

GTC ORF with score 250 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c25h2.) (nt:spbc25h2.14, unknown, len:235aa, similar eg. to) (le:32931:33032:33181:33251) (re:32981:33109:33184:33611) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769906	2757	24913	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501769916	2758	24914	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770156	2759	24915	519	173

Description

6500726143 hypothetical protein:similar to transposon protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddB yddB Bacillus subtilis 1423 -11530001 7000694824 yddb transposon protein homolog yddb (db:pir2.dat) C69775 C69775 Bacillus subtilis 1423 -11530001 7500965377 yddb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transposon protein) (le:133966) (re:135030) (di:direct) BSUB0003 Z99106 g2632791 Bacillus subtilis 1423 -11530001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770161	2760	24916	699	232

Description

6500726144 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddC yddC Bacillus subtilis 1423 -11530002 7000693198 yddc hypothetical protein yddc (db:pir2.dat) D69775 D69775 Bacillus subtilis 1423 -11530002 302747 yddc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:71297) (re:71545) (di:direct) AB001488 AB001488 g1881302 Bacillus subtilis 1423 -11530002 7500964166 yddc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:135042) (re:135290) (di:direct) BSUB0003 Z99106 g2632792 Bacillus subtilis 1423 -11530002

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770169	2761	24917	714	237

Description

6500726145 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddD yddD Bacillus subtilis 1423 -11530003 7000693199 yddd hypothetical protein yddd (db:pir2.dat) E69775 E69775 Bacillus subtilis 1423 -11530003 302748 yddd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:71558) (re:72082) (di:direct) AB001488 AB001488 g1881303 Bacillus subtilis 1423 -11530003 7500964167 yddd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:135303) (re:135827) (di:direct) BSUB0003 Z99106 g2632793 Bacillus subtilis 1423 -11530003

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770175	2762	24918	483	160

Description

6500726146 hypothetical protein:similar to transposon protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddE yddE Bacillus subtilis 1423 -11530004 7000694825 ydde transposon protein homolog ydde (db:pir2.dat) F69775 F69775 Bacillus subtilis 1423 -11530004 302749 ydde (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to orf16 of enterococcus faecalis) (le:71970) (re:74465) (di:direct) AB001488 AB001488 g1881304 Bacillus subtilis 1423 -11530004 7500965378 ydde (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transposon protein) (le:135715) (re:138210) (di:direct) BSUB0003 Z99106 g2632794 Bacillus subtilis 1423 -11530004

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770177	2763	24919	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770190	2764	24920	702	233

Description

6500726147 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddF yddF Bacillus subtilis 1423 -11530005 7000693200 yddf hypothetical protein yddf (db:pir2.dat) G69775 G69775 Bacillus subtilis 1423 -11530005 302750 yddf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:74484) (re:74810) (di:direct) AB001488 AB001488 g1881305 Bacillus subtilis 1423 -11530005 7500964168 yddf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:138229) (re:138555) (di:direct) BSUB0003 Z99106 g2632795 Bacillus subtilis 1423 -11530005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770196	2765	24921	1218	405

Description

6500726148 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddG yddG Bacillus subtilis 1423 -11530006 7000693201 yddg hypothetical protein yddg (db:pir2.dat) H69775 H69775 Bacillus subtilis 1423 -11530006 302751 yddg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:74814) (re:77261) (di:direct) AB001488 AB001488 g1881306 Bacillus subtilis 1423 -11530006 7500964169 yddg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:138559) (re:141006) (di:direct) BSUB0003 Z99106 g2632796 Bacillus subtilis 1423 -11530006

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770206	2766	24922	636	211

Description

6500726149 hypothetical protein:similar to transposon protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddH yddH Bacillus subtilis 1423 -11530007 7000694826 yddh transposon protein homolog yddh (db:pir2.dat) A69776 A69776 Bacillus subtilis 1423 -11530007 302752 yddh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to orf14 of enterococcus faecalis) (le:77258) (re:78247) (di:direct) AB001488 AB001488 g1881307 Bacillus subtilis 1423 -11530007 7500965379 yddh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transposon protein) (le:141003) (re:141992) (di:direct) BSUB0003 Z99106 g2632797 Bacillus subtilis 1423 -11530007

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770224	2767	24923	498	165

Description

6500726150 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddI yddI Bacillus subtilis 1423 -11530008 7000693202 yddi hypothetical protein yddi (db:pir2.dat) B69776 B69776 Bacillus subtilis 1423 -11530008 302753 yddi (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:78262) (re:78768) (di:direct) AB001488 AB001488 g1881308 Bacillus subtilis 1423 -11530008 7500964170 yddi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:142007) (re:142513) (di:direct) BSUB0003 Z99106 g2632798 Bacillus subtilis 1423 -11530008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770225	2768	24924	261	86

Description

6500726151 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddJ yddJ Bacillus subtilis 1423 -11530009 7000693203 yddj hypothetical protein yddj (db:pir2.dat) C69776 C69776 Bacillus subtilis 1423 -11530009 302754 yddj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:78831) (re:79211) (di:direct) AB001488 AB001488 g1881309 Bacillus subtilis 1423 -11530009 7500964171 yddj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:142576) (re:142956) (di:direct) BSUB0003 Z99106 g2632799 Bacillus subtilis 1423 -11530009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770228	2769	24925	615	204

Description

6500726152 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddK yddK Bacillus subtilis 1423 -11530010 7000693204 yddk hypothetical protein yddk (db:pir2.dat) D69776 D69776 Bacillus subtilis 1423 -11530010 302755 yddk (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:79402) (re:80202) (di:complement) AB001488 AB001488 g1881310 Bacillus subtilis 1423 -11530010 7500964172 yddk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:143147) (re:143947) (di:complement) BSUB0003 Z99106 g2632800 Bacillus subtilis 1423 -11530010

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770231	2770	24926	300	100

Description

GTC ORF with score 168 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone t16l1 (essaiiproject).) (nt:strong similarity to aspartate--trna ligase,) (le:70056:70473:70640) (re:70225:70530:70720) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770247	2771	24927	687	228

Description

6500726153 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddM yddM Bacillus subtilis 1423 -11530011 7000693205 yddm hypothetical protein yddm (db:pir2.dat) E69776 E69776 Bacillus subtilis 1423 -11530011 302757 yddm (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:81946) (re:82887) (di:direct) AB001488 AB001488 g1881312 Bacillus subtilis 1423 -11530011 7500964173 yddm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:145691) (re:146632) (di:direct) BSUB0003 Z99106 g2632803 Bacillus subtilis 1423 -11530011

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770250	2772	24928	654	218

Description

6500726154 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddN yddN Bacillus subtilis 1423 -11530012 7000692429 yddn conserved hypothetical protein yddn (cl:ynbw protein) (db:pir2.dat) F69776 F69776 Bacillus subtilis 1423 -11530012 302758 yddn (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to alkanal monooxygenase alpha chain.) (le:83458) (re:84477) (di:complement) AB001488 AB001488 g1881313 Bacillus subtilis 1423 -11530012 7500963589 yddn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:147203) (re:148222) (di:complement) BSUB0003 Z99106 g2632804 Bacillus subtilis 1423 -11530012

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770260	2773	24929	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770266	2774	24930	693	231

Description

6500726155 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddQ yddQ Bacillus subtilis 1423 -11530013 7000692430 yddq conserved hypothetical protein yddq (cl:hypothetical protein yddq) (db:pir2.dat) G69776 G69776 Bacillus subtilis 1423 -11530013 302761 yddq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:85834) (re:86376) (di:direct) AB001488 AB001488 g1881316 Bacillus subtilis 1423 -11530013 7500955948 yddq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:149579) (re:150121) (di:direct) BSUB0003 Z99106 g2632807 Bacillus subtilis 1423 -11530013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770274	2775	24931	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770289	2776	24932	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770298	2777	24933	432	143

Description

6500726156 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddR yddR Bacillus subtilis 1423 -11530014 7000693206 yddr hypothetical protein yddr (db:pir2.dat) H69776 H69776 Bacillus subtilis 1423 -11530014 302762 yddr (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:86929) (re:87693) (di:direct) AB001488 AB001488 g1881317 Bacillus subtilis 1423 -11530014 7500964174 yddr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:150674) (re:151438) (di:direct) BSUB0003 Z99106 g2632808 Bacillus subtilis 1423 -11530014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770315	2778	24934	453	150

Description

6500726157 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddS yddS Bacillus subtilis 1423 -11530015 7000692431 ydds conserved hypothetical protein ydds (db:pir2.dat) A69777 A69777 Bacillus subtilis 1423 -11530015 302763 ydds (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable metabolite transport protein, similar) (le:87887) (re:89197) (di:direct) AB001488 AB001488 g1881318 Bacillus subtilis 1423 -11530015 7500963590 ydds (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:151632) (re:152942) (di:direct) BSUB0003 Z99106 g2632809 Bacillus subtilis 1423 -11530015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770318	2779	24935	984	327

Description

6500726158 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yddT yddT Bacillus subtilis 1423 -11530016 7000693207 yddt hypothetical protein yddt (db:pir2.dat) B69777 B69777 Bacillus subtilis 1423 -11530016 302764 yddt (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:89981) (re:90667) (di:direct) AB001488 AB001488 g1881319 Bacillus subtilis 1423 -11530016 7500964175 yddt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:153726) (re:154412) (di:direct) BSUB0003 Z99106 g2632810 Bacillus subtilis 1423 -11530016

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770328	2780	24936	1341	446

Description

6500726159 hypothetical protein:similar to glyceraldehyde 3-phosphate dehydrogenase:glycolysis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeA ydeA Bacillus subtilis 1423 -11530017 7000693057 ydea hypothetical protein ydea (db:pir2.dat) C69777 C69777 Bacillus subtilis 1423 -11530017 302765 ydea (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:91627) (re:92220) (di:direct) AB001488 AB001488 g1881320 Bacillus subtilis 1423 -11530017 7500964030 ydea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to glyceraldehyde 3-phosphate dehydrogenase) (le:155372) (re:155965) (di:direct) BSUB0003 Z99106 g2632811 Bacillus subtilis 1423 -11530017

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770329	2781	24937	450	149

Description

GTC ORF with score 121 to: (or:Rattus norvegicus) (sr:norway rat) (db:genpept-rod) (de:rattus norvegicus class a calcium channel variant ria-i (bcca1)mrna, partial cds.) (nt:alternatively spliced; amino terminus of protein) (le:<1) (re:2376) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770351	2782	24938	1167	388

Description

6500726160 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeB ydeB Bacillus subtilis 1423 -11530018 7000692432 ydeb conserved hypothetical protein ydeb (db:pir2.dat) D69777 D69777 Bacillus subtilis 1423 -11530018 302767 ydeb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to transcription factor of myxococcus) (le:93370) (re:93831) (di:complement) AB001488 AB001488 g1881322 Bacillus subtilis 1423 -11530018 7500963591 ydeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:157115) (re:157576) (di:complement) BSUB0003 Z99106 g2632813 Bacillus subtilis 1423 -11530018

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770589	2783	24939	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770613	2784	24940	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770624	2785	24941	537	178

Description

6500726161 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydzE ydzE Bacillus subtilis 1423 -11530019 7000692458 ydze conserved hypothetical protein ydze (db:pir2.dat) F69790 F69790 Bacillus subtilis 1423 -11530019 7500963612 ydze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:158144) (re:158380) (di:complement) BSUB0003 Z99106 g2632814 Bacillus subtilis 1423 -11530019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770627	2786	24942	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770629	2787	24943	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770630	2788	24944	750	249

Description

6500726162 hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeC ydeC Bacillus subtilis 1423 -11530020 7000694714 ydec transcription regulator arac/xyls family homolog ydec (db:pir2.dat) E69777 E69777 Bacillus subtilis 1423 -11530020 302768 ydec (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable hth_arac_family of transcriptional) (le:94733) (re:95608) (di:complement) AB001488 AB001488 g1881323 Bacillus subtilis 1423 -11530020 7500965290 ydec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (arac/xyls) (le:158478) (re:159353) (di:complement) BSUB0003 Z99106 g2632815 Bacillus subtilis 1423 -11530020

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770655	2789	24945	1008	335

Description

6500726163 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeD ydeD Bacillus subtilis 1423 -11530021 7500922243 yded (de:hypothetical 35.3 kd protein in cspc-nap intergenic region) (db:swissprot) YDED_BACSU P96661 BACILLUS SUBTILIS 1423 -11530021 7000692433 yded conserved hypothetical protein yded (cl:hypothetical protein yded) (db:pir2.dat) F69777 F69777 Bacillus subtilis 1423 -11530021 302769 yded (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in e.coli.) (le:95721) (re:96680) (di:direct) AB001488 AB001488 g1881324 Bacillus subtilis 1423 -11530021 7500922246 yded (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:159466) (re:160425) (di:direct) BSUB0003 Z99106 g2632816 Bacillus subtilis 1423 -11530021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770666	2790	24946	1209	403

Description

6500726164 hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeE ydeE Bacillus subtilis 1423 -11530022 7000694715 ydee transcription regulator arac/xyls family homolog ydee (db:pir2.dat) G69777 G69777 Bacillus subtilis 1423 -11530022 302770 ydee (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable hth_arac_family of transcriptional) (le:96833) (re:97705) (di:complement) AB001488 AB001488 g1881325 Bacillus subtilis 1423 -11530022 7500965291 ydee (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (arac/xyls) (le:160578) (re:161450) (di:complement) BSUB0003 Z99106 g2632817 Bacillus subtilis 1423 -11530022

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770690	2791	24947	276	91

Description

6500726165 hypothetical protein:similar to transcriptional regulator:gntr family / aminotransferase:mocr-like (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeF ydeF Bacillus subtilis 1423 -11530023 7000694730 ydef transcription regulator gntr family homolog ydef (db:pir2.dat) H69777 H69777 Bacillus subtilis 1423 -11530023 302771 ydef (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to hypothetical transcriptional) (le:97923) (re:99320) (di:direct) AB001488 AB001488 g1881326 Bacillus subtilis 1423 -11530023 7500965304 ydef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (gntr family)) (le:161668) (re:163065) (di:direct) BSUB0003 Z99106 g2632818 Bacillus subtilis 1423 -11530023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770712	2792	24948	222	73

Description

6500726166 hypothetical protein:similar to metabolite transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeG ydeG Bacillus subtilis 1423 -11530024 7000694204 ydeg metabolite transport protein homolog ydeg (db:pir2.dat) A69778 A69778 Bacillus subtilis 1423 -11530024 302772 ydeg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to ydds_bacsu.) (le:99430) (re:100722) (di:direct) AB001488 AB001488 g1881327 Bacillus subtilis 1423 -11530024 7500964931 ydeg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to metabolite transport protein) (le:163175) (re:164467) (di:direct) BSUB0003 Z99106 g2632819 Bacillus subtilis 1423 -11530024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770713	2793	24949	1311	436

Description

6500726167 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeH ydeH Bacillus subtilis 1423 -11530025 7000693208 ydeh hypothetical protein ydeh (db:pir2.dat) B69778 B69778 Bacillus subtilis 1423 -11530025 302773 ydeh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:100881) (re:101327) (di:direct) AB001488 AB001488 g1881328 Bacillus subtilis 1423 -11530025 7500964176 ydeh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:164626) (re:165072) (di:direct) BSUB0003 Z99106 g2632820 Bacillus subtilis 1423 -11530025

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770719	2794	24950	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770737	2795	24951	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770738	2796	24952	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770747	2797	24953	420	139

Description

6500726168 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeI ydeI Bacillus subtilis 1423 -11530026 7000693209 ydei hypothetical protein ydei (db:pir2.dat) C69778 C69778 Bacillus subtilis 1423 -11530026 302774 ydei (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:101564) (re:102157) (di:direct) AB001488 AB001488 g1881329 Bacillus subtilis 1423 -11530026 7500964177 ydei (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:165309) (re:165902) (di:direct) BSUB0003 Z99106 g2632821 Bacillus subtilis 1423 -11530026

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770749	2798	24954	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770760	2799	24955	216	72

Description

6500726169 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeJ ydeJ Bacillus subtilis 1423 -11530027 7000693210 ydej hypothetical protein ydej (db:pir2.dat) D69778 D69778 Bacillus subtilis 1423 -11530027 302775 ydej (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:102509) (re:103168) (di:complement) AB001488 AB001488 g1881330 Bacillus subtilis 1423 -11530027 7500964178 ydej (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:166254) (re:166913) (di:complement) BSUB0003 Z99106 g2632822 Bacillus subtilis 1423 -11530027

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770763	2800	24956	909	302

Description

6500726170 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeK ydeK Bacillus subtilis 1423 -11530028 7000692434 ydek conserved hypothetical protein ydek (db:pir2.dat) E69778 E69778 Bacillus subtilis 1423 -11530028 302776 ydek (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in e. coli.) (le:103590) (re:104453) (di:complement) AB001488 AB001488 g1881331 Bacillus subtilis 1423 -11530028 7500963592 ydek (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:167335) (re:168198) (di:complement) BSUB0003 Z99106 g2632823 Bacillus subtilis 1423 -11530028

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770773	2801	24957	309	102

Description

6500726171 hypothetical protein:similar to transcriptional regulator:gntr family / aminotransferase:mocr-like (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeL ydeL Bacillus subtilis 1423 -11530029 7000694731 ydel transcription regulator gntr family homolog ydel (cl:hypothetical protein b1439) (db:pir2.dat) F69778 F69778 Bacillus subtilis 1423 -11530029 302777 ydel (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to the rhizopine catabolism (mocr) gene of) (le:104608) (re:105999) (di:direct) AB001488 AB001488 g1881332 Bacillus subtilis 1423 -11530029 7500965305 ydel (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (gntr family)) (le:168353) (re:169744) (di:direct) BSUB0003 Z99106 g2632824 Bacillus subtilis 1423 -11530029

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770774	2802	24958	678	225

Description

6500726172 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeM ydeM Bacillus subtilis 1423 -11530030 7000693211 ydem hypothetical protein ydem (db:pir2.dat) G69778 G69778 Bacillus subtilis 1423 -11530030 302778 ydem (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:106193) (re:106618) (di:direct) AB001488 AB001488 g1881333 Bacillus subtilis 1423 -11530030 7500964179 ydem (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:169938) (re:170363) (di:direct) BSUB0003 Z99106 g2632825 Bacillus subtilis 1423 -11530030

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770778	2803	24959	858	285

Description

6500726173 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeN ydeN Bacillus subtilis 1423 -11530031 7000693212 yden hypothetical protein yden (db:pir2.dat) H69778 H69778 Bacillus subtilis 1423 -11530031 302779 yden (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:106671) (re:107243) (di:complement) AB001488 AB001488 g1881334 Bacillus subtilis 1423 -11530031 7500964180 yden (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:170416) (re:170988) (di:complement) BSUB0003 Z99106 g2632826 Bacillus subtilis 1423 -11530031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501770790	2804	24960	663	220

Description

6500726174 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydzF ydzF Bacillus subtilis 1423 -11530032 7000692459 ydzf conserved hypothetical protein ydzf (cl:conserved hypothetical protein mth1285) (db:pir2.dat) G69790 G69790 Bacillus subtilis 1423 -11530032 7500963613 ydzf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:171070) (re:171399) (di:complement) BSUB0003 Z99106 g2632827 Bacillus subtilis 1423 -11530032

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771027	2805	24961	759	252

Description

6500726175 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeO ydeO Bacillus subtilis 1423 -11530033 7000692435 ydeo conserved hypothetical protein ydeo (cl:conserved hypothetical protein yitt) (db:pir2.dat) A69779 A69779 Bacillus subtilis 1423 -11530033 302780 ydeo (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to yqfu, yxkd, yitb of b. subtilis.) (le:107908) (re:108780) (di:direct) AB001488 AB001488 g1881335 Bacillus subtilis 1423 -11530033 7500963593 ydeo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:171654) (re:172526) (di:direct) BSUB0003 Z99106 g2632828 Bacillus subtilis 1423 -11530033

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771045	2806	24962	549	182

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771047	2807	24963	582	194

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771049	2808	24964	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771061	2809	24965	615	204

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771077	2810	24966	1701	567

Description

GTC ORF with score 194 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771095	2811	24967	450	149

Description

6500726176 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeP ydeP Bacillus subtilis 1423 -11530034 7000692436 ydep conserved hypothetical protein ydep (cl:conserved hypothetical protein mth1285) (db:pir2.dat) B69779 B69779 Bacillus subtilis 1423 -11530034 7500963594 ydep (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:172676) (re:173062) (di:complement) BSUB0003 Z99106 g2632829 Bacillus subtilis 1423 -11530034

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771120	2812	24968	492	163

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771121	2813	24969	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771139	2814	24970	1152	383

Description

6500726177 hypothetical protein:similar to nad:ph oxidoreductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeQ ydeQ Bacillus subtilis 1423 -11530035 7500922255 ydeq (ec:1.6.99.-) (de:putative nad(p)h oxidoreductase ydeq,) (db:swissprot) YDEQ_BACSU P96674 BACILLUS SUBTILIS 1423 -11530035 7000694299 ydeq nad p h oxidoreductase homolog ydeq (cl:probable nad(p)h oxidoreductase yabf) (db:pir2.dat) C69779 C69779 Bacillus subtilis 1423 -11530035 302782 ydeq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable nad(p)h oxidoreductase.) (le:109427) (re:110020) (di:direct) AB001488 AB001488 g1881337 Bacillus subtilis 1423 -11530035 7500922258 ydeq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to nad(p)h oxidoreductase) (le:173173) (re:173766) (di:direct) BSUB0003 Z99106 g2632830 Bacillus subtilis 1423 -11530035

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771149	2815	24971	453	150

Description

6500726178 hypothetical protein:similar to antibiotic resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeR ydeR Bacillus subtilis 1423 -11530036 7000692213 yder antibiotic resistance protein homolog yder (db:pir2.dat) D69779 D69779 Bacillus subtilis 1423 -11530036 302783 yder (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable integral membrane protein, similar to) (le:110164) (re:111351) (di:complement) AB001488 AB001488 g1881338 Bacillus subtilis 1423 -11530036 7500963419 yder (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to antibiotic resistance protein) (le:173910) (re:175097) (di:complement) BSUB0003 Z99106 g2632831 Bacillus subtilis 1423 -11530036

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771150	2816	24972	270	89

Description

6500726179 hypothetical protein:similar to transcriptional regulator:tetr/acrr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeS ydeS Bacillus subtilis 1423 -11530037 7000694783 ydes transcription regulator tetr/acrr family homolog ydes (db:pir2.dat) E69779 E69779 Bacillus subtilis 1423 -11530037 302784 ydes (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transcriptional regulator, similar to) (le:111555) (re:112151) (di:direct) AB001488 AB001488 g1881339 Bacillus subtilis 1423 -11530037 7500965345 ydes (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (tetr/acrr) (le:175301) (re:175897) (di:direct) BSUB0003 Z99106 g2632832 Bacillus subtilis 1423 -11530037

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771156	2817	24973	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771162	2818	24974	1140	380

Description

6500726180 hypothetical protein:similar to transcriptional regulator:arsr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydeT ydeT Bacillus subtilis 1423 -11530038 7000694722 ydet transcription regulator arsr family homolog ydet (cl:arsenical resistance operon repressor) (db:pir2.dat) F69779 F69779 Bacillus subtilis 1423 -11530038 302785 ydet (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transcriptional regulator, similar to) (le:112759) (re:113094) (di:direct) AB001488 AB001488 g1881340 Bacillus subtilis 1423 -11530038 7500965297 ydet (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (arsr family)) (le:176505) (re:176840) (di:direct) BSUB0003 Z99106 g2632833 Bacillus subtilis 1423 -11530038

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771177	2819	24975	699	232

Description

6500726181 hypothetical protein:similar to arsenical pump membrane protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfA ydfA Bacillus subtilis 1423 -11530039 7000692230 ydfa arsenical pump membrane protein homolog ydfa (cl:arsenical pump membrane protein) (db:pir2.dat) G69779 G69779 Bacillus subtilis 1423 -11530039 302786 ydfa (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to arsenical pump membrane protein.) (le:113107) (re:114414) (di:direct) AB001488 AB001488 g1881341 Bacillus subtilis 1423 -11530039 7500955281 ydfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to arsenical pump membrane protein) (le:176853) (re:178160) (di:direct) BSUB0003 Z99106 g2632834 Bacillus subtilis 1423 -11530039

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771179	2820	24976	666	221

Description

6500726182 hypothetical protein:similar to antibiotic resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfB ydfB Bacillus subtilis 1423 -11530040 7000692214 ydfb antibiotic resistance protein homolog ydfb (db:pir2.dat) H69779 H69779 Bacillus subtilis 1423 -11530040 302787 ydfb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to bacillus cereus zwittermicin) (le:114912) (re:115697) (di:direct) AB001488 AB001488 g1881342 Bacillus subtilis 1423 -11530040 7500963420 ydfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to antibiotic resistance protein) (le:178658) (re:179443) (di:direct) BSUB0003 Z99106 g2632835 Bacillus subtilis 1423 -11530040

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771432	2821	24977	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771455	2822	24978	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771465	2823	24979	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771469	2824	24980	819	272

Description

6500726183 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfC ydfC Bacillus subtilis 1423 -11530041 7000692437 ydfc conserved hypothetical protein ydfc (db:pir2.dat) A69780 A69780 Bacillus subtilis 1423 -11530041 302788 ydfc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in e. coli.) (le:115754) (re:116674) (di:complement) AB001488 AB001488 g1881343 Bacillus subtilis 1423 -11530041 7500963595 ydfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:179500) (re:180420) (di:complement) BSUB0003 Z99106 g2632836 Bacillus subtilis 1423 -11530041

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771483	2825	24981	678	225

Description

6500726184 hypothetical protein:similar to transcriptional regulator:gntr family / aminotransferase:mocr-like (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfD ydfD Bacillus subtilis 1423 -11530042 7000694732 ydfd transcription regulator gntr family homolog ydfd (db:pir2.dat) B69780 B69780 Bacillus subtilis 1423 -11530042 302789 ydfd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to the rhizopine catabolism (mocr) gene of) (le:116807) (re:118255) (di:direct) AB001488 AB001488 g1881344 Bacillus subtilis 1423 -11530042 7500965306 ydfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (gntr family)) (le:180553) (re:182001) (di:direct) BSUB0003 Z99106 g2632837 Bacillus subtilis 1423 -11530042

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771498	2826	24982	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771507	2827	24983	615	204

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771513	2828	24984	627	208

Description

6500726185 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfE ydfE Bacillus subtilis 1423 -11530043 7000693213 ydfe hypothetical protein ydfe (db:pir2.dat) C69780 C69780 Bacillus subtilis 1423 -11530043 302790 ydfe (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:118373) (re:118996) (di:complement) AB001488 AB001488 g1881345 Bacillus subtilis 1423 -11530043 7500964181 ydfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:182119) (re:182742) (di:complement) BSUB0003 Z99106 g2632838 Bacillus subtilis 1423 -11530043

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771524	2829	24985	1248	415

Description

6500726186 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfF ydfF Bacillus subtilis 1423 -11530044 7000693214 ydff hypothetical protein ydff (db:pir2.dat) D69780 D69780 Bacillus subtilis 1423 -11530044 302791 ydff (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:119086) (re:119766) (di:direct) AB001488 AB001488 g1881346 Bacillus subtilis 1423 -11530044 7500964182 ydff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:182832) (re:183512) (di:direct) BSUB0003 Z99106 g2632839 Bacillus subtilis 1423 -11530044

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771536	2830	24986	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771538	2831	24987	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771550	2832	24988	240	79

Description

6500726187 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfG ydfG Bacillus subtilis 1423 -11530045 7000692438 ydfg conserved hypothetical protein ydfg (db:pir2.dat) E69780 E69780 Bacillus subtilis 1423 -11530045 302792 ydfg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:119846) (re:120289) (di:complement) AB001488 AB001488 g1881347 Bacillus subtilis 1423 -11530045 7500963596 ydfg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:183592) (re:184035) (di:complement) BSUB0003 Z99106 g2632840 Bacillus subtilis 1423 -11530045

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771558	2833	24989	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771565	2834	24990	420	139

Description

6500726188 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfH ydfH Bacillus subtilis 1423 -11530046 7000694872 ydfh two-component sensor histidine kinase homolog ydfh (db:pir2.dat) F69780 F69780 Bacillus subtilis 1423 -11530046 302793 ydfh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:pobable sensory transduction histidine kinase.) (le:120962) (re:122185) (di:direct) AB001488 AB001488 g1881348 Bacillus subtilis 1423 -11530046 7500965409 ydfh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to two-component sensor histidine kinase) (le:184708) (re:185931) (di:direct) BSUB0003 Z99106 g2632841 Bacillus subtilis 1423 -11530046

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771577	2835	24991	228	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771578	2836	24992	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771585	2837	24993	363	120

Description

6500726189 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfI ydfI Bacillus subtilis 1423 -11530047 7000694843 ydfi two-component response regulator ydfh homolog ydfi) (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) G69780 G69780 Bacillus subtilis 1423 -11530047 302794 ydfi (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable regulatory component of sensory) (le:122178) (re:122819) (di:direct) AB001488 AB001488 g1881349 Bacillus subtilis 1423 -11530047 7500965392 ydfi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to two-component response regulator (ydfh)) (le:185924) (re:186565) (di:direct) BSUB0003 Z99106 g2632842 Bacillus subtilis 1423 -11530047

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771586	2838	24994	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771590	2839	24995	1185	395

Description

6500726190 hypothetical protein:similar to antibiotic transport-associated protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfJ ydfJ Bacillus subtilis 1423 -11530048 7000692221 ydfj antibiotic transport-associated protein homolog ydfj (db:pir2.dat) H69780 H69780 Bacillus subtilis 1423 -11530048 302795 ydfj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transport protein, similar to antibiotic) (le:122935) (re:125109) (di:direct) AB001488 AB001488 g1881350 Bacillus subtilis 1423 -11530048 7500963425 ydfj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to antibiotic transport-associated protein) (le:186681) (re:188855) (di:direct) BSUB0003 Z99106 g2632843 Bacillus subtilis 1423 -11530048

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771605	2840	24996	843	280

Description

6500726191 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfK ydfK Bacillus subtilis 1423 -11530049 7000692439 ydfk conserved hypothetical protein ydfk (cl:conserved hypothetical protein b2966) (db:pir2.dat) A69781 A69781 Bacillus subtilis 1423 -11530049 302797 ydfk (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in e.coli.) (le:126625) (re:127314) (di:complement) AB001488 AB001488 g1881352 Bacillus subtilis 1423 -11530049 7500963597 ydfk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:190371) (re:191060) (di:complement) BSUB0003 Z99106 g2632845 Bacillus subtilis 1423 -11530049

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771609	2841	24997	285	94

Description

6500726192 hypothetical protein:similar to multidrug-efflux transporter regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfL ydfL Bacillus subtilis 1423 -11530050 7000694261 ydfl multidrug-efflux transporter regulator homolog ydfl (db:pir2.dat) B69781 B69781 Bacillus subtilis 1423 -11530050 302798 ydfl (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable regulatory protein, similar to) (le:127404) (re:128216) (di:complement) AB001488 AB001488 g1881353 Bacillus subtilis 1423 -11530050 7500964980 ydfl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to multidrug-efflux transporter regulator) (le:191150) (re:191962) (di:complement) BSUB0003 Z99106 g2632846 Bacillus subtilis 1423 -11530050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771610	2842	24998	402	133

Description

6500726193 hypothetical protein:similar to cation efflux system (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfM ydfM Bacillus subtilis 1423 -11530051 7000692330 ydfm cation efflux system homolog ydfm (db:pir2.dat) C69781 C69781 Bacillus subtilis 1423 -11530051 302799 ydfm (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in synechocystis) (le:128327) (re:129220) (di:complement) AB001488 AB001488 g1881354 Bacillus subtilis 1423 -11530051 7500963498 ydfm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to cation efflux system) (le:192073) (re:192966) (di:complement) BSUB0003 Z99106 g2632847 Bacillus subtilis 1423 -11530051

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771624	2843	24999	420	139

Description

6500726194 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfN ydfN Bacillus subtilis 1423 -11530052 7000692440 ydfn conserved hypothetical protein ydfn (cl:nitroreductase) (db:pir2.dat) D69781 D69781 Bacillus subtilis 1423 -11530052 7500963598 ydfn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:193442) (re:194062) (di:direct) BSUB0003 Z99106 g2632848 Bacillus subtilis 1423 -11530052

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771625	2844	25000	909	302

Description

6500726195 hypothetical protein:similar to abc transporter:binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfO ydfO Bacillus subtilis 1423 -11530053 7000692112 ydfo abc transporter binding protein homolog ydfo (cl:probable abc transporter protein ydfo) (db:pir2.dat) E69781 E69781 Bacillus subtilis 1423 -11530053 302801 ydfo (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to pentachlorophenol-induced periplasmic) (le:130332) (re:131270) (di:direct) AB001488 AB001488 g1881356 Bacillus subtilis 1423 -11530053 7500963352 ydfo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to abc transporter (binding protein)) (le:194078) (re:195016) (di:direct) BSUB0003 Z99106 g2632849 Bacillus subtilis 1423 -11530053

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771639	2845	25001	834	277

Description

GTC ORF with score 159 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.).) (nt:similar to (pir accession number d35402)) (le:7040) (re:7951) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771643	2846	25002	582	194

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771910	2847	25003	1068	355

Description

GTC ORF with score 890 to: (sr:aspergillus fumigatus (library: cbs 144.89) (clone: fp4) myceliu) (db:genpept-pln1) (de:aspergillus fumigatus 88 kda secreted dipetidyl peptidase gene,complete cds.) (nt:putative) (le:326:461:571:860:1922) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771917	2848	25004	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771918	2849	25005	1071	357

Description

6500726196 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfP ydfP Bacillus subtilis 1423 -11530054 7000692441 ydfp conserved hypothetical protein ydfp (db:pir2.dat) F69781 F69781 Bacillus subtilis 1423 -11530054 302802 ydfp (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in e. coli and h.) (le:131372) (re:131761) (di:direct) AB001488 AB001488 g1881357 Bacillus subtilis 1423 -11530054 7500963599 ydfp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:195118) (re:195507) (di:direct) BSUB0003 Z99106 g2632850 Bacillus subtilis 1423 -11530054

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771926	2850	25006	555	184

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771928	2851	25007	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771932	2852	25008	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771969	2853	25009	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771976	2854	25010	201	66

Description

6500726197 hypothetical protein:similar to thioredoxin (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfQ ydfQ Bacillus subtilis 1423 -11530055 7000694681 ydfq thioredoxin homolog ydfq (db:pir2.dat) G69781 G69781 Bacillus subtilis 1423 -11530055 302803 ydfq (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to thioredoxin.) (le:131947) (re:132285) (di:direct) AB001488 AB001488 g1881358 Bacillus subtilis 1423 -11530055 7500965266 ydfq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to thioredoxin) (le:195693) (re:196031) (di:direct) BSUB0003 Z99106 g2632851 Bacillus subtilis 1423 -11530055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771978	2855	25011	237	78

Description

6500726198 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydzH ydzH Bacillus subtilis 1423 -11530056 7000692460 ydzh conserved hypothetical protein ydzh (cl:hypothetical protein ydgb) (db:pir2.dat) H69790 H69790 Bacillus subtilis 1423 -11530056 7500955944 ydzh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:196071) (re:196307) (di:complement) BSUB0003 Z99106 g2632852 Bacillus subtilis 1423 -11530056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771979	2856	25012	483	160

Description

6500726199 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfR ydfR Bacillus subtilis 1423 -11530057 7000692442 ydfr probable membrane protein ydfr (cl:probable membrane protein ycap) (db:pir2.dat) H69781 H69781 Bacillus subtilis 1423 -11530057 302804 ydfr (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to ydfs gene product of this entry) (le:133447) (re:134124) (di:complement) AB001488 AB001488 g1881359 Bacillus subtilis 1423 -11530057 7500955871 ydfr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:197193) (re:197870) (di:complement) BSUB0003 Z99106 g2632853 Bacillus subtilis 1423 -11530057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771980	2857	25013	342	113

Description

6500726200 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfS ydfS Bacillus subtilis 1423 -11530058 7000692443 ydfs probable membrane protein ydfs (cl:probable membrane protein ycap) (db:pir2.dat) A69782 A69782 Bacillus subtilis 1423 -11530058 302805 ydfs (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to ydfr gene product of this entry) (le:134237) (re:134944) (di:direct) AB001488 AB001488 g1881360 Bacillus subtilis 1423 -11530058 6000686368 ydfs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:197983) (re:198690) (di:direct) BSUB0003 Z99106 g2632854 Bacillus subtilis 1423 -11530058 7500955869 ydfs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:33) (re:740) (di:direct) BSUB0004 Z99107 g2632867 Bacillus subtilis 1423 -11530058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771982	2858	25014	270	89

Description

6500726201 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydfT ydfT Bacillus subtilis 1423 -11530059 7000693215 ydft hypothetical protein ydft (db:pir2.dat) B69782 B69782 Bacillus subtilis 1423 -11530059 302806 ydft (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:134959) (re:135390) (di:complement) AB001488 AB001488 g1881361 Bacillus subtilis 1423 -11530059 6000686370 ydft (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:198705) (re:199136) (di:complement) BSUB0003 Z99106 g2632855 Bacillus subtilis 1423 -11530059 7500964183 ydft (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:755) (re:1186) (di:complement) BSUB0004 Z99107 g2632868 Bacillus subtilis 1423 -11530059

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771985	2859	25015	564	188

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501771996	2860	25016	540	180

Description

6500726202 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgA ydgA Bacillus subtilis 1423 -11530060 7000692444 ydga conserved hypothetical protein ydga (cl:hypothetical protein ydgb) (db:pir2.dat) C69782 C69782 Bacillus subtilis 1423 -11530060 302807 ydga (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to ydgb gene product of this entry) (le:135403) (re:135645) (di:complement) AB001488 AB001488 g1881362 Bacillus subtilis 1423 -11530060 6000686372 ydga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:199149) (re:199391) (di:complement) BSUB0003 Z99106 g2632856 Bacillus subtilis 1423 -11530060 7500955943 ydga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:1199) (re:1441) (di:complement) BSUB0004 Z99107 g2632869 Bacillus subtilis 1423 -11530060

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772006	2861	25017	633	210

Description

6500726203 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgB ydgB Bacillus subtilis 1423 -11530061 7000692445 ydgb conserved hypothetical protein ydgb (cl:hypothetical protein ydgb) (db:pir2.dat) D69782 D69782 Bacillus subtilis 1423 -11530061 302808 ydgb (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to ydga gene product of this entry) (le:135659) (re:135931) (di:complement) AB001488 AB001488 g1881363 Bacillus subtilis 1423 -11530061 6000686374 ydgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins from b. subtilis) (le:199405) (re:199677) (di:complement) BSUB0003 Z99106 g2632857 Bacillus subtilis 1423 -11530061 7500955942 ydgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:1455) (re:1727) (di:complement) BSUB0004 Z99107 g2632870 Bacillus subtilis 1423 -11530061

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772010	2862	25018	690	229

Description

6500726204 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgC ydgC Bacillus subtilis 1423 -11530062 7000692446 ydgc conserved hypothetical protein ydgc (db:pir2.dat) E69782 E69782 Bacillus subtilis 1423 -11530062 302809 ydgc (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:136230) (re:136817) (di:direct) AB001488 AB001488 g1881364 Bacillus subtilis 1423 -11530062 6000686376 ydgc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:199976) (re:200563) (di:direct) BSUB0003 Z99106 g2632858 Bacillus subtilis 1423 -11530062 7500963600 ydgc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:2026) (re:2613) (di:direct) BSUB0004 Z99107 g2632871 Bacillus subtilis 1423 -11530062

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772018	2863	25019	1947	649

Description

6500726205 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgD ydgD Bacillus subtilis 1423 -11530063 7000693216 ydgd hypothetical protein ydgd (db:pir2.dat) F69782 F69782 Bacillus subtilis 1423 -11530063 302810 ydgd (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:136814) (re:137158) (di:direct) AB001488 AB001488 g1881365 Bacillus subtilis 1423 -11530063 6000686378 ydgd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (le:200560) (re:200904) (di:direct) BSUB0003 Z99106 g2632859 Bacillus subtilis 1423 -11530063 7500964184 ydgd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:2610) (re:2954) (di:direct) BSUB0004 Z99107 g2632872 Bacillus subtilis 1423 -11530063

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772042	2864	25020	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772059	2865	25021	627	208

Description

GTC ORF with score 162 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f12c20 genomic sequence,complete sequence.) (nt:unknown protein) (le:45171:46239:46705) (re:45637:46611:47409) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772066	2866	25022	222	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772068	2867	25023	1005	335

Description

6500726206 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgE ydgE Bacillus subtilis 1423 -11530064 7000692447 ydge conserved hypothetical protein ydge (db:pir2.dat) G69782 G69782 Bacillus subtilis 1423 -11530064 302811 ydge (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown, similar product in) (le:137321) (re:137794) (di:direct) AB001488 AB001488 g1881366 Bacillus subtilis 1423 -11530064 6000686380 ydge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to hypothetical proteins) (le:201067) (re:201540) (di:direct) BSUB0003 Z99106 g2632860 Bacillus subtilis 1423 -11530064 7500963601 ydge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:3117) (re:3590) (di:direct) BSUB0004 Z99107 g2632873 Bacillus subtilis 1423 -11530064

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772069	2868	25024	360	119

Description

6500726207 hypothetical protein:similar to amino acid abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgF ydgF Bacillus subtilis 1423 -11530065 7500922300 ydgf (de:hypothetical transport protein in expz-dinb intergenic region) (db:swissprot) YDGF_BACSU P96704 BACILLUS SUBTILIS 1423 -11530065 7000692191 ydgf amino acid abc transporter permease homolog ydgf (cl:arginine permease) (db:pir2.dat) H69782 H69782 Bacillus subtilis 1423 -11530065 302813 ydgf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable amino acid transport permiase.) (le:139917) (re:141293) (di:complement) AB001488 AB001488 g1881368 Bacillus subtilis 1423 -11530065 7500922302 ydgf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to amino acid abc transporter (permease)) (le:203663) (re:205039) (di:complement) BSUB0003 Z99106 g2632862 Bacillus subtilis 1423 -11530065 7500922303 ydgf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to amino acid abc transporter (permease)) (le:5713) (re:7089) (di:complement) BSUB0004 Z99107 g2632875 Bacillus subtilis 1423 -11530065 6000686384 ydgf (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable amino acid transport permiase.) (le:139917) (re:141293) (di:complement) AB001488 AB001488 g1881368 Bacillus subtilis 1423 -11530065

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772078	2869	25025	1149	383

Description

6500726208 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgG ydgG Bacillus subtilis 1423 -11530066 7000694763 ydgg transcription regulator marr family homolog ydgg (db:pir2.dat) A69783 A69783 Bacillus subtilis 1423 -11530066 302815 ydgg (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:function unknown.) (le:142152) (re:142610) (di:direct) AB001488 AB001488 g1881370 Bacillus subtilis 1423 -11530066 6000686388 ydgg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transcriptional regulator (marr family)) (le:205898) (re:206356) (di:direct) BSUB0003 Z99106 g2632864 Bacillus subtilis 1423 -11530066 7500965333 ydgg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (marr family)) (le:7948) (re:8406) (di:direct) BSUB0004 Z99107 g2632877 Bacillus subtilis 1423 -11530066

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772093	2870	25026	543	180

Description

6500726209 hypothetical protein:similar to transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgH ydgH Bacillus subtilis 1423 -11530067 7000694816 ydgh transporter homolog ydgh (db:pir2.dat) B69783 B69783 Bacillus subtilis 1423 -11530067 302816 ydgh (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:probable transport protein, similar product in) (le:142607) (re:145264) (di:direct) AB001488 AB001488 g1881371 Bacillus subtilis 1423 -11530067 6000686390 ydgh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.) (nt:similar to transporter) (le:206353) (re:209010) (di:direct) BSUB0003 Z99106 g2632865 Bacillus subtilis 1423 -11530067 7500965370 ydgh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transporter) (le:8403) (re:11060) (di:direct) BSUB0004 Z99107 g2632878 Bacillus subtilis 1423 -11530067

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772094	2871	25027	300	99

Description

6500726210 hypothetical protein:putative nad:ph nitroreductase (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgI ydgI Bacillus subtilis 1423 -11530068 5500686523 ydgi (ec:1.-.-.-) (de:putative nad(p)h nitroreductase ydgi,) (db:swissprot) YDGI_BACSU P96707 BACILLUS SUBTILIS 1423 -11530068 7000687544 ydgi nadh dehydrogenase homolog ydgi (cl:nitroreductase) (db:pir2.dat) C69783 C69783 Bacillus subtilis 1423 -11530068 302817 ydgi (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to nitroreductase.) (le:145410) (re:146039) (di:complement) AB001488 AB001488 g1881372 Bacillus subtilis 1423 -11530068 7500922307 ydgi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to nadh dehydrogenase) (le:11206) (re:11835) (di:complement) BSUB0004 Z99107 g2632879 Bacillus subtilis 1423 -11530068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772110	2872	25028	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772117	2873	25029	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772133	2874	25030	276	91

Description

6500726211 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgJ ydgJ Bacillus subtilis 1423 -11530069 7000694764 ydgj transcription regulator marr family homolog ydgj (cl:regulatory protein mpra) (db:pir2.dat) D69783 D69783 Bacillus subtilis 1423 -11530069 302818 ydgj (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to salmonella typhimurium slyy gene) (le:146055) (re:146549) (di:complement) AB001488 AB001488 g1881373 Bacillus subtilis 1423 -11530069 7500955821 ydgj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (marr family)) (le:11851) (re:12345) (di:complement) BSUB0004 Z99107 g2632880 Bacillus subtilis 1423 -11530069

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772136	2875	25031	489	162

Description

6500726212 hypothetical protein:similar to bicyclomycin resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydgK ydgK Bacillus subtilis 1423 -11530070 7000692268 ydgk bicyclomycin resistance protein homolog ydgk (cl:bicyclomycin resistance protein) (db:pir2.dat) E69783 E69783 Bacillus subtilis 1423 -11530070 302819 ydgk (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.) (nt:similar to bicyclomycin resistance protein.) (le:146860) (re:148068) (di:direct) AB001488 AB001488 g1881374 Bacillus subtilis 1423 -11530070 7500963449 ydgk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to bicyclomycin resistance protein) (le:12656) (re:13864) (di:direct) BSUB0004 Z99107 g2632881 Bacillus subtilis 1423 -11530070

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772146	2876	25032	267	88

Description

6500726213 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhB ydhB Bacillus subtilis 1423 -11530071 7000692448 ydhb conserved hypothetical protein ydhb (db:pir2.dat) F69783 F69783 Bacillus subtilis 1423 -11530071 1500693327 ydhb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:13859) (re:14638) (di:complement) BSUB0004 Z99107 g2632882 Bacillus subtilis 1423 -11530071 7500963602 ydhb (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:transmembrane) (le:861) (re:1640) (di:complement) D88802 D88802 g1945085 Bacillus subtilis 1423 -11530071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772147	2877	25033	687	228

Description

GTC ORF with score 635 to: (db:genpept-pln2) (de:emericella nidulans negative-acting regulatory protein (qutr) gene,complete cds; and unknown gene.) (nt:repressor protein; coding region predicted from dna) (le:3826) (re:6531) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772149	2878	25034	291	96

Description

GTC ORF with score 353 to: (db:genpept-pln2) (de:emericella nidulans negative-acting regulatory protein (qutr) gene,complete cds; and unknown gene.) (nt:repressor protein; coding region predicted from dna) (le:3826) (re:6531) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772152	2879	25035	486	161

Description

GTC ORF with score 205 to: (db:genpept-pln2) (de:emericella nidulans negative-acting regulatory protein (qutr) gene,complete cds; and unknown gene.) (nt:repressor protein; coding region predicted from dna) (le:3826) (re:6531) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772381	2880	25036	531	177

Description

6500726214 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhC ydhC Bacillus subtilis 1423 -11530072 7502851645 ydhc (de:hypothetical transcriptional regulator in dinb-phob intergenic region) (db:swissprot) YDHC_BACSU O05494 BACILLUS SUBTILIS 1423 -11530072 7000694736 ydhc transcription regulator gntr family homolog ydhc (db:pir2.dat) G69783 G69783 Bacillus subtilis 1423 -11530072 1500693328 ydhc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (gntr family)) (le:14887) (re:15561) (di:direct) BSUB0004 Z99107 g2632883 Bacillus subtilis 1423 -11530072 7500965309 ydhc (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis gluconate operon repressor; p10585) (le:1889) (re:2563) (di:direct) D88802 D88802 g1945086 Bacillus subtilis 1423 -11530072

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772383	2881	25037	585	195

Description

6500726215 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhD ydhD Bacillus subtilis 1423 -11530073 7000692449 ydhd conserved hypothetical protein ydhd (cl:hypothetical protein yaah) (db:pir2.dat) H69783 H69783 Bacillus subtilis 1423 -11530073 1500693329 ydhd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:15688) (re:17007) (di:direct) BSUB0004 Z99107 g2632884 Bacillus subtilis 1423 -11530073 7500963603 ydhd (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis yaah hypothetical protein; p37534) (le:2690) (re:4009) (di:direct) D88802 D88802 g1945087 Bacillus subtilis 1423 -11530073

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772384	2882	25038	513	171

Description

6500726216 hypothetical protein:similar to macrolide glycosyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhE ydhE Bacillus subtilis 1423 -11530074 7000694177 ydhe macrolide glycosyltransferase homolog ydhe (cl:glycosyltransferase) (db:pir2.dat) A69784 A69784 Bacillus subtilis 1423 -11530074 1500693330 ydhe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to macrolide glycosyltransferase) (le:17153) (re:18298) (di:direct) BSUB0004 Z99107 g2632885 Bacillus subtilis 1423 -11530074 7500954259 ydhe (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:s. lividans glycosyl transferase; js0636 (311)) (le:4155) (re:5300) (di:direct) D88802 D88802 g1945088 Bacillus subtilis 1423 -11530074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772387	2883	25039	516	171

Description

6500726217 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhF ydhF Bacillus subtilis 1423 -11530075 7000692450 ydhf conserved hypothetical protein ydhf (db:pir2.dat) B69784 B69784 Bacillus subtilis 1423 -11530075 7500963604 ydhf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:18337) (re:19047) (di:complement) BSUB0004 Z99107 g2632886 Bacillus subtilis 1423 -11530075

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772390	2884	25040	717	238

Description

6500726218 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhG ydhG Bacillus subtilis 1423 -11530076 7000692451 ydhg conserved hypothetical protein ydhg (db:pir2.dat) C69784 C69784 Bacillus subtilis 1423 -11530076 7500963605 ydhg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:20863) (re:21234) (di:direct) BSUB0004 Z99107 g2632888 Bacillus subtilis 1423 -11530076

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772392	2885	25041	450	149

Description

6500726219 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhH ydhH Bacillus subtilis 1423 -11530077 7000692452 ydhh conserved hypothetical protein ydhh (db:pir2.dat) D69784 D69784 Bacillus subtilis 1423 -11530077 1500693334 ydhh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:21310) (re:21807) (di:complement) BSUB0004 Z99107 g2632889 Bacillus subtilis 1423 -11530077 7500963606 ydhh (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:secretory) (le:8312) (re:8809) (di:complement) D88802 D88802 g1945092 Bacillus subtilis 1423 -11530077

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772399	2886	25042	216	71

Description

6500726220 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhI ydhI Bacillus subtilis 1423 -11530078 7502851646 ydhi (de:hypothetical 17.9 kd protein in phob-groes intergenic region) (db:swissprot) YDHI_BACSU O05501 BACILLUS SUBTILIS 1423 -11530078 7000692453 ydhi conserved hypothetical protein ydhi (db:pir2.dat) E69784 E69784 Bacillus subtilis 1423 -11530078 1500693335 ydhi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:21825) (re:22307) (di:complement) BSUB0004 Z99107 g2632890 Bacillus subtilis 1423 -11530078 7500963607 ydhi (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis yxar hypothetical protein; p46328) (le:8827) (re:9309) (di:complement) D88802 D88802 g1945093 Bacillus subtilis 1423 -11530078

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772400	2887	25043	564	188

Description

6500726221 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhJ ydhJ Bacillus subtilis 1423 -11530079 7000692454 ydhj conserved hypothetical protein ydhj (db:pir2.dat) F69784 F69784 Bacillus subtilis 1423 -11530079 1500693336 ydhj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:22390) (re:23367) (di:direct) BSUB0004 Z99107 g2632891 Bacillus subtilis 1423 -11530079 7500963608 ydhj (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (le:9392) (re:10369) (di:direct) D88802 D88802 g1945094 Bacillus subtilis 1423 -11530079

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772401	2888	25044	450	149

Description

6500726222 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhK ydhK Bacillus subtilis 1423 -11530080 7000693217 ydhk hypothetical protein ydhk (db:pir2.dat) G69784 G69784 Bacillus subtilis 1423 -11530080 1500693337 ydhk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:23509) (re:24126) (di:direct) BSUB0004 Z99107 g2632892 Bacillus subtilis 1423 -11530080 7500964185 ydhk (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:membrane protein) (le:10511) (re:11128) (di:direct) D88802 D88802 g1945095 Bacillus subtilis 1423 -11530080

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772408	2889	25045	1005	334

Description

6500726223 hypothetical protein:similar to chloramphenicol resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhL ydhL Bacillus subtilis 1423 -11530081 7000692364 ydhl chloramphenicol resistance protein homolog ydhl (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) H69784 H69784 Bacillus subtilis 1423 -11530081 1500693338 ydhl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to chloramphenicol resistance protein) (le:24142) (re:25419) (di:complement) BSUB0004 Z99107 g2632893 Bacillus subtilis 1423 -11530081 7500963527 ydhl (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:s. lividans chloramphenicol resistance protein;) (le:11144) (re:12421) (di:complement) D88802 D88802 g1945096 Bacillus subtilis 1423 -11530081

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772424	2890	25046	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772441	2891	25047	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772448	2892	25048	1044	348

Description

6500726224 hypothetical protein:similar to cellobiose phosphotransferase system enzyme ii (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhM ydhM Bacillus subtilis 1423 -11530082 7000692351 ydhm cellobiose phosphotransferase system enzym homolog ydhm (cl:phosphotransferase system enzyme ii cellobiose-specific factor iib) (db:pir2.dat) A69785 A69785 Bacillus subtilis 1423 -11530082 1500693339 ydhm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to cellobiose phosphotransferase system) (le:25638) (re:25949) (di:direct) BSUB0004 Z99107 g2632894 Bacillus subtilis 1423 -11530082 7500963515 ydhm (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis, cellobiose phosphotransferase system,) (le:12640) (re:12951) (di:direct) D88802 D88802 g1945097 Bacillus subtilis 1423 -11530082

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772449	2893	25049	903	300

Description

GTC ORF with score 98 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f8k4 sequence, completesequence.) (nt:contains similarity to gb|u51898 ca2+-independent) (le:33258:33792:34028:34442) (re:33695:33939:34126:34647) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772454	2894	25050	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772457	2895	25051	441	147

Description

6500726225 hypothetical protein:similar to cellobiose phosphotransferase system enzyme ii (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhN ydhN Bacillus subtilis 1423 -11530083 7000692352 ydhn cellobiose phosphotransferase system enzym homolog ydhn (cl:phosphotransferase system lactose-specific enzyme ii, factor iii) (db:pir2.dat) B69785 B69785 Bacillus subtilis 1423 -11530083 1500693340 ydhn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to cellobiose phosphotransferase system) (le:25949) (re:26281) (di:direct) BSUB0004 Z99107 g2632895 Bacillus subtilis 1423 -11530083 7500963516 ydhn (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis cellobiose phosphotransferase system) (le:12951) (re:13283) (di:direct) D88802 D88802 g1945098 Bacillus subtilis 1423 -11530083

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772461	2896	25052	192	63

Description

6500726226 hypothetical protein:similar to cellobiose phosphotransferase system enzyme ii (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhO ydhO Bacillus subtilis 1423 -11530084 7000692353 ydho cellobiose phosphotransferase system enzym homolog ydho (cl:phosphotransferase system enzyme ii factor ii, phosphoenolpyruvate-dependent) (db:pir2.dat) C69785 C69785 Bacillus subtilis 1423 -11530084 1500693341 ydho (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to cellobiose phosphotransferase system) (le:26300) (re:27628) (di:direct) BSUB0004 Z99107 g2632896 Bacillus subtilis 1423 -11530084 7500963517 ydho (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis cellobiose phosphotransferase system) (le:13302) (re:14630) (di:direct) D88802 D88802 g1945099 Bacillus subtilis 1423 -11530084

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772464	2897	25053	1395	464

Description

6500726227 hypothetical protein:similar to beta-glucosidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhP ydhP Bacillus subtilis 1423 -11530085 7000692263 ydhp beta-glucosidase homolog ydhp (cl:agrobacterium beta-glucosidase) (db:pir2.dat) D69785 D69785 Bacillus subtilis 1423 -11530085 1500693342 ydhp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to beta-glucosidase) (le:27646) (re:29043) (di:direct) BSUB0004 Z99107 g2632897 Bacillus subtilis 1423 -11530085 7500963445 ydhp (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:c. thermocellum beta-glucosidase; p26208 (985)) (le:14648) (re:16045) (di:direct) D88802 D88802 g1945100 Bacillus subtilis 1423 -11530085

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772475	2898	25054	1002	333

Description

GTC ORF with score 253 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772478	2899	25055	264	87

Description

6500726228 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhQ ydhQ Bacillus subtilis 1423 -11530086 7000694737 ydhq transcription regulator gntr family homolog ydhq (cl:transcription regulator gntr) (db:pir2.dat) E69785 E69785 Bacillus subtilis 1423 -11530086 1500693343 ydhq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (gntr family)) (le:29186) (re:29899) (di:direct) BSUB0004 Z99107 g2632898 Bacillus subtilis 1423 -11530086 7500965310 ydhq (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:k. aerogenes, histidine utilization repressor;) (le:16188) (re:16901) (di:direct) D88802 D88802 g1945101 Bacillus subtilis 1423 -11530086

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772480	2900	25056	231	76

Description

6500726229 hypothetical protein:similar to fructokinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhR ydhR Bacillus subtilis 1423 -11530087 7502851647 ydhr (ec:2.7.1.4) (de:putative fructokinase,) (db:swissprot) SCRK_BACSU O05510 BACILLUS SUBTILIS 1423 -11530087 7000693008 ydhr fructokinase homolog ydhr (cl:fructokinase:glucose kinase homology) (db:pir2.dat) F69785 F69785 Bacillus subtilis 1423 -11530087 1500693344 ydhr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to fructokinase) (le:29928) (re:30827) (di:direct) BSUB0004 Z99107 g2632899 Bacillus subtilis 1423 -11530087 7500963995 ydhr (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:s. mutans fructokinase; q07211 (665)) (le:16930) (re:17829) (di:direct) D88802 D88802 g1945102 Bacillus subtilis 1423 -11530087

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772492	2901	25057	246	81

Description

6500726230 hypothetical protein:similar to mannose-6-phosphate isomerase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhS ydhS Bacillus subtilis 1423 -11530088 7000694197 ydhs mannose-6-phosphate isomerase homolog ydhs (db:pir2.dat) G69785 G69785 Bacillus subtilis 1423 -11530088 1500693345 ydhs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to mannose-6-phosphate isomerase) (le:30824) (re:31771) (di:direct) BSUB0004 Z99107 g2632900 Bacillus subtilis 1423 -11530088 7500964924 ydhs (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis mannose-6-phosphate isomerase; p39841) (le:17826) (re:18773) (di:direct) D88802 D88802 g1945103 Bacillus subtilis 1423 -11530088

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772501	2902	25058	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772511	2903	25059	357	118

Description

6500726231 hypothetical protein:similar to mannan endo-1:4-beta-mannosidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhT ydhT Bacillus subtilis 1423 -11530089 7000694196 ydht mannan endo-1:4-beta-mannosidase homolog ydht (db:pir2.dat) H69785 H69785 Bacillus subtilis 1423 -11530089 1500693346 ydht (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to mannan endo-1,4-beta-mannosidase) (le:31790) (re:32878) (di:direct) BSUB0004 Z99107 g2632901 Bacillus subtilis 1423 -11530089 7500964923 ydht (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:bacillus sp. mannan endo-1, 4-beta-mannosidase;) (le:18792) (re:19880) (di:direct) D88802 D88802 g1945104 Bacillus subtilis 1423 -11530089

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772538	2904	25060	777	258

Description

6500726232 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydhU ydhU Bacillus subtilis 1423 -11530090 7000687553 ydhu (de:hypothetical 17.1 kd protein in phob-groes intergenic region) (db:swissprot) YDHU_BACSU O05513 BACILLUS SUBTILIS 1423 -11530090 7000687554 ydhu hypothetical protein ydhu (db:pir2.dat) A69786 A69786 Bacillus subtilis 1423 -11530090 1500693347 ydhu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:32939) (re:33394) (di:complement) BSUB0004 Z99107 g2632902 Bacillus subtilis 1423 -11530090 7500922335 ydhu (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (le:19941) (re:20396) (di:complement) D88802 D88802 g1945105 Bacillus subtilis 1423 -11530090

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772540	2905	25061	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772541	2906	25062	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772812	2907	25063	540	180

Description

6500726233 ydxa:ydia hypothetical protein:similar to thiamin-monophosphate kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiA ydiA Bacillus subtilis 1423 -11530091 7000694675 ydia thiamin-monophosphate kinase homolog ydia (db:pir2.dat) B69786 B69786 Bacillus subtilis 1423 -11530091 7500965260 ydia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: ydxa; similar to) (le:39678) (re:40655) (di:direct) BSUB0004 Z99107 g2632903 Bacillus subtilis 1423 -11530091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772817	2908	25064	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772834	2909	25065	408	135

Description

6500726234 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiB ydiB Bacillus subtilis 1423 -11530092 7000692455 ydib conserved hypothetical protein ydib (cl:hypothetical protein hi0065) (db:pir2.dat) C69786 C69786 Bacillus subtilis 1423 -11530092 1500693349 ydib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:40670) (re:41146) (di:direct) BSUB0004 Z99107 g2632904 Bacillus subtilis 1423 -11530092 7500963609 ydib (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:e. coli hypothetical protein; p31805 (267)) (le:27672) (re:28148) (di:direct) D88802 D88802 g1945107 Bacillus subtilis 1423 -11530092

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772836	2910	25066	315	104

Description

6500726235 hypothetical protein:similar to glycoprotein endopeptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiC ydiC Bacillus subtilis 1423 -11530093 7000693070 ydic glycoprotein endopeptidase homolog ydic (db:pir2.dat) D69786 D69786 Bacillus subtilis 1423 -11530093 1500693350 ydic (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to glycoprotein endopeptidase) (le:41127) (re:41816) (di:direct) BSUB0004 Z99107 g2632905 Bacillus subtilis 1423 -11530093 7500964038 ydic (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:h. influenzae hypothetical protein; p43990 (182)) (le:28129) (re:28818) (di:direct) D88802 D88802 g1945108 Bacillus subtilis 1423 -11530093

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772839	2911	25067	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772862	2912	25068	525	174

Description

GTC ORF with score 105 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t18h9.) (nt:coded for by c. elegans cdna yk68a8.5) (le:25268:25502:25795:26180) (re:25334:25749:26001:26566) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772865	2913	25069	1110	369

Description

6500726236 hypothetical protein:similar to ribosomal-protein-alanine n-acetyltransferase (gtcfc:14.1) (ec:2.3.1.128) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiD ydiD Bacillus subtilis 1423 -11530094 7000694544 ydid ribosomal-protein-alanine n-acetyltransfer homolog ydid (cl:escherichia coli peptide n-acetyltransferase rimi) (db:pir2.dat) E69786 E69786 Bacillus subtilis 1423 -11530094 1500693351 ydid (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to ribosomal-protein-alanine) (le:41826) (re:42281) (di:direct) BSUB0004 Z99107 g2632906 Bacillus subtilis 1423 -11530094 7500965160 ydid (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:h. influenzae, ribosomal protein alanine) (le:28828) (re:29283) (di:direct) D88802 D88802 g1945109 Bacillus subtilis 1423 -11530094

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772870	2914	25070	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772889	2915	25071	921	306

Description

GTC ORF with score 167 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completecds.) (nt:putative oxo-ketoglutarate dioxygenase; orf3) (le:2783) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772892	2916	25072	288	95

Description

6500726237 hypothetical protein:similar to glycoprotein endopeptidase (gtcfc:14.1) (ec:3.4.24.57) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiE ydiE Bacillus subtilis 1423 -11530095 7500922342 ydie (de:hypothetical 36.8 kd protein in phob-groes intergenic region) (db:swissprot) YDIE_BACSU O05518 BACILLUS SUBTILIS 1423 -11530095 7000693071 ydie glycoprotein endopeptidase homolog ydie (cl:o-sialoglycoprotein endopeptidase) (db:pir2.dat) F69786 F69786 Bacillus subtilis 1423 -11530095 7500922344 ydie (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to glycoprotein endopeptidase) (le:42274) (re:43314) (di:direct) BSUB0004 Z99107 g2632907 Bacillus subtilis 1423 -11530095 1500693352 ydie (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:p. haemolytica o-sialoglycoprotein endopeptidase;) (le:29276) (re:30316) (di:direct) D88802 D88802 g1945110 Bacillus subtilis 1423 -11530095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772896	2917	25073	666	221

Description

6500726238 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiF ydiF Bacillus subtilis 1423 -11530096 7500922346 ydif (de:hypothetical abc transporter atp-binding protein ydif) (db:swissprot) YDIF_BACSU O05519 BACILLUS SUBTILIS 1423 -11530096 7000692081 ydif abc transporter atp-binding protein homolog ydif (cl:atp-binding cassette homology) (db:pir2.dat) G69786 G69786 Bacillus subtilis 1423 -11530096 7500922348 ydif (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to abc transporter (atp-binding protein)) (le:43544) (re:45472) (di:complement) BSUB0004 Z99107 g2632908 Bacillus subtilis 1423 -11530096 1500693353 ydif (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:h. influenzae hypothetical abc transporter; p44808) (le:30546) (re:32474) (di:complement) D88802 D88802 g1945111 Bacillus subtilis 1423 -11530096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772898	2918	25074	528	176

Description

6500726239 hypothetical protein:similar to molybdopterin precursor biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiG ydiG Bacillus subtilis 1423 -11530097 7000694231 ydig molybdenum cofactor biosynthesis protein c homolog ydig (cl:molybdenum cofactor biosynthesis protein c) (db:pir2.dat) H69786 H69786 Bacillus subtilis 1423 -11530097 1500693354 ydig (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to molybdopterin precursor biosynthesis) (le:45598) (re:46110) (di:direct) BSUB0004 Z99107 g2632909 Bacillus subtilis 1423 -11530097 7500955524 ydig (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:e. coli moac protein; p30747 (368)) (le:32600) (re:33112) (di:direct) D88802 D88802 g1945112 Bacillus subtilis 1423 -11530097

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772911	2919	25075	933	310

Description

6500726240 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiH ydiH Bacillus subtilis 1423 -11530098 7000693218 ydih hypothetical protein ydih (db:pir2.dat) A69787 A69787 Bacillus subtilis 1423 -11530098 1500693355 ydih (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:46107) (re:46754) (di:direct) BSUB0004 Z99107 g2632910 Bacillus subtilis 1423 -11530098 7500964186 ydih (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (le:33109) (re:33756) (di:direct) D88802 D88802 g1945113 Bacillus subtilis 1423 -11530098

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772912	2920	25076	414	137

Description

6500726241 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiI ydiI Bacillus subtilis 1423 -11530099 7000693219 ydii hypothetical protein ydii (cl:conserved hypothetical secreted protein hp0320) (db:pir2.dat) B69787 B69787 Bacillus subtilis 1423 -11530099 1500693356 ydii (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:46776) (re:46949) (di:direct) BSUB0004 Z99107 g2632911 Bacillus subtilis 1423 -11530099 7500964187 ydii (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:membrane protein) (le:33778) (re:33951) (di:direct) D88802 D88802 g1945114 Bacillus subtilis 1423 -11530099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772924	2921	25077	534	177

Description

6500726242 hypothetical protein:hypothetical 29.1 kd protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiJ ydiJ Bacillus subtilis 1423 -11530100 5500686543 ydij (de:hypothetical 29.1 kd protein in phob-groes intergenic region) (db:swissprot) YDIJ_BACSU O05523 BACILLUS SUBTILIS 1423 -11530100 7000687561 ydij conserved hypothetical protein ydij (cl:conserved hypothetical protein hi0188) (db:pir2.dat) C69787 C69787 Bacillus subtilis 1423 -11530100 1500693357 ydij (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:46956) (re:47720) (di:direct) BSUB0004 Z99107 g2632912 Bacillus subtilis 1423 -11530100 7500922353 ydij (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:b. subtilis ycbt hypothetical protein; p42252 (519)) (le:33958) (re:34722) (di:direct) D88802 D88802 g1945115 Bacillus subtilis 1423 -11530100

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772949	2922	25078	378	125

Description

GTC ORF with score 181 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772956	2923	25079	189	62

Description

GTC ORF with score 120 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772957	2924	25080	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772966	2925	25081	873	290

Description

6500726243 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiK ydiK Bacillus subtilis 1423 -11530101 7000693220 ydik hypothetical protein ydik (db:pir2.dat) D69787 D69787 Bacillus subtilis 1423 -11530101 1500693358 ydik (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:47758) (re:47949) (di:complement) BSUB0004 Z99107 g2632913 Bacillus subtilis 1423 -11530101 7500964188 ydik (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:secretory) (le:34760) (re:34951) (di:complement) D88802 D88802 g1945116 Bacillus subtilis 1423 -11530101

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772971	2926	25082	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772975	2927	25083	357	118

Description

GTC ORF with score 177 to: (sr:n.crassa (strain 74a) dna) (db:genpept-pln1) (de:n.crassa vacuolar atpase 67-kd subunit (vma-1) gene, complete cds.) (nt:vacuolar atpase vma-1) (le:1155:1295:1406:1493) (re:1163:1331:1427:1541) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772980	2928	25084	423	140

Description

6500726244 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiL ydiL Bacillus subtilis 1423 -11530102 7000693221 ydil hypothetical protein ydil (db:pir2.dat) E69787 E69787 Bacillus subtilis 1423 -11530102 1500693359 ydil (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:47946) (re:48680) (di:complement) BSUB0004 Z99107 g2632914 Bacillus subtilis 1423 -11530102 7500964189 ydil (sr:bacillus subtilis (sub_species:marburg, strain:168, isolate:jh642) (db:genpept-bct1) (de:bacillus subtilis dna for phob-rrne-groesl region, complete cds.) (nt:transmembrane) (le:34948) (re:35682) (di:complement) D88802 D88802 g1945117 Bacillus subtilis 1423 -11530102

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772982	2929	25085	1278	426

Description

6500726245 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiM ydiM Bacillus subtilis 1423 -11530103 7000693222 ydim hypothetical protein ydim (db:pir2.dat) F69787 F69787 Bacillus subtilis 1423 -11530103 5500704087 ydim (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:function unknown) (le:3520) (re:3900) (di:direct) AB007637 AB007637 g2521995 Bacillus subtilis 1423 -11530103 7500964190 ydim (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:52448) (re:52828) (di:direct) BSUB0004 Z99107 g2632917 Bacillus subtilis 1423 -11530103

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772992	2930	25086	1104	368

Description

6500726246 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiN ydiN Bacillus subtilis 1423 -11530104 7000693223 ydin hypothetical protein ydin (db:pir2.dat) G69787 G69787 Bacillus subtilis 1423 -11530104 5500704088 ydin (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:function unknown) (le:5067) (re:5282) (di:direct) AB007637 AB007637 g2521996 Bacillus subtilis 1423 -11530104 7500964191 ydin (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:53995) (re:54210) (di:direct) BSUB0004 Z99107 g2632918 Bacillus subtilis 1423 -11530104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772993	2931	25087	444	147

Description

GTC ORF with score 168 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1086.) (nt:similar to saccharomyces cerevisiae orf yor091w,) (le:<1) (re:870) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501772996	2932	25088	276	91

Description

6500726247 hypothetical protein:similar to dna-methyltransferase:cytosine-specific (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiO ydiO Bacillus subtilis 1423 -11530105 7000692952 ydio dna-methyltransferase cytosine-specific homolog ydio (db:pir2.dat) H69787 H69787 Bacillus subtilis 1423 -11530105 5500704089 ydio (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:similar to modification methylase) (le:5312) (re:6595) (di:direct) AB007637 AB007637 g2521997 Bacillus subtilis 1423 -11530105 7500963963 ydio (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to dna-methyltransferase) (le:54240) (re:55523) (di:direct) BSUB0004 Z99107 g2632919 Bacillus subtilis 1423 -11530105

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773002	2933	25089	888	295

Description

6500726248 hypothetical protein:similar to dna-methyltransferase:cytosine-specific (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiP ydiP Bacillus subtilis 1423 -11530106 7000692953 ydip dna-methyltransferase cytosine-specific homolog ydip (db:pir2.dat) A69788 A69788 Bacillus subtilis 1423 -11530106 5500704090 ydip (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:probable modification methlase) (le:6617) (re:7786) (di:direct) AB007637 AB007637 g2521998 Bacillus subtilis 1423 -11530106 7500963964 ydip (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to dna-methyltransferase) (le:55545) (re:56714) (di:direct) BSUB0004 Z99107 g2632920 Bacillus subtilis 1423 -11530106

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773009	2934	25090	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773014	2935	25091	492	163

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773017	2936	25092	408	135

Description

6500726249 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiQ ydiQ Bacillus subtilis 1423 -11530107 7000693224 ydiq hypothetical protein ydiq (db:pir2.dat) B69788 B69788 Bacillus subtilis 1423 -11530107 5500704091 ydiq (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:function unknown) (le:8272) (re:8460) (di:direct) AB007637 AB007637 g2521999 Bacillus subtilis 1423 -11530107 7500964192 ydiq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:57200) (re:57388) (di:direct) BSUB0004 Z99107 g2632921 Bacillus subtilis 1423 -11530107

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773018	2937	25093	528	176

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773325	2938	25094	243	80

Description

6500726250 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiR ydiR Bacillus subtilis 1423 -11530108 7000693225 ydir hypothetical protein ydir (db:pir2.dat) C69788 C69788 Bacillus subtilis 1423 -11530108 5500704092 ydir (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:function unknown) (le:9712) (re:10653) (di:direct) AB007637 AB007637 g2522000 Bacillus subtilis 1423 -11530108 7500964193 ydir (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:58640) (re:59581) (di:direct) BSUB0004 Z99107 g2632922 Bacillus subtilis 1423 -11530108

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773328	2939	25095	1716	572

Description

6500726251 hypothetical protein:similar to dna restriction (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydiS ydiS Bacillus subtilis 1423 -11530109 7000692945 ydis dna restriction homolog ydis (db:pir2.dat) D69788 D69788 Bacillus subtilis 1423 -11530109 5500704093 ydis (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:weakly similar to 5-methylcytosine-specific) (le:10685) (re:11716) (di:direct) AB007637 AB007637 g2522001 Bacillus subtilis 1423 -11530109 7500963956 ydis (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to dna restriction) (le:59613) (re:60644) (di:direct) BSUB0004 Z99107 g2632923 Bacillus subtilis 1423 -11530109

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773342	2940	25096	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773355	2941	25097	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773363	2942	25098	864	288

Description

6500726252 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjA ydjA Bacillus subtilis 1423 -11530110 7000693226 ydja hypothetical protein ydja (db:pir2.dat) E69788 E69788 Bacillus subtilis 1423 -11530110 5500704094 ydja (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:function unknown) (le:11719) (re:13116) (di:direct) AB007637 AB007637 g2522002 Bacillus subtilis 1423 -11530110 7500964194 ydja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:60647) (re:62044) (di:direct) BSUB0004 Z99107 g2632924 Bacillus subtilis 1423 -11530110

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773367	2943	25099	1068	355

Description

6500726253 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjB ydjB Bacillus subtilis 1423 -11530111 7000693227 ydjb hypothetical protein ydjb (db:pir2.dat) F69788 F69788 Bacillus subtilis 1423 -11530111 5500704095 ydjb (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:function unknown) (le:13690) (re:14025) (di:direct) AB007637 AB007637 g2522003 Bacillus subtilis 1423 -11530111 7500964195 ydjb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:62618) (re:62953) (di:direct) BSUB0004 Z99107 g2632925 Bacillus subtilis 1423 -11530111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773374	2944	25100	306	101

Description

6500726254 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjC ydjC Bacillus subtilis 1423 -11530112 7000693228 ydjc hypothetical protein ydjc (db:pir2.dat) G69788 G69788 Bacillus subtilis 1423 -11530112 5500704096 ydjc (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing groes to gutr region, 48degree.) (nt:function unknown) (le:14408) (re:14758) (di:direct) AB007637 AB007637 g2522004 Bacillus subtilis 1423 -11530112 7500964196 ydjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:63336) (re:63686) (di:direct) BSUB0004 Z99107 g2632926 Bacillus subtilis 1423 -11530112

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773376	2945	25101	285	94

Description

6500726255 hypothetical protein:similar to h+-symporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjD ydjD Bacillus subtilis 1423 -11530113 5500704097 guta (de:putative sugar transport protein guta) (db:swissprot) GUTA_BACSU O34368 BACILLUS SUBTILIS 1423 -11530113 7000693079 ydjd h+-symporter homolog ydjd (cl:melibiose carrier protein) (db:pir2.dat) H69788 H69788 Bacillus subtilis 1423 -11530113 7500964043 guta sugar transport protein (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:putative) (le:93) (re:1484) (di:direct) AB007638 AB007638 g2522008 Bacillus subtilis 1423 -11530113 7502851648 ydjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to h+-symporter) (le:67618) (re:69009) (di:direct) BSUB0004 Z99107 g2632929 Bacillus subtilis 1423 -11530113

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773383	2946	25102	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773388	2947	25103	315	105

Description

6500726256 hypothetical protein:similar to fructokinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjE ydjE Bacillus subtilis 1423 -11530114 5500704098 ydje:fruc (de:hypothetical sugar kinase in guta-cota intergenic region) (db:swissprot) YDJE_BACSU O34768 BACILLUS SUBTILIS 1423 -11530114 7000693009 ydje fructokinase homolog ydje (cl:ribokinase) (db:pir2.dat) A69789 A69789 Bacillus subtilis 1423 -11530114 7500963996 fruc sugar transport protein (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:putative) (le:1579) (re:2541) (di:direct) AB007638 AB007638 g2522009 Bacillus subtilis 1423 -11530114 7502851649 ydje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to fructokinase) (le:69104) (re:70066) (di:direct) BSUB0004 Z99107 g2632930 Bacillus subtilis 1423 -11530114

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773395	2948	25104	888	295

Description

6500726257 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjF ydjF Bacillus subtilis 1423 -11530115 7000692456 ydjf conserved hypothetical protein ydjf (db:pir2.dat) B69789 B69789 Bacillus subtilis 1423 -11530115 5500704099 ydjf membrane protein (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:putative) (le:2737) (re:3420) (di:direct) AB007638 AB007638 g2522010 Bacillus subtilis 1423 -11530115 7500963610 ydjf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:70262) (re:70945) (di:direct) BSUB0004 Z99107 g2632931 Bacillus subtilis 1423 -11530115

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773396	2949	25105	294	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773401	2950	25106	201	66

Description

6500726258 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjG ydjG Bacillus subtilis 1423 -11530116 7000693229 ydjg hypothetical protein ydjg (db:pir2.dat) C69789 C69789 Bacillus subtilis 1423 -11530116 5500704100 ydjg (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:function unknown) (le:3486) (re:4511) (di:direct) AB007638 AB007638 g2522011 Bacillus subtilis 1423 -11530116 7500964197 ydjg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:71011) (re:72036) (di:direct) BSUB0004 Z99107 g2632932 Bacillus subtilis 1423 -11530116

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773403	2951	25107	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773416	2952	25108	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773419	2953	25109	561	186

Description

6500726259 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjH ydjH Bacillus subtilis 1423 -11530117 7000693230 ydjh hypothetical protein ydjh (db:pir2.dat) D69789 D69789 Bacillus subtilis 1423 -11530117 5500704101 ydjh (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:function unknown) (le:4511) (re:5275) (di:direct) AB007638 AB007638 g2522012 Bacillus subtilis 1423 -11530117 7500964198 ydjh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:72036) (re:72800) (di:direct) BSUB0004 Z99107 g2632933 Bacillus subtilis 1423 -11530117

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773430	2954	25110	1089	362

Description

6500726260 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjI ydjI Bacillus subtilis 1423 -11530118 7000693231 ydji hypothetical protein ydji (db:pir2.dat) E69789 E69789 Bacillus subtilis 1423 -11530118 5500704102 ydji (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:function unknown) (le:5306) (re:6277) (di:direct) AB007638 AB007638 g2522013 Bacillus subtilis 1423 -11530118 7500964199 ydji (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:72831) (re:73802) (di:direct) BSUB0004 Z99107 g2632934 Bacillus subtilis 1423 -11530118

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773443	2955	25111	1017	339

Description

6500726261 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjJ ydjJ Bacillus subtilis 1423 -11530119 7000693232 ydjj hypothetical protein ydjj (db:pir2.dat) F69789 F69789 Bacillus subtilis 1423 -11530119 5500704103 ydjj (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:function unknown) (le:6324) (re:7349) (di:complement) AB007638 AB007638 g2522014 Bacillus subtilis 1423 -11530119 7500964200 ydjj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:73849) (re:74874) (di:complement) BSUB0004 Z99107 g2632935 Bacillus subtilis 1423 -11530119

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773454	2956	25112	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773469	2957	25113	228	75

Description

6500726262 hypothetical protein:similar to sugar transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjK ydjK Bacillus subtilis 1423 -11530120 7000694650 ydjk sugar transporter homolog ydjk (cl:glucose transport protein) (db:pir2.dat) G69789 G69789 Bacillus subtilis 1423 -11530120 5500704104 ydjk metabolite transport protein (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:putative) (le:7934) (re:9355) (di:direct) AB007638 AB007638 g2522015 Bacillus subtilis 1423 -11530120 7500965234 ydjk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to sugar transporter) (le:75459) (re:76880) (di:direct) BSUB0004 Z99107 g2632936 Bacillus subtilis 1423 -11530120

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773471	2958	25114	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773472	2959	25115	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773473	2960	25116	288	95

Description

GTC ORF with score 342 to: (fn:high-copy number suppressor of the prp20) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:yeast gtp-binding protein (gsp2) gene, complete cds.) (nt:putative) (le:555) (re:1217) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773475	2961	25117	288	95

Description

6500726263 hypothetical protein:similar to l-iditol 2-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjL ydjL Bacillus subtilis 1423 -11530121 7000694149 ydjl l-iditol 2-dehydrogenase:homolog ydjl:sorbitol dehydrogenase homolog (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.14) (db:pir1.dat) H69789 H69789 Bacillus subtilis 1423 -11530121 5500704105 ydjl dehydrogenase (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:putative) (le:9403) (re:10443) (di:complement) AB007638 AB007638 g2522016 Bacillus subtilis 1423 -11530121 7500953161 ydjl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to l-iditol 2-dehydrogenase) (le:76928) (re:77968) (di:complement) BSUB0004 Z99107 g2632937 Bacillus subtilis 1423 -11530121

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773484	2962	25118	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773497	2963	25119	660	219

Description

6500726264 yzva:ydjm hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjM ydjM Bacillus subtilis 1423 -11530122 7000692457 ydjm conserved hypothetical protein ydjm (db:pir2.dat) A69790 A69790 Bacillus subtilis 1423 -11530122 5500704106 ydjm (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:function unknown) (le:10882) (re:11253) (di:direct) AB007638 AB007638 g2522017 Bacillus subtilis 1423 -11530122 7500963611 ydjm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yzva; similar to hypothetical) (le:78407) (re:78778) (di:direct) BSUB0004 Z99107 g2632938 Bacillus subtilis 1423 -11530122

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773501	2964	25120	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773510	2965	25121	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773513	2966	25122	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773524	2967	25123	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773533	2968	25124	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773538	2969	25125	375	124

Description

GTC ORF with score 193 to: (fn:involved in ribosome assembly) (sr:saccharomyces cerevisiae (strain drs1) dna) (db:genpept-pln1) (de:saccharomyces cerevisiae atp-dependent rna helicase gene, completecds.) (nt:putative) (le:121) (re:2289) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773542	2970	25126	552	183

Description

6500726265 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjN ydjN Bacillus subtilis 1423 -11530123 7000693233 ydjn hypothetical protein ydjn (db:pir2.dat) B69790 B69790 Bacillus subtilis 1423 -11530123 5500704107 ydjn (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:function unknown) (le:11319) (re:12365) (di:direct) AB007638 AB007638 g2522018 Bacillus subtilis 1423 -11530123 7500964201 ydjn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:78844) (re:79890) (di:direct) BSUB0004 Z99107 g2632939 Bacillus subtilis 1423 -11530123

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773548	2971	25127	1344	448

Description

6500726266 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjO ydjO Bacillus subtilis 1423 -11530124 7000693234 ydjo hypothetical protein ydjo (db:pir2.dat) C69790 C69790 Bacillus subtilis 1423 -11530124 5500704109 ydjo (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:function unknown) (le:12747) (re:12956) (di:complement) AB007638 AB007638 g2522020 Bacillus subtilis 1423 -11530124 7500964202 ydjo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:80272) (re:80481) (di:complement) BSUB0004 Z99107 g2632940 Bacillus subtilis 1423 -11530124

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773558	2972	25128	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773560	2973	25129	432	143

Description

6500726267 hypothetical protein:similar to arylesterase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ydjP ydjP Bacillus subtilis 1423 -11530125 7000692232 ydjp probable halide peroxidase:ydjp (ec:1.11.1.-) (db:pir2.dat) D69790 D69790 Bacillus subtilis 1423 -11530125 5500704110 ydjp peroxidase (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:putative) (le:13039) (re:13854) (di:complement) AB007638 AB007638 g2522021 Bacillus subtilis 1423 -11530125 7500963431 ydjp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to arylesterase) (le:80564) (re:81379) (di:complement) BSUB0004 Z99107 g2632941 Bacillus subtilis 1423 -11530125

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773566	2974	25130	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773567	2975	25131	759	252

Description

6500726268 ydjq:yeaa hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeaA yeaA Bacillus subtilis 1423 -11530126 7000693236 yeaa hypothetical protein yeaa (db:pir2.dat) A69791 A69791 Bacillus subtilis 1423 -11530126 5500704111 ydjq peroxidase (sr:bacillus subtilis (strain:marburg 168) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna containing guta to cota region, 48degree.) (nt:putative) (le:13867) (re:14856) (di:complement) AB007638 AB007638 g2522022 Bacillus subtilis 1423 -11530126 7500964204 yeaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: ydjq) (le:81392) (re:82381) (di:complement) BSUB0004 Z99107 g2632942 Bacillus subtilis 1423 -11530126

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773584	2976	25132	543	180

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773885	2977	25133	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773912	2978	25134	561	186

Description

6500726269 ydxt:yeab hypothetical protein:hypothetical 31.8 kd protein in gabp-guaa intergenic region:orfx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeaB yeaB Bacillus subtilis 1423 -11530127 111386 yeab (de:hypothetical 31.8 kd protein in gabp-guaa intergenic region (orfx)) (db:swissprot) YEAB_BACSU P46348 BACILLUS SUBTILIS 1423 -11530127 7000687582 yeab cation efflux system membrane protein homolog yeab (cl:conserved hypothetical protein mj0449) (db:pir2.dat) B69791 B69791 Bacillus subtilis 1423 -11530127 220055 yeab yeab (fn:membrane protein) (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:similar to alcaligenes eutrophu... BSU51115 U51115 g1708640 Bacillus subtilis 1423 -11530127 298013 yeab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: ydxt; similar to cation efflux) (le:85979) (re:86851) (di:direct) BSUB0004 Z99107 g2632945 Bacillus subtilis 1423 -11530127

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773915	2979	25135	1002	333

Description

6500726270 hypothetical protein:similar to methanol dehydrogenase regulation (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeaC yeaC Bacillus subtilis 1423 -11530128 7000694210 yeac methanol dehydrogenase regulation homolog yeac (cl:methanol dehydrogenase regulatory protein) (db:pir2.dat) C69791 C69791 Bacillus subtilis 1423 -11530128 220056 yeac yeac (fn:membrane protein) (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:similar to moxr protein of para... BSU51115 U51115 g1708641 Bacillus subtilis 1423 -11530128 298014 yeac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to methanol dehydrogenase regulation) (le:87004) (re:87966) (di:direct) BSUB0004 Z99107 g2632946 Bacillus subtilis 1423 -11530128

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773918	2980	25136	243	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773929	2981	25137	282	94

Description

GTC ORF with score 128 to: (or:Arabidopsis thaliana) (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f17i5 (essaiiproject).) (nt:strong similarity to extensin-like protein, zea) (le:64328) (re:66427) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773936	2982	25138	564	188

Description

6500726271 hypothetical protein:hypothetical 30.5 kd protein in gabp-guaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeaD yeaD Bacillus subtilis 1423 -11530129 5500686564 yead (de:hypothetical 30.5 kd protein in gabp-guaa intergenic region) (db:swissprot) YEAD_BACSU P94475 BACILLUS SUBTILIS 1423 -11530129 7000687584 yead conserved hypothetical protein yead (db:pir2.dat) D69791 D69791 Bacillus subtilis 1423 -11530129 220057 yead (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (le:6761) (re:7573) (di:direct) BSU51115 U51115 g1708642 Bacillus subtilis 1423 -11530129 298015 yead (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:88350) (re:89162) (di:direct) BSUB0004 Z99107 g2632947 Bacillus subtilis 1423 -11530129

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773941	2983	25139	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773942	2984	25140	324	107

Description

6500726272 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yebA yebA Bacillus subtilis 1423 -11530130 7000692461 yeba conserved hypothetical protein yeba (db:pir2.dat) E69791 E69791 Bacillus subtilis 1423 -11530130 220058 yeba yeba (fn:membrane protein) (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:encodes 5 transmembrane helixes... BSU51115 U51115 g1708643 Bacillus subtilis 1423 -11530130 298016 yeba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:89359) (re:91326) (di:direct) BSUB0004 Z99107 g2632948 Bacillus subtilis 1423 -11530130

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773959	2985	25141	324	107

Description

6500726273 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yebB yebB Bacillus subtilis 1423 -11530131 7000692462 yebb conserved hypothetical protein yebb (cl:conserved hypothetical protein hi0125) (db:pir2.dat) F69791 F69791 Bacillus subtilis 1423 -11530131 4000714506 unknown protein (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:transmembrane protein; similar to hypothetical) (le:1... BSU51115 U51115 g2239289 Bacillus subtilis 1423 -11530131 7500963614 yebb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:93480) (re:94802) (di:direct) BSUB0004 Z99107 g2632950 Bacillus subtilis 1423 -11530131

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773965	2986	25142	756	251

Description

6500726274 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yebC yebC Bacillus subtilis 1423 -11530132 7000693237 yebc hypothetical protein yebc (db:pir2.dat) G69791 G69791 Bacillus subtilis 1423 -11530132 4000714507 unknown (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:yebc; similar to human amp desaminase) (le:13415) (re... BSU51115 U51115 g2239290 Bacillus subtilis 1423 -11530132 7500964205 yebc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:95004) (re:95807) (di:direct) BSUB0004 Z99107 g2632951 Bacillus subtilis 1423 -11530132

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773975	2987	25143	486	161

Description

6500726275 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yebD yebD Bacillus subtilis 1423 -11530133 7000693238 yebd hypothetical protein yebd (db:pir2.dat) H69791 H69791 Bacillus subtilis 1423 -11530133 4000714508 unknown (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:yebd) (le:14377) (re:14598) (di:direct) BSU51115 U51115 g2239291 Bacillus subtilis 1423 -11530133 7500964206 yebd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:95966) (re:96187) (di:direct) BSUB0004 Z99107 g2632952 Bacillus subtilis 1423 -11530133

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501773976	2988	25144	732	244

Description

6500726276 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yebE yebE Bacillus subtilis 1423 -11530134 7000693239 yebe hypothetical protein yebe (db:pir2.dat) A69792 A69792 Bacillus subtilis 1423 -11530134 4000714509 unknown (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:yebe) (le:14761) (re:15003) (di:direct) BSU51115 U51115 g2239292 Bacillus subtilis 1423 -11530134 7500964207 yebe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:96350) (re:96592) (di:direct) BSUB0004 Z99107 g2632953 Bacillus subtilis 1423 -11530134

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774003	2989	25145	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774015	2990	25146	219	72

Description

6500726277 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yebF yebF Bacillus subtilis 1423 -11530135 7000693240 yebf hypothetical protein yebf (db:pir2.dat) B69792 B69792 Bacillus subtilis 1423 -11530135 4000714510 unknown (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:yebf) (le:15046) (re:15312) (di:direct) BSU51115 U51115 g2239293 Bacillus subtilis 1423 -11530135 7500964208 yebf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:96635) (re:96901) (di:direct) BSUB0004 Z99107 g2632954 Bacillus subtilis 1423 -11530135

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774027	2991	25147	684	227

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774039	2992	25148	387	128

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774040	2993	25149	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774048	2994	25150	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774067	2995	25151	717	239

Description

6500726278 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yebG yebG Bacillus subtilis 1423 -11530136 7000693241 yebg hypothetical protein yebg (db:pir2.dat) C69792 C69792 Bacillus subtilis 1423 -11530136 4000714511 unknown (db:genpept-bct1) (de:bacillus subtilis cota (cota), gabp (gabp), yeab (yeab), yeac(yeac), yeba (yeba), gmp synthetase (guaa) genes, complete cds, andair carboxylase i (pure) gene, partial cds.) (nt:yebg) (le:15312) (re:15509) (di:direct) BSU51115 U51115 g2239294 Bacillus subtilis 1423 -11530136 7500964209 yebg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:96901) (re:97098) (di:direct) BSUB0004 Z99107 g2632955 Bacillus subtilis 1423 -11530136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774073	2996	25152	477	158

Description

5000689565 hypothetical protein:hypothetical 9.7 kd protein in pur operon (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yexA yexA Bacillus subtilis 1423 -11530137 111730 yexa (de:hypothetical 9.7 kd protein in purc-purl intergenic region) (db:swissprot) YEXA_BACSU P12049 BACILLUS SUBTILIS 1423 -11530137 7000687671 yexa conserved hypothetical protein yexa:hypothetical protein pur operon (cl:conserved hypothetical protein mj1593) (db:pir2.dat) E29326 E29326 Bacillus subtilis 1423 -11530137 7500923186 yexa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:101124) (re:101378) (di:direct) BSUB0004 Z99107 g2632960 Bacillus subtilis 1423 -11530137 170083 yexa conserved hypothetical protein yexa:hypothetical protein pur operon (db:pir) E29326 E29326 Bacillus subtilis 1423 -11530137 6500726279 hypothetical protein:hypothetical 9.7 kd protein in pur operon (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yexA yexA Bacillus subtilis 1423 -11530137

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774074	2997	25153	189	62

Description

6500726280 hypothetical protein:similar to transcriptional regulator:lrp/asnc family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yezC yezC Bacillus subtilis 1423 -11530138 7000694749 yezc transcription regulator lrp/asnc family homolog yezc (db:pir2.dat) H69799 H69799 Bacillus subtilis 1423 -11530138 7500965320 yezc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (lrp/asnc) (le:110424) (re:110681) (di:complement) BSUB0004 Z99107 g2632968 Bacillus subtilis 1423 -11530138

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774089	2998	25154	1212	404

Description

6500726281 hypothetical protein:similar to amino acid permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yecA yecA Bacillus subtilis 1423 -11530139 7000692196 yeca amino acid permease homolog yeca (db:pir2.dat) D69792 D69792 Bacillus subtilis 1423 -11530139 5500687236 yeca yeca (db:genpept-bct1) (de:bacillus subtilis phosphoribosylaminoimidazole-carboxamideformyltransferase (purh-j) gene, partial cds,phosphoribosylglycinamide synthetase (purd), yeca (yeca), putativeadenine deaminase (yecb), yecc (yecc), and yecd (yecd) genes,... AF011544 AF011544 g2465562 Bacillus subtilis 1423 -11530139 7500963403 yeca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to amino acid permease) (le:110825) (re:112216) (di:direct) BSUB0004 Z99107 g2632969 Bacillus subtilis 1423 -11530139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774112	2999	25155	255	85

Description

6500726282 hypothetical protein:similar to adenine deaminase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerA yerA Bacillus subtilis 1423 -11530140 7502851650 yera:yecb (de:hypothetical 66.6 kd protein in purd-sapb intergenic region) (db:swissprot) YERA_BACSU O34909 BACILLUS SUBTILIS 1423 -11530140 7000692155 yera adenine deaminase homolog yera (db:pir2.dat) H69793 H69793 Bacillus subtilis 1423 -11530140 5500704845 yera (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to adenine deaminase) (le:112470) (re:114212) (di:direct) BSUB0004 Z99107 g2632970 Bacillus subtilis 1423 -11530140 7500963383 yera yera protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (nt:similar to bacillus subtilis adec adenine deaminase) (le:115) (re:1857) (di:direct) BSYERABCD Y15254 g2577960 Bacillus subtilis 1423 -11530140

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774118	3000	25156	315	104

Description

6500726283 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerB yerB Bacillus subtilis 1423 -11530141 7000693246 yerb hypothetical protein yerb (db:pir2.dat) A69794 A69794 Bacillus subtilis 1423 -11530141 5500704846 yerb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:114239) (re:115234) (di:direct) BSUB0004 Z99107 g2632971 Bacillus subtilis 1423 -11530141 7500964214 yerb yerb protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (le:1884) (re:2879) (di:direct) BSYERABCD Y15254 g2577961 Bacillus subtilis 1423 -11530141

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774122	3001	25157	222	73

Description

6500726284 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerC yerC Bacillus subtilis 1423 -11530142 7000693247 yerc hypothetical protein yerc (db:pir2.dat) B69794 B69794 Bacillus subtilis 1423 -11530142 5500687239 yecd yecd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis phosphoribosylaminoimidazole-carboxamideformyltransferase (purh-j) gene, partial cds,phosphoribosylglycinamide synthetase (purd), yeca (yeca), putativeadenine deaminase (yecb), yecc (yecc), and yecd ... AF011544 AF011544 g2465565 Bacillus subtilis 1423 -11530142 5500687240 yerc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:115237) (re:115551) (di:direct) BSUB0004 Z99107 g2632972 Bacillus subtilis 1423 -11530142 7500964215 yerc yerc protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (le:2882) (re:3196) (di:direct) BSYERABCD Y15254 g2577962 Bacillus subtilis 1423 -11530142

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774124	3002	25158	390	129

Description

6500726285 hypothetical protein:similar to glutamate synthase:ferredoxin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerD yerD Bacillus subtilis 1423 -11530143 7000693046 yerd glutamate synthase ferredoxin homolog yerd (db:pir2.dat) C69794 C69794 Bacillus subtilis 1423 -11530143 5500704847 yerd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to glutamate synthase (ferredoxin)) (le:115586) (re:117163) (di:complement) BSUB0004 Z99107 g2632973 Bacillus subtilis 1423 -11530143 7500964023 yerd yerd protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (nt:similar to plectonema boryanum large subunit of) (le:3231) (re:4808) (di:complement) BSYERABCD Y15254 g2577963 Bacillus subtilis 1423 -11530143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774125	3003	25159	468	156

Description

6500726286 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerE yerE Bacillus subtilis 1423 -11530144 7000692467 yere conserved hypothetical protein yere (cl:pcrb protein) (db:pir2.dat) D69794 D69794 Bacillus subtilis 1423 -11530144 5500704848 yere (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:117428) (re:118114) (di:direct) BSUB0004 Z99107 g2632974 Bacillus subtilis 1423 -11530144 7500963619 pcrb pcrb protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (nt:similar to staphylococcus aureus pcrb (acc. no.) (le:5073) (re:5759) (di:direct) BSYERABCD Y15254 g2577964 Bacillus subtilis 1423 -11530144

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774426	3004	25160	957	319

Description

6500726287 hypothetical protein:similar to atp-dependent dna helicase (gtcfc:14.1) (ec:3.6.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerF yerF Bacillus subtilis 1423 -11530145 7000692248 yerf atp-dependent dna helicase homolog yerf (cl:helicase ii) (db:pir2.dat) E69794 E69794 Bacillus subtilis 1423 -11530145 5500704849 yerf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to atp-dependent dna helicase) (le:118176) (re:120395) (di:direct) BSUB0004 Z99107 g2632975 Bacillus subtilis 1423 -11530145 7500963440 pcra pcra protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (nt:similar to staphylococcus aureus pcra dna-helicase) (le:5821) (re:8040) (di:direct) BSYERABCD Y15254 g2577965 Bacillus subtilis 1423 -11530145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774435	3005	25161	303	100

Description

6500726288 hypothetical protein:similar to dna ligase (gtcfc:14.1) (ec:6.5.1.2) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerG yerG Bacillus subtilis 1423 -11530146 7000692930 yerg dna ligase nad+ (cl:polydeoxyribonucleotide synthase (nad+)) (ec:6.5.1.2) (db:pir1.dat) F69794 F69794 Bacillus subtilis 1423 -11530146 7500953391 yerg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to dna ligase) (le:120419) (re:122425) (di:direct) BSUB0004 Z99107 g2632976 Bacillus subtilis 1423 -11530146

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774437	3006	25162	693	230

Description

6500726289 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerH yerH Bacillus subtilis 1423 -11530147 7000693248 yerh hypothetical protein yerh (db:pir2.dat) G69794 G69794 Bacillus subtilis 1423 -11530147 5500704850 yerh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:122441) (re:123631) (di:direct) BSUB0004 Z99107 g2632977 Bacillus subtilis 1423 -11530147 7500964216 yerh yerh protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (le:10086) (re:11276) (di:direct) BSYERABCD Y15254 g2577966 Bacillus subtilis 1423 -11530147

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774445	3007	25163	1107	369

Description

6500726290 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerI yerI Bacillus subtilis 1423 -11530148 7000693249 yeri hypothetical protein yeri (db:pir2.dat) H69794 H69794 Bacillus subtilis 1423 -11530148 5500704851 yeri (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:123793) (re:124803) (di:direct) BSUB0004 Z99107 g2632978 Bacillus subtilis 1423 -11530148 7500964217 yeri yeri protein (db:genpept-bct2) (de:bacillus subtilis 13kb dna fragment, from yera to sapb gene.) (le:11438) (re:12448) (di:direct) BSYERABCD Y15254 g2577967 Bacillus subtilis 1423 -11530148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774461	3008	25164	198	65

Description

6500726291 hypothetical protein:sapb protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) sapB sapB Bacillus subtilis 1423 -11530149 5500685953 sapb (de:sapb protein) (db:swissprot) SAPB_BACSU Q45514 BACILLUS SUBTILIS 1423 -11530149 7000686556 sapb mutant activates alkaline phosphatase during sporulation indep sapb (cl:mg2+-transporting atpase) (db:pir2.dat) G69703 G69703 Bacillus subtilis 1423 -11530149 220139 sapb sapb (db:genpept-bct1) (de:bacillus subtilis sapb (sapb), opue (opue), yeda (yeda) genes,complete cds, and yedb (yedb) gene, partial cds.) (le:163) (re:861) (di:complement) AF011545 AF011545 g2465555 Bacillus subtilis 1423 -11530149 5500685954 sapb sapb (sr:bacillus subtilis strain=168) (db:genpept-bct1) (de:bacillus subtilis sapb gene, complete cds.) (nt:initiates at ttg as formyl-methionine; mutant) (le:510) (re:1208) (di:direct) BSU59128 U59128 g1399815 Bacillus subtilis 1423 -11530149 7500891310 sapb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:mutant activates alkaline phosphatase during) (le:124841) (re:125539) (di:complement) BSUB0004 Z99107 g2632979 Bacillus subtilis 1423 -11530149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774480	3009	25165	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774495	3010	25166	879	292

Description

6500726292 yeda:yerl hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerL yerL Bacillus subtilis 1423 -11530150 7000692468 yerl conserved hypothetical protein yerl (cl:probable glu-trna amidotransferase c chain) (db:pir2.dat) A69795 A69795 Bacillus subtilis 1423 -11530150 1500696452 gatc glu-trnagln amidotransferase subunit c (db:genpept-bct1) (de:bacillus subtilis glu-trnagln amidotransferase subunits c (gatc), a(gata) and b (gatb) genes, complete cds.) (le:412) (re:702) (di:direct) AF008553 AF008553 g2589194 Bacillus subtilis 1423 -11530150 5500687787 (db:genpept-bct1) (de:bacillus subtilis strain jh642 amidase-like protein, partial cds,osmoregulated proline transporter (opue) gene, complete cds andsapb (sapb) gene, partial cds.) (nt:similar to synechocystis sp. hypothetical protein,) (le:278) (re:5... BSU92466 U92466 g2114425 Bacillus subtilis 1423 -11530150 7500963620 yerl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yeda; similar to hypothetical) (le:127538) (re:127828) (di:direct) BSUB0004 Z99107 g2632981 Bacillus subtilis 1423 -11530150

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774500	3011	25167	723	241

Description

6500726293 yedb:yerm hypothetical protein:similar to amidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerM yerM Bacillus subtilis 1423 -11530151 7000692183 yerm amidase homolog yerm (cl:indoleacetamide hydrolase) (db:pir2.dat) B69795 B69795 Bacillus subtilis 1423 -11530151 7500954385 yerm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yedb; similar to amidase) (le:127844) (re:129301) (di:direct) BSUB0004 Z99107 g2632982 Bacillus subtilis 1423 -11530151

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774518	3012	25168	255	84

Description

6500726294 hypothetical protein:similar to pet112-like protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerN yerN Bacillus subtilis 1423 -11530152 7000694364 yern pet112-like protein homolog yern (cl:pet112 protein) (db:pir2.dat) C69795 C69795 Bacillus subtilis 1423 -11530152 7500965050 yern (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to pet112-like protein) (le:129492) (re:130745) (di:direct) BSUB0004 Z99107 g2632983 Bacillus subtilis 1423 -11530152

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774519	3013	25169	1266	421

Description

6500726295 hypothetical protein:similar to transcriptional regulator:tetr/acrr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerO yerO Bacillus subtilis 1423 -11530153 7000694784 yero transcription regulator tetr/acrr family homolog yero (db:pir2.dat) D69795 D69795 Bacillus subtilis 1423 -11530153 7500965346 yero (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (tetr/acrr) (le:130760) (re:131629) (di:complement) BSUB0004 Z99107 g2632984 Bacillus subtilis 1423 -11530153

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774528	3014	25170	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774532	3015	25171	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774541	3016	25172	1017	338

Description

6500726296 hypothetical protein:similar to acriflavin resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerP yerP Bacillus subtilis 1423 -11530154 7000692147 yerp acriflavin resistance protein homolog yerp (db:pir2.dat) E69795 E69795 Bacillus subtilis 1423 -11530154 7500963375 yerp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to acriflavin resistance protein) (le:131722) (re:134919) (di:direct) BSUB0004 Z99107 g2632985 Bacillus subtilis 1423 -11530154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774547	3017	25173	561	186

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774566	3018	25174	543	180

Description

6500726297 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yerQ yerQ Bacillus subtilis 1423 -11530155 7000692469 yerq conserved hypothetical protein yerq (db:pir2.dat) F69795 F69795 Bacillus subtilis 1423 -11530155 7500963621 yerq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:135242) (re:136153) (di:direct) BSUB0004 Z99107 g2632986 Bacillus subtilis 1423 -11530155

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774567	3019	25175	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774568	3020	25176	282	93

Description

6500726298 yers:yefa hypothetical protein:similar to rna methyltransferase (gtcfc:14.1) (ec:2.1.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yefA yefA Bacillus subtilis 1423 -11530156 7000694550 yefa rna methyltransferase homolog yefa (db:pir2.dat) E69793 E69793 Bacillus subtilis 1423 -11530156 7500965163 yefa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yers; similar to rna) (le:136409) (re:137788) (di:direct) BSUB0004 Z99107 g2632987 Bacillus subtilis 1423 -11530156

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774582	3021	25177	825	274

Description

6500726299 hypothetical protein:similar to site-specific recombinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yefB yefB Bacillus subtilis 1423 -11530157 7000694590 yefb site-specific recombinase homolog yefb (db:pir2.dat) F69793 F69793 Bacillus subtilis 1423 -11530157 5500687248 yefb yefb (db:genpept-bct1) (de:bacillus subtilis strain 168 trpc2 yefa (yefa) gene, partial cds,and yefb (yefb), yefc (yefc), yeea (yeea), yeeb (yeeb), yeec(yeec), yeed (yeed), yeee (yeee) and yeef (yeef) genes, completecds.) (le:227) (re:1129) (di:complement) AF012532 AF012532 g2318059 Bacillus subtilis 1423 -11530157 7500965189 yefb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to site-specific recombinase) (le:137801) (re:138703) (di:complement) BSUB0004 Z99107 g2632988 Bacillus subtilis 1423 -11530157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774600	3022	25178	432	143

Description

6500726300 hypothetical protein:similar to resolvase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yefC yefC Bacillus subtilis 1423 -11530158 7000694493 yefc resolvase homolog yefc (db:pir2.dat) G69793 G69793 Bacillus subtilis 1423 -11530158 5500687249 yefc yefc (db:genpept-bct1) (de:bacillus subtilis strain 168 trpc2 yefa (yefa) gene, partial cds,and yefb (yefb), yefc (yefc), yeea (yeea), yeeb (yeeb), yeec(yeec), yeed (yeed), yeee (yeee) and yeef (yeef) genes, completecds.) (nt:similar to enterococcus faecali... AF012532 AF012532 g2318060 Bacillus subtilis 1423 -11530158 7500965132 yefc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to resolvase) (le:138642) (re:139019) (di:direct) BSUB0004 Z99107 g2632989 Bacillus subtilis 1423 -11530158

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774603	3023	25179	294	97

Description

6500726301 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeA yeeA Bacillus subtilis 1423 -11530159 7000692463 yeea conserved hypothetical protein yeea (db:pir2.dat) E69792 E69792 Bacillus subtilis 1423 -11530159 7500963615 yeea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:139094) (re:141733) (di:direct) BSUB0004 Z99107 g2632990 Bacillus subtilis 1423 -11530159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774604	3024	25180	225	74

Description

6500726302 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeB yeeB Bacillus subtilis 1423 -11530160 7000693242 yeeb hypothetical protein yeeb (db:pir2.dat) F69792 F69792 Bacillus subtilis 1423 -11530160 5500687251 yeeb yeeb (db:genpept-bct1) (de:bacillus subtilis strain 168 trpc2 yefa (yefa) gene, partial cds,and yefb (yefb), yefc (yefc), yeea (yeea), yeeb (yeeb), yeec(yeec), yeed (yeed), yeee (yeee) and yeef (yeef) genes, completecds.) (le:4171) (re:5967) (di:direct) AF012532 AF012532 g2318062 Bacillus subtilis 1423 -11530160 7500964210 yeeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:141745) (re:143541) (di:direct) BSUB0004 Z99107 g2632991 Bacillus subtilis 1423 -11530160

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774605	3025	25181	330	109

Description

6500726303 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeC yeeC Bacillus subtilis 1423 -11530161 7000693243 yeec hypothetical protein yeec (db:pir2.dat) G69792 G69792 Bacillus subtilis 1423 -11530161 5500687252 yeec yeec (db:genpept-bct1) (de:bacillus subtilis strain 168 trpc2 yefa (yefa) gene, partial cds,and yefb (yefb), yefc (yefc), yeea (yeea), yeeb (yeeb), yeec(yeec), yeed (yeed), yeee (yeee) and yeef (yeef) genes, completecds.) (le:6080) (re:7228) (di:direct) AF012532 AF012532 g2318063 Bacillus subtilis 1423 -11530161 7500964211 yeec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:143654) (re:144802) (di:direct) BSUB0004 Z99107 g2632992 Bacillus subtilis 1423 -11530161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774622	3026	25182	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774626	3027	25183	573	190

Description

GTC ORF with score 123 to: (or:Homo sapiens) (sr:human) (db:genpept-pri2) (de:human chromosome 12p13 sequence, complete sequence.) (nt:human dentatorubral and pallidoluysian atrophy) (le:146011:146185:146474) (re:146037:146322:146587) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774630	3028	25184	684	227

Description

GTC ORF with score 141 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774635	3029	25185	432	143

Description

6500726304 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeD yeeD Bacillus subtilis 1423 -11530162 7000693244 yeed hypothetical protein yeed (db:pir2.dat) H69792 H69792 Bacillus subtilis 1423 -11530162 5500687253 yeed yeed (db:genpept-bct1) (de:bacillus subtilis strain 168 trpc2 yefa (yefa) gene, partial cds,and yefb (yefb), yefc (yefc), yeea (yeea), yeeb (yeeb), yeec(yeec), yeed (yeed), yeee (yeee) and yeef (yeef) genes, completecds.) (le:7490) (re:7795) (di:complement) AF012532 AF012532 g2318064 Bacillus subtilis 1423 -11530162 7500964212 yeed (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:145064) (re:145369) (di:complement) BSUB0004 Z99107 g2632993 Bacillus subtilis 1423 -11530162

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774650	3030	25186	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774651	3031	25187	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774677	3032	25188	1173	390

Description

6500726305 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yezA yezA Bacillus subtilis 1423 -11530163 7000693257 yeza hypothetical protein yeza (db:pir2.dat) F69799 F69799 Bacillus subtilis 1423 -11530163 7500964225 yeza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:145436) (re:145642) (di:complement) BSUB0004 Z99107 g2632994 Bacillus subtilis 1423 -11530163

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774959	3033	25189	342	113

Description

6500726306 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeF yeeF Bacillus subtilis 1423 -11530164 7000692464 yeef conserved hypothetical protein yeef (db:pir2.dat) A69793 A69793 Bacillus subtilis 1423 -11530164 7500963616 yeef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:145882) (re:148365) (di:complement) BSUB0004 Z99107 g2632995 Bacillus subtilis 1423 -11530164

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774966	3034	25190	1149	383

Description

6500726307 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeG yeeG Bacillus subtilis 1423 -11530165 7000693245 yeeg hypothetical protein yeeg (db:pir2.dat) B69793 B69793 Bacillus subtilis 1423 -11530165 7500964213 yeeg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:148501) (re:149598) (di:direct) BSUB0004 Z99107 g2632996 Bacillus subtilis 1423 -11530165

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774990	3035	25191	1014	338

Description

6500726308 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeI yeeI Bacillus subtilis 1423 -11530166 7000692465 yeei conserved hypothetical protein yeei (cl:hypothetical protein mg332) (db:pir2.dat) C69793 C69793 Bacillus subtilis 1423 -11530166 7500963617 yeei (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:151216) (re:151938) (di:direct) BSUB0004 Z99107 g2632998 Bacillus subtilis 1423 -11530166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501774997	3036	25192	198	65

Description

6500726309 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yeeK yeeK Bacillus subtilis 1423 -11530167 7000692466 yeek conserved hypothetical protein yeek (db:pir2.dat) D69793 D69793 Bacillus subtilis 1423 -11530167 7500963618 yeek (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:152073) (re:153209) (di:direct) BSUB0004 Z99107 g2632999 Bacillus subtilis 1423 -11530167

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775004	3037	25193	282	94

Description

6500726310 yeel:yese hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesE yesE Bacillus subtilis 1423 -11530168 7000693250 yese hypothetical protein yese (db:pir2.dat) G69795 G69795 Bacillus subtilis 1423 -11530168 7500964218 yese (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yeel) (le:153288) (re:153731) (di:direct) BSUB0004 Z99107 g2633000 Bacillus subtilis 1423 -11530168

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775005	3038	25194	840	279

Description

6500726311 yeem:yfxb:yesf hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesF yesF Bacillus subtilis 1423 -11530169 7000692470 yesf conserved hypothetical protein yesf (db:pir2.dat) H69795 H69795 Bacillus subtilis 1423 -11530169 7500963622 yesf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yeem, yfxb; similar to) (le:153728) (re:154588) (di:direct) BSUB0004 Z99107 g2633001 Bacillus subtilis 1423 -11530169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775014	3039	25195	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775015	3040	25196	561	186

Description

6500726312 yeen:yfxc:yfxd:yesj hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesJ yesJ Bacillus subtilis 1423 -11530170 7000692471 yesj conserved hypothetical protein yesj (db:pir2.dat) A69796 A69796 Bacillus subtilis 1423 -11530170 7500963623 yesj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yeen, yfxc, yfxd; similar to) (le:155919) (re:156461) (di:direct) BSUB0004 Z99107 g2633005 Bacillus subtilis 1423 -11530170

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775019	3041	25197	426	141

Description

GTC ORF with score 210 to: (fn:ribosomal protein) (db:genpept-pln1) (de:filobasidiella neoformans ubiquitin-carboxy extension proteinfusion, complete cds.) (nt:similar to the ubi1 protein of s. cerevisiae) (le:293:390:755:902:1020) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775022	3042	25198	402	133

Description

6500726313 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesK yesK Bacillus subtilis 1423 -11530171 7000693251 yesk hypothetical protein yesk (db:pir2.dat) B69796 B69796 Bacillus subtilis 1423 -11530171 7500964219 yesk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:156397) (re:156786) (di:direct) BSUB0004 Z99107 g2633006 Bacillus subtilis 1423 -11530171

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775026	3043	25199	261	86

Description

6500726314 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesL yesL Bacillus subtilis 1423 -11530172 7000692472 yesl conserved hypothetical protein yesl (cl:bacillus subtilis conserved hypothetical protein yusy) (db:pir2.dat) C69796 C69796 Bacillus subtilis 1423 -11530172 7500963624 yesl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:156901) (re:157530) (di:direct) BSUB0004 Z99107 g2633007 Bacillus subtilis 1423 -11530172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775027	3044	25200	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775034	3045	25201	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775048	3046	25202	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775068	3047	25203	231	76

Description

6500726315 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesM yesM Bacillus subtilis 1423 -11530173 7000694873 yesm two-component sensor histidine kinase homolog yesm (db:pir2.dat) D69796 D69796 Bacillus subtilis 1423 -11530173 7500965410 yesm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to two-component sensor histidine kinase) (le:157527) (re:159260) (di:direct) BSUB0004 Z99107 g2633008 Bacillus subtilis 1423 -11530173

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775069	3048	25204	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775074	3049	25205	417	138

Description

6500726316 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesN yesN Bacillus subtilis 1423 -11530174 7000694844 yesn two-component response regulator yesm homolog yesn) (cl:response regulator homology) (db:pir2.dat) E69796 E69796 Bacillus subtilis 1423 -11530174 7500965393 yesn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to two-component response regulator (yesm)) (le:159260) (re:160366) (di:direct) BSUB0004 Z99107 g2633009 Bacillus subtilis 1423 -11530174

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775075	3050	25206	225	75

Description

6500726317 hypothetical protein:similar to sugar-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesO yesO Bacillus subtilis 1423 -11530175 7000694651 yeso sugar-binding protein homolog yeso (db:pir2.dat) F69796 F69796 Bacillus subtilis 1423 -11530175 7500965235 yeso (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to sugar-binding protein) (le:160515) (re:161753) (di:direct) BSUB0004 Z99107 g2633010 Bacillus subtilis 1423 -11530175

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775082	3051	25207	285	95

Description

6500726318 hypothetical protein:similar to lactose permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesP yesP Bacillus subtilis 1423 -11530176 7000694155 yesp lactose permease homolog yesp (cl:inner membrane protein ugpa) (db:pir2.dat) G69796 G69796 Bacillus subtilis 1423 -11530176 7500964888 yesp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to lactose permease) (le:161750) (re:162679) (di:direct) BSUB0004 Z99107 g2633011 Bacillus subtilis 1423 -11530176

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775104	3052	25208	363	120

Description

GTC ORF with score 171 to: (sr:homo sapiens cerebral cortex cdna to mrna, clone:delta3) (db:genpept-pri2) (de:homo sapiens mrna for protein phosphatase 2a delta (b'') regulatorysubunit, delta3 isoform, complete cds.) (nt:possible splice variant) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775114	3053	25209	1143	381

Description

6500726319 hypothetical protein:similar to lactose permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesQ yesQ Bacillus subtilis 1423 -11530177 7000694156 yesq lactose permease homolog yesq (cl:maltose transport protein malg) (db:pir2.dat) H69796 H69796 Bacillus subtilis 1423 -11530177 7500964889 yesq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to lactose permease) (le:162683) (re:163573) (di:direct) BSUB0004 Z99107 g2633012 Bacillus subtilis 1423 -11530177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775117	3054	25210	687	228

Description

6500726320 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesR yesR Bacillus subtilis 1423 -11530178 7000692473 yesr conserved hypothetical protein yesr (db:pir2.dat) A69797 A69797 Bacillus subtilis 1423 -11530178 7500963625 yesr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:163589) (re:164623) (di:direct) BSUB0004 Z99107 g2633013 Bacillus subtilis 1423 -11530178

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775121	3055	25211	465	154

Description

6500726321 hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesS yesS Bacillus subtilis 1423 -11530179 7000694716 yess transcription regulator arac/xyls family homolog yess (db:pir2.dat) B69797 B69797 Bacillus subtilis 1423 -11530179 7500965292 yess (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (arac/xyls) (le:164646) (re:166931) (di:direct) BSUB0004 Z99107 g2633014 Bacillus subtilis 1423 -11530179

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775132	3056	25212	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775145	3057	25213	402	133

Description

6500726322 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesT yesT Bacillus subtilis 1423 -11530180 7000692474 yest conserved hypothetical protein yest (cl:hypothetical protein yest) (db:pir2.dat) C69797 C69797 Bacillus subtilis 1423 -11530180 7500955866 yest (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:166945) (re:167643) (di:direct) BSUB0004 Z99107 g2633015 Bacillus subtilis 1423 -11530180

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775153	3058	25214	402	133

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775154	3059	25215	540	179

Description

6500726323 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesU yesU Bacillus subtilis 1423 -11530181 7000693252 yesu hypothetical protein yesu (db:pir2.dat) D69797 D69797 Bacillus subtilis 1423 -11530181 7500964220 yesu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:167636) (re:168298) (di:direct) BSUB0004 Z99107 g2633016 Bacillus subtilis 1423 -11530181

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775368	3060	25216	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775391	3061	25217	327	108

Description

6500726324 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesV yesV Bacillus subtilis 1423 -11530182 7000692475 yesv conserved hypothetical protein yesv (cl:bacillus subtilis conserved hypothetical protein yusy) (db:pir2.dat) E69797 E69797 Bacillus subtilis 1423 -11530182 7500963626 yesv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:168295) (re:168921) (di:direct) BSUB0004 Z99107 g2633017 Bacillus subtilis 1423 -11530182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775392	3062	25218	213	70

Description

6500726325 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesW yesW Bacillus subtilis 1423 -11530183 7000692476 yesw conserved hypothetical protein yesw (db:pir2.dat) F69797 F69797 Bacillus subtilis 1423 -11530183 7500963627 yesw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:169042) (re:170904) (di:direct) BSUB0004 Z99107 g2633018 Bacillus subtilis 1423 -11530183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775397	3063	25219	246	82

Description

6500726326 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesX yesX Bacillus subtilis 1423 -11530184 7000692477 yesx conserved hypothetical protein yesx (db:pir2.dat) G69797 G69797 Bacillus subtilis 1423 -11530184 7500963628 yesx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:170950) (re:172788) (di:direct) BSUB0004 Z99107 g2633019 Bacillus subtilis 1423 -11530184

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775404	3064	25220	651	217

Description

6500726327 hypothetical protein:similar to rhamnogalacturonan acetylesterase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesY yesY Bacillus subtilis 1423 -11530185 7000694508 yesy rhamnogalacturonan acetylesterase homolog yesy (cl:hypothetical protein yest) (db:pir2.dat) H69797 H69797 Bacillus subtilis 1423 -11530185 7500955867 yesy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to rhamnogalacturonan acetylesterase) (le:172946) (re:173599) (di:direct) BSUB0004 Z99107 g2633020 Bacillus subtilis 1423 -11530185

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775414	3065	25221	462	153

Description

6500726328 hypothetical protein:similar to beta-galactosidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yesZ yesZ Bacillus subtilis 1423 -11530186 7000692260 yesz beta-galactosidase homolog yesz (cl:bacillus beta-galactosidase) (db:pir2.dat) A69798 A69798 Bacillus subtilis 1423 -11530186 7500954271 yesz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to beta-galactosidase) (le:173607) (re:175598) (di:direct) BSUB0004 Z99107 g2633021 Bacillus subtilis 1423 -11530186

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775427	3066	25222	633	210

Description

6500726329 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetA yetA Bacillus subtilis 1423 -11530187 7000693253 yeta hypothetical protein yeta (db:pir2.dat) B69798 B69798 Bacillus subtilis 1423 -11530187 7500964221 yeta (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:175642) (re:178215) (di:direct) BSUB0004 Z99107 g2633022 Bacillus subtilis 1423 -11530187

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775432	3067	25223	426	141

Description

GTC ORF with score 190 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775441	3068	25224	798	265

Description

6500726330 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetF yetF Bacillus subtilis 1423 -11530188 7000692478 yetf probable membrane protein yetf (cl:probable membrane protein ycap) (db:pir2.dat) C69798 C69798 Bacillus subtilis 1423 -11530188 7500955868 yetf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:183189) (re:183884) (di:direct) BSUB0004 Z99107 g2633027 Bacillus subtilis 1423 -11530188

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775452	3069	25225	345	115

Description

6500726331 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetG yetG Bacillus subtilis 1423 -11530189 7000693254 yetg hypothetical protein yetg (db:pir2.dat) D69798 D69798 Bacillus subtilis 1423 -11530189 7500964222 yetg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:183921) (re:184298) (di:complement) BSUB0004 Z99107 g2633028 Bacillus subtilis 1423 -11530189

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775455	3070	25226	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775457	3071	25227	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775460	3072	25228	747	248

Description

6500726332 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetH yetH Bacillus subtilis 1423 -11530190 7000692479 yeth conserved hypothetical protein yeth (db:pir2.dat) E69798 E69798 Bacillus subtilis 1423 -11530190 7500963629 yeth (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:184351) (re:184713) (di:complement) BSUB0004 Z99107 g2633029 Bacillus subtilis 1423 -11530190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775470	3073	25229	666	221

Description

6500726333 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetI yetI Bacillus subtilis 1423 -11530191 7000692480 yeti conserved hypothetical protein yeti (db:pir2.dat) F69798 F69798 Bacillus subtilis 1423 -11530191 7500963630 yeti (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:184993) (re:186078) (di:direct) BSUB0004 Z99107 g2633030 Bacillus subtilis 1423 -11530191

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775482	3074	25230	519	172

Description

6500726334 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yezB yezB Bacillus subtilis 1423 -11530192 7000692482 yezb conserved hypothetical protein yezb (db:pir2.dat) G69799 G69799 Bacillus subtilis 1423 -11530192 7500963631 yezb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:186084) (re:186368) (di:direct) BSUB0004 Z99107 g2633031 Bacillus subtilis 1423 -11530192

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775483	3075	25231	282	93

Description

6500726335 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yezD yezD Bacillus subtilis 1423 -11530193 7000693258 yezd hypothetical protein yezd (db:pir2.dat) A69800 A69800 Bacillus subtilis 1423 -11530193 7500964226 yezd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:186523) (re:186690) (di:direct) BSUB0004 Z99107 g2633032 Bacillus subtilis 1423 -11530193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775492	3076	25232	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775499	3077	25233	1506	502

Description

6500726336 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetJ yetJ Bacillus subtilis 1423 -11530194 7000693255 yetj hypothetical protein yetj (cl:hypothetical protein yetj) (db:pir2.dat) G69798 G69798 Bacillus subtilis 1423 -11530194 7500964223 yetj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:186800) (re:187444) (di:direct) BSUB0004 Z99107 g2633033 Bacillus subtilis 1423 -11530194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775504	3078	25234	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775506	3079	25235	246	81

Description

6500726337 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetK yetK Bacillus subtilis 1423 -11530195 7000692481 yetk conserved hypothetical protein yetk (cl:hypothetical protein yded) (db:pir2.dat) H69798 H69798 Bacillus subtilis 1423 -11530195 7500955911 yetk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:187444) (re:188436) (di:direct) BSUB0004 Z99107 g2633034 Bacillus subtilis 1423 -11530195

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775517	3080	25236	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775528	3081	25237	273	90

Description

6500726338 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetL yetL Bacillus subtilis 1423 -11530196 7000694765 yetl transcription regulator marr family homolog yetl (db:pir2.dat) A69799 A69799 Bacillus subtilis 1423 -11530196 7500965334 yetl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (marr family)) (le:188460) (re:188963) (di:complement) BSUB0004 Z99107 g2633035 Bacillus subtilis 1423 -11530196

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775529	3082	25238	795	264

Description

6500726339 hypothetical protein:similar to salicylate 1-monooxygenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetM yetM Bacillus subtilis 1423 -11530197 7000694571 yetm salicylate 1-monooxygenase homolog yetm (db:pir2.dat) B69799 B69799 Bacillus subtilis 1423 -11530197 1500696753 yetm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to salicylate 1-monooxygenase) (le:189126) (re:190235) (di:direct) BSUB0004 Z99107 g2633036 Bacillus subtilis 1423 -11530197 7500965171 yfnl (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfnl, yfnk, yfnj, complete cds.) (le:149) (re:1258) (di:direct) D87979 D87979 g2116972 Bacillus subtilis 1423 -11530197

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775536	3083	25239	939	312

Description

6500726340 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetN yetN Bacillus subtilis 1423 -11530198 7000693256 yetn hypothetical protein yetn (db:pir2.dat) C69799 C69799 Bacillus subtilis 1423 -11530198 1500696754 yetn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:190270) (re:191340) (di:complement) BSUB0004 Z99107 g2633037 Bacillus subtilis 1423 -11530198 7500964224 yfnk (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfnl, yfnk, yfnj, complete cds.) (le:1293) (re:2363) (di:complement) D87979 D87979 g2116973 Bacillus subtilis 1423 -11530198

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775557	3084	25240	477	159

Description

GTC ORF with score 385 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775857	3085	25241	426	141

Description

6500726341 yfnj:yeto hypothetical protein:similar to cytochrome p450 / nadph-cytochrome p450 reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yetO yetO Bacillus subtilis 1423 -11530199 7000692899 yeto cytochrome p450 / nadph-cytochrome p450 r homolog yeto (cl:p450 bifunctional enzyme cyp102:flavodoxin homology:nadph--ferrihemoprotein reductase homology) (db:pir2.dat) D69799 D69799 Bacillus subtilis 1423 -11530199 1500696755 yeto (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yfnj; similar to cytochrome) (le:191490) (re:194675) (di:direct) BSUB0004 Z99107 g2633038 Bacillus subtilis 1423 -11530199 7500953863 yfnj (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfnl, yfnk, yfnj, complete cds.) (le:2513) (re:5698) (di:direct) D87979 D87979 g2116974 Bacillus subtilis 1423 -11530199

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775865	3086	25242	336	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775872	3087	25243	474	157

Description

6500726342 yetp:yfni hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnI yfnI Bacillus subtilis 1423 -11530200 7000692506 yfni conserved hypothetical protein yfni (db:pir2.dat) D69815 D69815 Bacillus subtilis 1423 -11530200 1500696651 yfni (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:alternate gene name: yetp; similar to hypothetical) (le:195080) (re:197041) (di:direct) BSUB0004 Z99107 g2633039 Bacillus subtilis 1423 -11530200 7500963644 yfni (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:16150) (re:18111) (di:complement) D86418 D86418 g2116767 Bacillus subtilis 1423 -11530200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775892	3088	25244	612	203

Description

6500726343 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnF yfnF Bacillus subtilis 1423 -11530201 7000692505 yfnf conserved hypothetical protein yfnf (cl:hypothetical protein yfnd) (db:pir2.dat) A69815 A69815 Bacillus subtilis 1423 -11530201 1500696648 yfnf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:199040) (re:199951) (di:direct) BSUB0004 Z99107 g2633042 Bacillus subtilis 1423 -11530201 7500955951 yfnf (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:13240) (re:14151) (di:complement) D86418 D86418 g2116764 Bacillus subtilis 1423 -11530201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775893	3089	25245	270	89

Description

6500726344 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnE yfnE Bacillus subtilis 1423 -11530202 7000693312 yfne hypothetical protein yfne (db:pir2.dat) H69814 H69814 Bacillus subtilis 1423 -11530202 7500964268 yfne (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:199980) (re:201158) (di:direct) BSUB0004 Z99107 g2633043 Bacillus subtilis 1423 -11530202

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775894	3090	25246	270	89

Description

6500726345 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnD yfnD Bacillus subtilis 1423 -11530203 7000692504 yfnd conserved hypothetical protein yfnd (cl:hypothetical protein yfnd) (db:pir2.dat) G69814 G69814 Bacillus subtilis 1423 -11530203 7500955950 yfnd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins from b. subtilis) (le:201159) (re:202094) (di:direct) BSUB0004 Z99107 g2633044 Bacillus subtilis 1423 -11530203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775896	3091	25247	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775909	3092	25248	771	257

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775911	3093	25249	276	91

Description

6500726346 hypothetical protein:similar to fosmidmycin resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnC yfnC Bacillus subtilis 1423 -11530204 7000693007 yfnc fosmidmycin resistance protein homolog yfnc (cl:fosmidmycin resistance protein) (db:pir2.dat) F69814 F69814 Bacillus subtilis 1423 -11530204 1500696645 yfnc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to fosmidmycin resistance protein) (le:202125) (re:203354) (di:complement) BSUB0004 Z99107 g2633045 Bacillus subtilis 1423 -11530204 6000690270 yfnc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to fosmidmycin resistance protein) (le:5) (re:1234) (di:complement) BSUB0005 Z99108 g2633056 Bacillus subtilis 1423 -11530204 7500955914 yfnc (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:9837) (re:11066) (di:direct) D86418 D86418 g2116761 Bacillus subtilis 1423 -11530204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775919	3094	25250	270	90

Description

6500726347 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnB yfnB Bacillus subtilis 1423 -11530205 7000692503 yfnb conserved hypothetical protein yfnb (db:pir2.dat) E69814 E69814 Bacillus subtilis 1423 -11530205 1500696644 yfnb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to hypothetical proteins) (le:203465) (re:204172) (di:complement) BSUB0004 Z99107 g2633046 Bacillus subtilis 1423 -11530205 6000690272 yfnb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:1345) (re:2052) (di:complement) BSUB0005 Z99108 g2633057 Bacillus subtilis 1423 -11530205 7500963643 yfnb (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:9019) (re:9726) (di:direct) D86418 D86418 g2116760 Bacillus subtilis 1423 -11530205

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775958	3095	25251	1077	358

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775971	3096	25252	438	146

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775973	3097	25253	390	130

Description

6500726348 hypothetical protein:similar to metabolite transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfnA yfnA Bacillus subtilis 1423 -11530206 7000694208 yfna metabolite transporter homolog yfna (cl:arginine permease) (db:pir2.dat) D69814 D69814 Bacillus subtilis 1423 -11530206 6000690274 yfna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to metabolite transporter) (le:204264) (re:205649) (di:complement) BSUB0004 Z99107 g2633047 Bacillus subtilis 1423 -11530206 7500964935 yfna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to metabolite transporter) (le:2144) (re:3529) (di:complement) BSUB0005 Z99108 g2633058 Bacillus subtilis 1423 -11530206

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775978	3098	25254	537	178

Description

6500726349 hypothetical protein:similar to benzaldehyde dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmT yfmT Bacillus subtilis 1423 -11530207 7000692259 yfmt benzaldehyde dehydrogenase homolog yfmt (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) C69814 C69814 Bacillus subtilis 1423 -11530207 1500696642 yfmt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to benzaldehyde dehydrogenase) (le:205899) (re:207356) (di:direct) BSUB0004 Z99107 g2633048 Bacillus subtilis 1423 -11530207 6000690276 yfmt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to benzaldehyde dehydrogenase) (le:3779) (re:5236) (di:direct) BSUB0005 Z99108 g2633059 Bacillus subtilis 1423 -11530207 7500963444 yfmt (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:5835) (re:7292) (di:complement) D86418 D86418 g2116758 Bacillus subtilis 1423 -11530207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775983	3099	25255	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775989	3100	25256	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501775991	3101	25257	879	292

Description

6500726350 hypothetical protein:similar to methyl-accepting chemotaxis protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmS yfmS Bacillus subtilis 1423 -11530208 7000694213 yfms methyl-accepting chemotaxis protein homolog yfms (db:pir2.dat) B69814 B69814 Bacillus subtilis 1423 -11530208 1500696641 yfms (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to methyl-accepting chemotaxis protein) (le:207370) (re:208230) (di:direct) BSUB0004 Z99107 g2633049 Bacillus subtilis 1423 -11530208 6000690278 yfms (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to methyl-accepting chemotaxis protein) (le:5250) (re:6110) (di:direct) BSUB0005 Z99108 g2633060 Bacillus subtilis 1423 -11530208 7500964938 yfms (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:4961) (re:5821) (di:complement) D86418 D86418 g2116757 Bacillus subtilis 1423 -11530208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776022	3102	25258	1017	338

Description

6500726351 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmR yfmR Bacillus subtilis 1423 -11530209 7000692086 yfmr abc transporter atp-binding protein homolog yfmr (cl:atp-binding cassette homology) (db:pir2.dat) A69814 A69814 Bacillus subtilis 1423 -11530209 1500696640 yfmr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to abc transporter (atp-binding protein)) (le:208365) (re:210254) (di:direct) BSUB0004 Z99107 g2633050 Bacillus subtilis 1423 -11530209 6000690280 yfmr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:6245) (re:8134) (di:direct) BSUB0005 Z99108 g2633061 Bacillus subtilis 1423 -11530209 7500963325 yfmr (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:2937) (re:4826) (di:complement) D86418 D86418 g2116756 Bacillus subtilis 1423 -11530209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776044	3103	25259	762	253

Description

6500726352 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmQ yfmQ Bacillus subtilis 1423 -11530210 7000693311 yfmq hypothetical protein yfmq (db:pir2.dat) H69813 H69813 Bacillus subtilis 1423 -11530210 1500696639 yfmq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:210377) (re:210823) (di:direct) BSUB0004 Z99107 g2633051 Bacillus subtilis 1423 -11530210 6000690282 yfmq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:8257) (re:8703) (di:direct) BSUB0005 Z99108 g2633062 Bacillus subtilis 1423 -11530210 7500964267 yfmq (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:2368) (re:2814) (di:complement) D86418 D86418 g2116755 Bacillus subtilis 1423 -11530210

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776052	3104	25260	642	214

Description

6500726353 hypothetical protein:similar to transcriptional regulator:merr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmP yfmP Bacillus subtilis 1423 -11530211 7000694775 yfmp transcription regulator merr family homolog yfmp (db:pir2.dat) G69813 G69813 Bacillus subtilis 1423 -11530211 1500696638 yfmp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to transcriptional regulator (merr family)) (le:210948) (re:211370) (di:direct) BSUB0004 Z99107 g2633052 Bacillus subtilis 1423 -11530211 6000690284 yfmp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to transcriptional regulator (merr family)) (le:8828) (re:9250) (di:direct) BSUB0005 Z99108 g2633063 Bacillus subtilis 1423 -11530211 7500965338 yfmp (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:1821) (re:2243) (di:complement) D86418 D86418 g2116754 Bacillus subtilis 1423 -11530211

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776057	3105	25261	1038	345

Description

6500726354 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmO yfmO Bacillus subtilis 1423 -11530212 7000694254 yfmo multidrug-efflux transporter homolog yfmo (db:pir2.dat) F69813 F69813 Bacillus subtilis 1423 -11530212 1500696637 yfmo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (nt:similar to multidrug-efflux transporter) (le:211436) (re:212626) (di:direct) BSUB0004 Z99107 g2633053 Bacillus subtilis 1423 -11530212 6000690286 yfmo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to multidrug-efflux transporter) (le:9316) (re:10506) (di:direct) BSUB0005 Z99108 g2633064 Bacillus subtilis 1423 -11530212 7500964976 yfmo (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:565) (re:1755) (di:complement) D86418 D86418 g2116753 Bacillus subtilis 1423 -11530212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776063	3106	25262	444	148

Description

6500726355 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmN yfmN Bacillus subtilis 1423 -11530213 7000693310 yfmn hypothetical protein yfmn (db:pir2.dat) E69813 E69813 Bacillus subtilis 1423 -11530213 1500696636 yfmn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.) (le:212917) (re:213072) (di:direct) BSUB0004 Z99107 g2633054 Bacillus subtilis 1423 -11530213 5500687927 yfmn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:10797) (re:10952) (di:direct) BSUB0005 Z99108 g2633065 Bacillus subtilis 1423 -11530213 6000690288 yfmn (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:37569) (re:37724) (di:complement) D86417 D86417 g2443257 Bacillus subtilis 1423 -11530213 7500964266 yfmn (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna 69-70 degree region, partialsequence.) (le:119) (re:274) (di:complement) D86418 D86418 g2116752 Bacillus subtilis 1423 -11530213

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776076	3107	25263	261	87

Description

GTC ORF with score 118 to: (sr:human) (db:genpept-pri2) (de:homo sapiens chromosome 9, p1 clone 11659, complete sequence.) (nt:hypothetical 96.6 kda putative membrane protein;) (le:68640:69524:69916) (re:68671:69730:70122) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776092	3108	25264	1332	444

Description

6500726356 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmM yfmM Bacillus subtilis 1423 -11530214 7000692085 yfmm abc transporter atp-binding protein homolog yfmm (cl:atp-binding cassette homology) (db:pir2.dat) D69813 D69813 Bacillus subtilis 1423 -11530214 5500687926 yfmm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:11072) (re:12628) (di:complement) BSUB0005 Z99108 g2633066 Bacillus subtilis 1423 -11530214 7500963324 yfmm (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:35893) (re:37449) (di:direct) D86417 D86417 g2443256 Bacillus subtilis 1423 -11530214

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776093	3109	25265	798	266

Description

6500726357 hypothetical protein:similar to rna helicase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmL yfmL Bacillus subtilis 1423 -11530215 7000694549 yfml rna helicase homolog yfml (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) C69813 C69813 Bacillus subtilis 1423 -11530215 5500687925 yfml (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to rna helicase) (le:12801) (re:13931) (di:direct) BSUB0005 Z99108 g2633067 Bacillus subtilis 1423 -11530215 7500954383 yfml (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:34590) (re:35720) (di:complement) D86417 D86417 g2443255 Bacillus subtilis 1423 -11530215

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776094	3110	25266	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776105	3111	25267	663	220

Description

6500726358 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmK yfmK Bacillus subtilis 1423 -11530216 7000693309 yfmk hypothetical protein yfmk (db:pir2.dat) B69813 B69813 Bacillus subtilis 1423 -11530216 5500687924 yfmk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:13999) (re:14445) (di:direct) BSUB0005 Z99108 g2633068 Bacillus subtilis 1423 -11530216 7500964265 yfmk (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:34076) (re:34522) (di:complement) D86417 D86417 g2443254 Bacillus subtilis 1423 -11530216

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776107	3112	25268	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776111	3113	25269	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776410	3114	25270	477	158

Description

6500726359 hypothetical protein:similar to quinone oxidoreductase (gtcfc:9.12) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmJ yfmJ Bacillus subtilis 1423 -11530217 7000694488 yfmj quinone oxidoreductase homolog yfmj (db:pir2.dat) A69813 A69813 Bacillus subtilis 1423 -11530217 5500687923 yfmj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to quinone oxidoreductase) (le:14498) (re:15517) (di:complement) BSUB0005 Z99108 g2633069 Bacillus subtilis 1423 -11530217 7500965127 yfmj (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:33004) (re:34023) (di:direct) D86417 D86417 g2443253 Bacillus subtilis 1423 -11530217

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776424	3115	25271	618	205

Description

6500726360 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmI yfmI Bacillus subtilis 1423 -11530218 7000692502 yfmi conserved hypothetical protein yfmi (db:pir2.dat) H69812 H69812 Bacillus subtilis 1423 -11530218 5500687922 yfmi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:15999) (re:17219) (di:complement) BSUB0005 Z99108 g2633070 Bacillus subtilis 1423 -11530218 7500963642 yfmi (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:31302) (re:32522) (di:direct) D86417 D86417 g2443252 Bacillus subtilis 1423 -11530218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776434	3116	25272	429	143

Description

6500726361 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmH yfmH Bacillus subtilis 1423 -11530219 7000693308 yfmh hypothetical protein yfmh (db:pir2.dat) G69812 G69812 Bacillus subtilis 1423 -11530219 5500687921 yfmh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:17417) (re:17488) (di:direct) BSUB0005 Z99108 g2633071 Bacillus subtilis 1423 -11530219 7500964264 yfmh (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:31033) (re:31104) (di:complement) D86417 D86417 g2443251 Bacillus subtilis 1423 -11530219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776435	3117	25273	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776447	3118	25274	1113	370

Description

6500726362 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmG yfmG Bacillus subtilis 1423 -11530220 7000693307 yfmg hypothetical protein yfmg (db:pir2.dat) F69812 F69812 Bacillus subtilis 1423 -11530220 5500687920 yfmg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:17555) (re:19018) (di:direct) BSUB0005 Z99108 g2633072 Bacillus subtilis 1423 -11530220 7500964263 yfmg (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:29503) (re:30966) (di:complement) D86417 D86417 g2443250 Bacillus subtilis 1423 -11530220

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776450	3119	25275	198	65

Description

6500726363 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmB yfmB Bacillus subtilis 1423 -11530221 7000693306 yfmb hypothetical protein yfmb (db:pir2.dat) A69812 A69812 Bacillus subtilis 1423 -11530221 5500687915 yfmb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:23531) (re:23899) (di:complement) BSUB0005 Z99108 g2633077 Bacillus subtilis 1423 -11530221 7500964262 yfmb (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:24622) (re:24990) (di:direct) D86417 D86417 g2443245 Bacillus subtilis 1423 -11530221

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776452	3120	25276	264	87

Description

6500726364 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfmA yfmA Bacillus subtilis 1423 -11530222 7000693305 yfma hypothetical protein yfma (db:pir2.dat) H69811 H69811 Bacillus subtilis 1423 -11530222 5500687914 yfma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:23940) (re:24107) (di:direct) BSUB0005 Z99108 g2633078 Bacillus subtilis 1423 -11530222 7500964261 yfma (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:24414) (re:24581) (di:complement) D86417 D86417 g2443244 Bacillus subtilis 1423 -11530222

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776463	3121	25277	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776477	3122	25278	1212	403

Description

6500726365 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflT yflT Bacillus subtilis 1423 -11530223 7000693304 yflt hypothetical protein yflt (db:pir2.dat) G69811 G69811 Bacillus subtilis 1423 -11530223 5500687913 yflt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:24143) (re:24490) (di:direct) BSUB0005 Z99108 g2633079 Bacillus subtilis 1423 -11530223 7500964260 yflt (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:24031) (re:24378) (di:complement) D86417 D86417 g2443243 Bacillus subtilis 1423 -11530223

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776488	3123	25279	441	147

Description

6500726366 hypothetical protein:similar to 2-oxoglutarate/malate translocator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflS yflS Bacillus subtilis 1423 -11530224 7000692039 yfls 2-oxoglutarate/malate translocator homolog yfls (cl:2-oxoglutarate/malate translocator) (db:pir2.dat) F69811 F69811 Bacillus subtilis 1423 -11530224 5500687912 yfls (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to 2-oxoglutarate/malate translocator) (le:26070) (re:27506) (di:direct) BSUB0005 Z99108 g2633081 Bacillus subtilis 1423 -11530224 7500963291 yfls (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:21015) (re:22451) (di:complement) D86417 D86417 g2443241 Bacillus subtilis 1423 -11530224

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776491	3124	25280	459	153

Description

6500726367 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflP yflP Bacillus subtilis 1423 -11530225 7000693303 yflp hypothetical protein yflp (db:pir2.dat) E69811 E69811 Bacillus subtilis 1423 -11530225 5500687909 yflp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:30096) (re:30875) (di:direct) BSUB0005 Z99108 g2633084 Bacillus subtilis 1423 -11530225 7500964259 yflp (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:17646) (re:18425) (di:complement) D86417 D86417 g2443238 Bacillus subtilis 1423 -11530225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776497	3125	25281	516	172

Description

6500726368 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflN yflN Bacillus subtilis 1423 -11530226 7000693302 yfln hypothetical protein yfln (db:pir2.dat) D69811 D69811 Bacillus subtilis 1423 -11530226 5500687907 yfln (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:32428) (re:33222) (di:direct) BSUB0005 Z99108 g2633086 Bacillus subtilis 1423 -11530226 7500964258 yfln (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:15300) (re:16094) (di:complement) D86417 D86417 g2443236 Bacillus subtilis 1423 -11530226

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776505	3126	25282	408	135

Description

6500726369 hypothetical protein:similar to nitric-oxide synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflM yflM Bacillus subtilis 1423 -11530227 7000694325 yflm nitric-oxide synthase homolog yflm (db:pir2.dat) C69811 C69811 Bacillus subtilis 1423 -11530227 5500687906 yflm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to nitric-oxide synthase) (le:33422) (re:34432) (di:direct) BSUB0005 Z99108 g2633087 Bacillus subtilis 1423 -11530227 7500965023 yflm (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:14090) (re:15100) (di:complement) D86417 D86417 g2443235 Bacillus subtilis 1423 -11530227

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776507	3127	25283	522	174

Description

GTC ORF with score 295 to: (db:genpept-bct2) (de:pseudomonas fluorescens cyclohexanone monooxygenase homolog gene,partial cds; lactone-specific esterase (estf1) gene, complete cds;and alkane-1 monooxygenase homolog gene, partial cds.) (nt:orf1) (le:<1)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776509	3128	25284	585	194

Description

6500726370 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflL yflL Bacillus subtilis 1423 -11530228 7500876542 yfll (ec:3.6.1.7) (de:phosphohydrolase)) (db:swissprot) ACYP_BACSU O35031 BACILLUS SUBTILIS 1423 -11530228 7000692501 yfll conserved hypothetical protein yfll (cl:acylphosphatase) (db:pir2.dat) B69811 B69811 Bacillus subtilis 1423 -11530228 7500876544 yfll (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:34423) (re:34698) (di:complement) BSUB0005 Z99108 g2633088 Bacillus subtilis 1423 -11530228 5500687905 yfll (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:13824) (re:14099) (di:direct) D86417 D86417 g2443234 Bacillus subtilis 1423 -11530228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776519	3129	25285	312	103

Description

6500726371 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflK yflK Bacillus subtilis 1423 -11530229 7000692500 yflk conserved hypothetical protein yflk (cl:hypothetical protein hi0278) (db:pir2.dat) A69811 A69811 Bacillus subtilis 1423 -11530229 5500687904 yflk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:34765) (re:35430) (di:direct) BSUB0005 Z99108 g2633089 Bacillus subtilis 1423 -11530229 7500955826 yflk (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:13092) (re:13757) (di:complement) D86417 D86417 g2443233 Bacillus subtilis 1423 -11530229

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776524	3130	25286	642	213

Description

6500726372 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflJ yflJ Bacillus subtilis 1423 -11530230 7000693301 yflj hypothetical protein yflj (db:pir2.dat) H69810 H69810 Bacillus subtilis 1423 -11530230 5500687903 yflj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:35471) (re:35608) (di:complement) BSUB0005 Z99108 g2633090 Bacillus subtilis 1423 -11530230 7500964257 yflj (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:12914) (re:13051) (di:direct) D86417 D86417 g2443232 Bacillus subtilis 1423 -11530230

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776525	3131	25287	696	232

Description

6500726373 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflI yflI Bacillus subtilis 1423 -11530231 7000693300 yfli hypothetical protein yfli (db:pir2.dat) G69810 G69810 Bacillus subtilis 1423 -11530231 5500687902 yfli (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:35765) (re:35920) (di:complement) BSUB0005 Z99108 g2633091 Bacillus subtilis 1423 -11530231 7500964256 yfli (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:12602) (re:12757) (di:direct) D86417 D86417 g2443231 Bacillus subtilis 1423 -11530231

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776536	3132	25288	585	194

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776545	3133	25289	336	112

Description

6500726374 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflH yflH Bacillus subtilis 1423 -11530232 7000692499 yflh conserved hypothetical protein yflh (cl:hypothetical protein yflh) (db:pir2.dat) F69810 F69810 Bacillus subtilis 1423 -11530232 5500687901 yflh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins from b. subtilis) (le:36027) (re:36341) (di:complement) BSUB0005 Z99108 g2633092 Bacillus subtilis 1423 -11530232 7500955912 yflh (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:12181) (re:12495) (di:direct) D86417 D86417 g2443230 Bacillus subtilis 1423 -11530232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776548	3134	25290	420	140

Description

6500726375 hypothetical protein:similar to methionine aminopeptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflG yflG Bacillus subtilis 1423 -11530233 7000694211 yflg methionine aminopeptidase homolog yflg (cl:escherichia coli methionyl aminopeptidase) (db:pir2.dat) E69810 E69810 Bacillus subtilis 1423 -11530233 5500687900 yflg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to methionine aminopeptidase) (le:36423) (re:37172) (di:complement) BSUB0005 Z99108 g2633093 Bacillus subtilis 1423 -11530233 7500964936 yflg (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:11350) (re:12099) (di:direct) D86417 D86417 g2443229 Bacillus subtilis 1423 -11530233

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776550	3135	25291	1044	347

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776572	3136	25292	657	218

Description

GTC ORF with score 139 to: (sr:clostridium thermosulfurogenes (library: genomic in puc 18; ds) (db:genpept-bct1) (ec:3.2.1.23) (de:clostridium thermosulfurogenes beta-galactosidase (lacz) gene,complete cds.) (le:252) (re:2402) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776574	3137	25293	564	187

Description

GTC ORF with score 172 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776600	3138	25294	924	307

Description

6500726376 hypothetical protein:similar to phosphotransferase system enzyme ii (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflF yflF Bacillus subtilis 1423 -11530234 7000694424 yflf phosphotransferase system enzyme ii:factor ii homolog yflf (cl:phosphotransferase system glucose-specific enzyme ii, factor ii:phosphotransferase system glucose-specific enzyme ii, factor ii homology) (ec:2.7.1.69) (db:pir2.dat) D69810 D69810 Bacillus subtilis 1423 -11530234 5500687899 yflf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to phosphotransferase system enzyme ii) (le:37344) (re:38702) (di:direct) BSUB0005 Z99108 g2633094 Bacillus subtilis 1423 -11530234 7500965080 yflf (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:9820) (re:11178) (di:complement) D86417 D86417 g2443228 Bacillus subtilis 1423 -11530234

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776606	3139	25295	1236	412

Description

6500726377 hypothetical protein:similar to anion-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflE yflE Bacillus subtilis 1423 -11530235 7000692210 yfle anion-binding protein homolog yfle (db:pir2.dat) C69810 C69810 Bacillus subtilis 1423 -11530235 5500687898 yfle (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to anion-binding protein) (le:38735) (re:40684) (di:complement) BSUB0005 Z99108 g2633095 Bacillus subtilis 1423 -11530235 7500963417 yfle (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:7838) (re:9787) (di:direct) D86417 D86417 g2443227 Bacillus subtilis 1423 -11530235

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776628	3140	25296	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776631	3141	25297	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776638	3142	25298	525	174

Description

GTC ORF with score 111 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f6i18 (essaiiproject).) (nt:similarity to various predicted proteins) (le:99829:100130:100273) (re:100055:100228:100404) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776653	3143	25299	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776921	3144	25300	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776923	3145	25301	603	201

Description

GTC ORF with score 698 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c3h8.) (nt:spac3h8.10, sec14 homologue, len: 286, similar to) (le:23063:23270:23769:23955) (re:23221:23572:23891:24230) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776924	3146	25302	306	101

Description

GTC ORF with score 175 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c3h8.) (nt:spac3h8.10, sec14 homologue, len: 286, similar to) (le:23063:23270:23769:23955) (re:23221:23572:23891:24230) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776928	3147	25303	315	104

Description

GTC ORF with score 172 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c3h8.) (nt:spac3h8.10, sec14 homologue, len: 286, similar to) (le:23063:23270:23769:23955) (re:23221:23572:23891:24230) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776944	3148	25304	378	125

Description

6500726378 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflD yflD Bacillus subtilis 1423 -11530236 7000693299 yfld hypothetical protein yfld (db:pir2.dat) B69810 B69810 Bacillus subtilis 1423 -11530236 5500687897 yfld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:40785) (re:40922) (di:direct) BSUB0005 Z99108 g2633096 Bacillus subtilis 1423 -11530236 7500964255 yfld (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:7600) (re:7737) (di:complement) D86417 D86417 g2443226 Bacillus subtilis 1423 -11530236

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776947	3149	25305	285	95

Description

6500726379 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflC yflC Bacillus subtilis 1423 -11530237 7000693298 yflc hypothetical protein yflc (db:pir2.dat) A69810 A69810 Bacillus subtilis 1423 -11530237 5500687896 yflc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:40938) (re:41090) (di:direct) BSUB0005 Z99108 g2633097 Bacillus subtilis 1423 -11530237 7500964254 yflc (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:7432) (re:7584) (di:complement) D86417 D86417 g2443225 Bacillus subtilis 1423 -11530237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776950	3150	25306	315	104

Description

6500726380 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflB yflB Bacillus subtilis 1423 -11530238 7000693297 yflb hypothetical protein yflb (db:pir2.dat) H69809 H69809 Bacillus subtilis 1423 -11530238 5500687895 yflb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:41072) (re:41332) (di:direct) BSUB0005 Z99108 g2633098 Bacillus subtilis 1423 -11530238 7500964253 yflb (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:7190) (re:7450) (di:complement) D86417 D86417 g2443224 Bacillus subtilis 1423 -11530238

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776961	3151	25307	570	189

Description

6500726381 hypothetical protein:similar to aminoacid carrier protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yflA yflA Bacillus subtilis 1423 -11530239 7000692203 yfla aminoacid carrier protein homolog yfla (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) G69809 G69809 Bacillus subtilis 1423 -11530239 5500687894 yfla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to aminoacid carrier protein) (le:41457) (re:42872) (di:direct) BSUB0005 Z99108 g2633099 Bacillus subtilis 1423 -11530239 7500963411 yfla (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:5650) (re:7065) (di:complement) D86417 D86417 g2443223 Bacillus subtilis 1423 -11530239

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776978	3152	25308	402	133

Description

6500726382 hypothetical protein:similar to spore germination protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkT yfkT Bacillus subtilis 1423 -11530240 7000694626 yfkt spore germination protein homolog yfkt (db:pir2.dat) F69809 F69809 Bacillus subtilis 1423 -11530240 5500687893 yfkt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to spore germination protein) (le:42869) (re:43945) (di:complement) BSUB0005 Z99108 g2633100 Bacillus subtilis 1423 -11530240 7500965221 yfkt (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:4577) (re:5653) (di:direct) D86417 D86417 g2443222 Bacillus subtilis 1423 -11530240

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776979	3153	25309	1170	389

Description

6500726383 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkS yfkS Bacillus subtilis 1423 -11530241 7000693296 yfks hypothetical protein yfks (db:pir2.dat) E69809 E69809 Bacillus subtilis 1423 -11530241 5500687892 yfks (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:43969) (re:44169) (di:complement) BSUB0005 Z99108 g2633101 Bacillus subtilis 1423 -11530241 7500964252 yfks (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:4353) (re:4553) (di:direct) D86417 D86417 g2443221 Bacillus subtilis 1423 -11530241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501776993	3154	25310	741	246

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777009	3155	25311	1164	388

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777019	3156	25312	459	152

Description

6500726384 hypothetical protein:similar to spore germination protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkR yfkR Bacillus subtilis 1423 -11530242 7000694625 yfkr spore germination protein homolog yfkr (db:pir2.dat) D69809 D69809 Bacillus subtilis 1423 -11530242 5500687891 yfkr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to spore germination protein) (le:44185) (re:45339) (di:complement) BSUB0005 Z99108 g2633102 Bacillus subtilis 1423 -11530242 7500965220 yfkr (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:3183) (re:4337) (di:direct) D86417 D86417 g2443220 Bacillus subtilis 1423 -11530242

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777020	3157	25313	720	239

Description

6500726385 hypothetical protein:similar to spore germination response (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkQ yfkQ Bacillus subtilis 1423 -11530243 7000694630 yfkq spore germination response homolog yfkq (cl:spore germination protein gerba) (db:pir2.dat) C69809 C69809 Bacillus subtilis 1423 -11530243 5500687890 yfkq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to spore germination response) (le:45320) (re:46861) (di:complement) BSUB0005 Z99108 g2633103 Bacillus subtilis 1423 -11530243 7500965223 yfkq (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis 35.7 kb genomic dna, 70-73 degree region,complete cds.) (le:1661) (re:3202) (di:direct) D86417 D86417 g2443219 Bacillus subtilis 1423 -11530243

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777028	3158	25314	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777029	3159	25315	717	238

Description

6500726386 hypothetical protein:similar to nad:ph-flavin oxidoreductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkO yfkO Bacillus subtilis 1423 -11530244 7502851651 yfko (ec:1.-.-.-) (de:putative nad(p)h nitroreductase yfko,) (db:swissprot) YFKO_BACSU O34475 BACILLUS SUBTILIS 1423 -11530244 7000694302 yfko nad p h-flavin oxidoreductase homolog yfko (cl:nitroreductase) (db:pir2.dat) B69809 B69809 Bacillus subtilis 1423 -11530244 6000690330 yfko (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to nad(p)h-flavin oxidoreductase) (le:51099) (re:51764) (di:direct) BSUB0005 Z99108 g2633107 Bacillus subtilis 1423 -11530244 7500965009 yfko (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:16157) (re:16822) (di:complement) D83967 D83967 g2626827 Bacillus subtilis 1423 -11530244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777033	3160	25316	738	246

Description

6500726387 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkM yfkM Bacillus subtilis 1423 -11530245 7000692498 yfkm conserved hypothetical protein yfkm (cl:archaeoglobus intracellular proteinase i) (db:pir2.dat) H69808 H69808 Bacillus subtilis 1423 -11530245 6000690334 yfkm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:56432) (re:56950) (di:direct) BSUB0005 Z99108 g2633109 Bacillus subtilis 1423 -11530245 7500963641 yfkm (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:10971) (re:11489) (di:complement) D83967 D83967 g2626825 Bacillus subtilis 1423 -11530245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777045	3161	25317	666	221

Description

6500726388 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkL yfkL Bacillus subtilis 1423 -11530246 7000694243 yfkl multidrug resistance protein homolog yfkl (cl:hypothetical protein b1691) (db:pir2.dat) G69808 G69808 Bacillus subtilis 1423 -11530246 6000690336 yfkl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to multidrug resistance protein) (le:56990) (re:58180) (di:complement) BSUB0005 Z99108 g2633110 Bacillus subtilis 1423 -11530246 7500964969 yfkl (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:9741) (re:10931) (di:direct) D83967 D83967 g2626824 Bacillus subtilis 1423 -11530246

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777056	3162	25318	261	86

Description

6500726389 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkK yfkK Bacillus subtilis 1423 -11530247 7000693295 yfkk hypothetical protein yfkk (db:pir2.dat) F69808 F69808 Bacillus subtilis 1423 -11530247 6000690338 yfkk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:58273) (re:58488) (di:complement) BSUB0005 Z99108 g2633111 Bacillus subtilis 1423 -11530247 7500964251 yfkk (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:9433) (re:9648) (di:direct) D83967 D83967 g2626823 Bacillus subtilis 1423 -11530247

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777057	3163	25319	420	140

Description

6500726390 hypothetical protein:similar to protein-tyrosine phosphatase (gtcfc:14.1) (ec:3.1.3.48) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkJ yfkJ Bacillus subtilis 1423 -11530248 7000694460 yfkj protein-tyrosine phosphatase homolog yfkj (cl:protein-tyrosine-phosphatase, low molecular weight) (db:pir2.dat) E69808 E69808 Bacillus subtilis 1423 -11530248 6000690340 yfkj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to protein-tyrosine phosphatase) (le:58691) (re:59161) (di:direct) BSUB0005 Z99108 g2633112 Bacillus subtilis 1423 -11530248 7500965110 yfkj (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:8760) (re:9230) (di:complement) D83967 D83967 g2626822 Bacillus subtilis 1423 -11530248

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777085	3164	25320	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777092	3165	25321	297	98

Description

6500726391 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkI yfkI Bacillus subtilis 1423 -11530249 7000693294 yfki hypothetical protein yfki (db:pir2.dat) D69808 D69808 Bacillus subtilis 1423 -11530249 6000690342 yfki (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:59179) (re:59499) (di:direct) BSUB0005 Z99108 g2633113 Bacillus subtilis 1423 -11530249 7500964250 yfki (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:8422) (re:8742) (di:complement) D83967 D83967 g2626821 Bacillus subtilis 1423 -11530249

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777094	3166	25322	378	125

Description

6500726392 hypothetical protein:similar to transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkH yfkH Bacillus subtilis 1423 -11530250 7000694817 yfkh transporter homolog yfkh (db:pir2.dat) C69808 C69808 Bacillus subtilis 1423 -11530250 6000690344 yfkh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to transporter) (le:59523) (re:60350) (di:direct) BSUB0005 Z99108 g2633114 Bacillus subtilis 1423 -11530250 7500965371 yfkh (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:7571) (re:8398) (di:complement) D83967 D83967 g2626820 Bacillus subtilis 1423 -11530250

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777095	3167	25323	561	186

Description

6500726393 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkF yfkF Bacillus subtilis 1423 -11530251 7000694253 yfkf multidrug-efflux transporter homolog yfkf (db:pir2.dat) B69808 B69808 Bacillus subtilis 1423 -11530251 6000690346 yfkf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to multidrug-efflux transporter) (le:60549) (re:61724) (di:complement) BSUB0005 Z99108 g2633115 Bacillus subtilis 1423 -11530251 7500964975 yfkf (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:6197) (re:7372) (di:direct) D83967 D83967 g2626818 Bacillus subtilis 1423 -11530251

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777099	3168	25324	558	186

Description

6500726394 hypothetical protein:similar to h+/ca2+ exchanger (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkE yfkE Bacillus subtilis 1423 -11530252 7000693081 yfke h+/ca2+ exchanger homolog yfke (cl:ca2+/h+-exchanging protein) (db:pir2.dat) A69808 A69808 Bacillus subtilis 1423 -11530252 6000690348 yfke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to h+/ca2+ exchanger) (le:61892) (re:62947) (di:direct) BSUB0005 Z99108 g2633116 Bacillus subtilis 1423 -11530252 7500964045 yfke (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:4974) (re:6029) (di:complement) D83967 D83967 g2626817 Bacillus subtilis 1423 -11530252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777113	3169	25325	714	237

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777116	3170	25326	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777127	3171	25327	585	194

Description

6500726395 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkD yfkD Bacillus subtilis 1423 -11530253 7000693293 yfkd hypothetical protein yfkd (db:pir2.dat) H69807 H69807 Bacillus subtilis 1423 -11530253 6000690350 yfkd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:63018) (re:63812) (di:direct) BSUB0005 Z99108 g2633117 Bacillus subtilis 1423 -11530253 7500964249 yfkd (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:4109) (re:4903) (di:complement) D83967 D83967 g2626816 Bacillus subtilis 1423 -11530253

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777128	3172	25328	666	221

Description

6500726396 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkC yfkC Bacillus subtilis 1423 -11530254 7000692497 yfkc conserved hypothetical protein yfkc (db:pir2.dat) G69807 G69807 Bacillus subtilis 1423 -11530254 6000690352 yfkc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:63851) (re:64693) (di:complement) BSUB0005 Z99108 g2633118 Bacillus subtilis 1423 -11530254 7500963640 yfkc (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:3228) (re:4070) (di:direct) D83967 D83967 g2626815 Bacillus subtilis 1423 -11530254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777148	3173	25329	915	304

Description

6500726397 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkB yfkB Bacillus subtilis 1423 -11530255 7000693292 yfkb hypothetical protein yfkb (db:pir2.dat) F69807 F69807 Bacillus subtilis 1423 -11530255 6000690354 yfkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:64694) (re:65155) (di:complement) BSUB0005 Z99108 g2633119 Bacillus subtilis 1423 -11530255 7500964248 yfkb (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:2766) (re:3227) (di:direct) D83967 D83967 g2626814 Bacillus subtilis 1423 -11530255

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777152	3174	25330	714	237

Description

6500726398 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfkA yfkA Bacillus subtilis 1423 -11530256 7000693291 yfka hypothetical protein yfka (db:pir2.dat) E69807 E69807 Bacillus subtilis 1423 -11530256 6000690356 yfka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:65350) (re:65814) (di:complement) BSUB0005 Z99108 g2633120 Bacillus subtilis 1423 -11530256 7500964247 yfka (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:2107) (re:2571) (di:direct) D83967 D83967 g2626813 Bacillus subtilis 1423 -11530256

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777155	3175	25331	696	231

Description

GTC ORF with score 280 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777156	3176	25332	189	62

Description

GTC ORF with score 94 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completecds.) (nt:similar to salicylate hydroxylase; orf7) (le:10288) (re:11433) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777157	3177	25333	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777452	3178	25334	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777453	3179	25335	363	120

Description

6500726399 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjT yfjT Bacillus subtilis 1423 -11530257 7000693289 yfjt hypothetical protein yfjt (db:pir2.dat) C69807 C69807 Bacillus subtilis 1423 -11530257 6000690358 yfjt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:65959) (re:66144) (di:direct) BSUB0005 Z99108 g2633121 Bacillus subtilis 1423 -11530257 7500964245 yfjt (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:1777) (re:1962) (di:complement) D83967 D83967 g2626812 Bacillus subtilis 1423 -11530257

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777460	3180	25336	234	77

Description

GTC ORF with score 118 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid b0261.) (nt:similar to drosophila rlc1 gene product) (le:4962:5131:5242:5457) (re:5053:5187:5406:5562) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777467	3181	25337	834	277

Description

6500726400 hypothetical protein:similar to polysaccharide deacetylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjS yfjS Bacillus subtilis 1423 -11530258 7000694436 yfjs polysaccharide deacetylase homolog yfjs (cl:nodulation protein nodb:nodb homology) (db:pir2.dat) B69807 B69807 Bacillus subtilis 1423 -11530258 6000690360 yfjs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to polysaccharide deacetylase) (le:66245) (re:67036) (di:direct) BSUB0005 Z99108 g2633122 Bacillus subtilis 1423 -11530258 7500955385 yfjs (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:885) (re:1676) (di:complement) D83967 D83967 g2626811 Bacillus subtilis 1423 -11530258

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777468	3182	25338	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777479	3183	25339	585	194

Description

6500726401 hypothetical protein:similar to 3-hydroxyisobutyrate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjR yfjR Bacillus subtilis 1423 -11530259 7500923559 yfjr (de:hypothetical 27.9 kd protein in trer-acoa intergenic region) (db:swissprot) YFJR_BACSU O34969 BACILLUS SUBTILIS 1423 -11530259 7000692046 yfjr 3-hydroxyisobutyrate dehydrogenase homolog yfjr (db:pir2.dat) A69807 A69807 Bacillus subtilis 1423 -11530259 7000692047 yfjr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to 3-hydroxyisobutyrate dehydrogenase) (le:67074) (re:67859) (di:complement) BSUB0005 Z99108 g2633123 Bacillus subtilis 1423 -11530259 7500923561 yfjr (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:18466) (re:19251) (di:direct) D78509 D78509 g2780402 Bacillus subtilis 1423 -11530259 6000690362 yfjr (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis genomic dna, 74 degree region.) (le:62) (re:847) (di:direct) D83967 D83967 g2626810 Bacillus subtilis 1423 -11530259

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777480	3184	25340	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777481	3185	25341	816	272

Description

GTC ORF with score 538 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmids 9379, 9581, andlambda clone 4678.) (nt:similar to hypothetical protein f42a10.1 from) (le:5607) (re:7439) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777498	3186	25342	1191	396

Description

6500726402 hypothetical protein:similar to divalent cation transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjQ yfjQ Bacillus subtilis 1423 -11530260 7000692925 yfjq divalent cation transport protein homolog yfjq (cl:magnesium and cobalt transport protein) (db:pir2.dat) H69806 H69806 Bacillus subtilis 1423 -11530260 7000692926 yfjq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to divalent cation transport protein) (le:68033) (re:68992) (di:complement) BSUB0005 Z99108 g2633124 Bacillus subtilis 1423 -11530260 7500963943 yfjq (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:17333) (re:18292) (di:direct) D78509 D78509 g2780401 Bacillus subtilis 1423 -11530260

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777505	3187	25343	855	284

Description

6500726403 hypothetical protein:similar to dna-3-methyladenine glycosidase ii (gtcfc:14.1) (ec:3.2.2.21) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjP yfjP Bacillus subtilis 1423 -11530261 7000692950 yfjp dna-3-methyladenine glycosidase ii homolog yfjp (db:pir2.dat) G69806 G69806 Bacillus subtilis 1423 -11530261 7000692951 yfjp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to dna-3-methyladenine glycosidase ii) (le:69111) (re:69974) (di:direct) BSUB0005 Z99108 g2633125 Bacillus subtilis 1423 -11530261 7500963961 yfjp (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:16351) (re:17214) (di:complement) D78509 D78509 g2780400 Bacillus subtilis 1423 -11530261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777509	3188	25344	252	83

Description

6500726404 hypothetical protein:similar to rna methyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjO yfjO Bacillus subtilis 1423 -11530262 7000694551 yfjo rna methyltransferase homolog yfjo (db:pir2.dat) F69806 F69806 Bacillus subtilis 1423 -11530262 7000694552 yfjo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to rna methyltransferase) (le:70088) (re:71488) (di:direct) BSUB0005 Z99108 g2633126 Bacillus subtilis 1423 -11530262 7500965164 yfjo (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:14837) (re:16237) (di:complement) D78509 D78509 g2780399 Bacillus subtilis 1423 -11530262

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777519	3189	25345	855	284

Description

6500726405 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjN yfjN Bacillus subtilis 1423 -11530263 7000692495 yfjn conserved hypothetical protein yfjn (db:pir2.dat) E69806 E69806 Bacillus subtilis 1423 -11530263 7000692496 yfjn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:73112) (re:74089) (di:direct) BSUB0005 Z99108 g2633127 Bacillus subtilis 1423 -11530263 7500963639 yfjn (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:12236) (re:13213) (di:complement) D78509 D78509 g2780398 Bacillus subtilis 1423 -11530263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777522	3190	25346	309	103

Description

6500726406 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjM yfjM Bacillus subtilis 1423 -11530264 7000693287 yfjm hypothetical protein yfjm (db:pir2.dat) D69806 D69806 Bacillus subtilis 1423 -11530264 7000693288 yfjm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:74285) (re:74737) (di:direct) BSUB0005 Z99108 g2633128 Bacillus subtilis 1423 -11530264 7500964244 yfjm (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:11588) (re:12040) (di:complement) D78509 D78509 g2780397 Bacillus subtilis 1423 -11530264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777523	3191	25347	582	193

Description

6500726407 yzta:yfjl hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjL yfjL Bacillus subtilis 1423 -11530265 7000693285 yfjl hypothetical protein yfjl (db:pir2.dat) C69806 C69806 Bacillus subtilis 1423 -11530265 7000693286 yfjl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yzta) (le:74767) (re:75456) (di:direct) BSUB0005 Z99108 g2633129 Bacillus subtilis 1423 -11530265 7500964243 yfjl (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis yfjg-yfjr genes, complete cds.) (le:10869) (re:11558) (di:complement) D78509 D78509 g2780396 Bacillus subtilis 1423 -11530265

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777534	3192	25348	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777552	3193	25349	891	297

Description

6500726408 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjU yfjU Bacillus subtilis 1423 -11530266 7000693290 yfju hypothetical protein yfju (db:pir2.dat) D69807 D69807 Bacillus subtilis 1423 -11530266 7500964246 yfju (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:82315) (re:82494) (di:direct) BSUB0005 Z99108 g2633135 Bacillus subtilis 1423 -11530266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777558	3194	25350	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777562	3195	25351	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777574	3196	25352	198	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777577	3197	25353	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777579	3198	25354	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777611	3199	25355	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777618	3200	25356	468	155

Description

6500726409 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjF yfjF Bacillus subtilis 1423 -11530267 7500923544 yfjf (de:hypothetical 11.9 kd protein in acor-glva intergenic region) (db:swissprot) YFJF_BACSU O31553 BACILLUS SUBTILIS 1423 -11530267 7000692494 yfjf conserved hypothetical protein yfjf (cl:hypothetical protein b1582) (db:pir2.dat) B69806 B69806 Bacillus subtilis 1423 -11530267 7500923546 yfjf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:82530) (re:82859) (di:complement) BSUB0005 Z99108 g2633136 Bacillus subtilis 1423 -11530267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777620	3201	25357	204	67

Description

6500726410 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjE yfjE Bacillus subtilis 1423 -11530268 7000692493 yfje conserved hypothetical protein yfje (db:pir2.dat) A69806 A69806 Bacillus subtilis 1423 -11530268 7500963638 yfje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins from b. subtilis) (le:82909) (re:83367) (di:complement) BSUB0005 Z99108 g2633137 Bacillus subtilis 1423 -11530268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777637	3202	25358	615	204

Description

6500726411 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjD yfjD Bacillus subtilis 1423 -11530269 7000692492 yfjd conserved hypothetical protein yfjd (db:pir2.dat) H69805 H69805 Bacillus subtilis 1423 -11530269 7500963637 yfjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins from b. subtilis) (le:83461) (re:84018) (di:complement) BSUB0005 Z99108 g2633138 Bacillus subtilis 1423 -11530269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777638	3203	25359	813	271

Description

6500726412 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjC yfjC Bacillus subtilis 1423 -11530270 7000693284 yfjc hypothetical protein yfjc (db:pir2.dat) G69805 G69805 Bacillus subtilis 1423 -11530270 7500964242 yfjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:84050) (re:84817) (di:complement) BSUB0005 Z99108 g2633139 Bacillus subtilis 1423 -11530270

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777645	3204	25360	480	159

Description

6500726413 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjB yfjB Bacillus subtilis 1423 -11530271 7000693283 yfjb hypothetical protein yfjb (db:pir2.dat) F69805 F69805 Bacillus subtilis 1423 -11530271 7500964241 yfjb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:84829) (re:86052) (di:complement) BSUB0005 Z99108 g2633140 Bacillus subtilis 1423 -11530271

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777659	3205	25361	252	83

Description

6500726414 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfjA yfjA Bacillus subtilis 1423 -11530272 7000693282 yfja hypothetical protein yfja (db:pir2.dat) E69805 E69805 Bacillus subtilis 1423 -11530272 7500964240 yfja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:86058) (re:86372) (di:complement) BSUB0005 Z99108 g2633141 Bacillus subtilis 1423 -11530272

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777665	3206	25362	234	77

Description

6500726415 hypothetical protein:hypothetical 29.3 kd protein in glvg-glvbc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiA yfiA Bacillus subtilis 1423 -11530273 111926 yfia (de:hypothetical 29.3 kd protein in glvg-glvbc intergenic region) (db:swissprot) YFIA_BACSU P54717 BACILLUS SUBTILIS 1423 -11530273 7000687715 yfia conserved hypothetical protein yfia (db:pir2.dat) D69802 D69802 Bacillus subtilis 1423 -11530273 222682 yfia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:88122) (re:88886) (di:direct) BSUB0005 Z99108 g2633143 Bacillus subtilis 1423 -11530273 7500923509 yfia unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:1798) (re:2562) (di:direct) D50543 D50543 g1486242 Bacillus subtilis 1423 -11530273

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777667	3207	25363	423	140

Description

5000689154 hypothetical protein:hypothetical abc transporter atp-binding protein 1 in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiB yfiB Bacillus subtilis 1423 -11530274 111928 yfib (de:hypothetical abc transporter atp-binding protein 1 in glvbc 3'region) (db:swissprot) YFIB_BACSU P54718 BACILLUS SUBTILIS 1423 -11530274 7000687716 yfib abc transporter atp-binding protein homolog yfib (cl:atp-binding cassette homology) (db:pir2.dat) E69802 E69802 Bacillus subtilis 1423 -11530274 222684 yfib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:90590) (re:92311) (di:direct) BSUB0005 Z99108 g2633145 Bacillus subtilis 1423 -11530274 7500923510 yfib unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:4266) (re:5987) (di:direct) D50543 D50543 g1486244 Bacillus subtilis 1423 -11530274 6500726416 hypothetical protein:hypothetical abc transporter atp-binding protein 1 in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiB yfiB Bacillus subtilis 1423 -11530274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777673	3208	25364	420	139

Description

5000689155 hypothetical protein:hypothetical abc transporter atp-binding protein 2 in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiC yfiC Bacillus subtilis 1423 -11530275 111931 yfic (de:hypothetical abc transporter atp-binding protein 2 in glvbc 3'region) (db:swissprot) YFIC_BACSU P54719 BACILLUS SUBTILIS 1423 -11530275 7000687718 yfic abc transporter atp-binding protein homolog yfic (cl:atp-binding cassette homology) (db:pir2.dat) F69802 F69802 Bacillus subtilis 1423 -11530275 222685 yfic (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:92305) (re:94119) (di:direct) BSUB0005 Z99108 g2633146 Bacillus subtilis 1423 -11530275 7500923512 yfic unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:5981) (re:7795) (di:direct) D50543 D50543 g1486245 Bacillus subtilis 1423 -11530275 6500726417 hypothetical protein:hypothetical abc transporter atp-binding protein 2 in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiC yfiC Bacillus subtilis 1423 -11530275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777691	3209	25365	552	184

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777692	3210	25366	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777697	3211	25367	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777708	3212	25368	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777710	3213	25369	285	94

Description

5000689156 hypothetical protein:hypothetical protein in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiD yfiD Bacillus subtilis 1423 -11530276 111934 yfid (de:hypothetical protein in glvbc 3'region) (db:swissprot) YFID_BACSU P54720 BACILLUS SUBTILIS 1423 -11530276 7000687719 yfid conserved hypothetical protein yfid (db:pir2.dat) G69802 G69802 Bacillus subtilis 1423 -11530276 222686 yfid (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:94274) (re:94678) (di:direct) BSUB0005 Z99108 g2633147 Bacillus subtilis 1423 -11530276 7500923514 yfid unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:7950) (re:8354) (di:direct) D50543 D50543 g1486246 Bacillus subtilis 1423 -11530276 6500726418 hypothetical protein:hypothetical protein in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiD yfiD Bacillus subtilis 1423 -11530276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777714	3214	25370	339	112

Description

5000689157 hypothetical protein:hypothetical 31.5 kd protein in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiE yfiE Bacillus subtilis 1423 -11530277 111938 yfie (de:hypothetical 31.5 kd protein in glvbc 3'region) (db:swissprot) YFIE_BACSU P54721 BACILLUS SUBTILIS 1423 -11530277 7000687721 yfie conserved hypothetical protein yfie (db:pir2.dat) H69802 H69802 Bacillus subtilis 1423 -11530277 222687 yfie (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins from b. subtilis) (le:94696) (re:95553) (di:direct) BSUB0005 Z99108 g2633148 Bacillus subtilis 1423 -11530277 7500923517 yfie unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:8372) (re:9229) (di:direct) D50543 D50543 g1486247 Bacillus subtilis 1423 -11530277 6500726419 hypothetical protein:hypothetical 31.5 kd protein in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiE yfiE Bacillus subtilis 1423 -11530277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501777734	3215	25371	987	329

Description

5000689158 hypothetical protein:hypothetical transcriptional regulator in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiF yfiF Bacillus subtilis 1423 -11530278 111940 yfif (de:hypothetical transcriptional regulator in glvc-lipb intergenic region) (db:swissprot) YFIF_BACSU P54722 BACILLUS SUBTILIS 1423 -11530278 7000687722 yfif transcription regulator arac/xyls family homolog yfif (db:pir2.dat) A69803 A69803 Bacillus subtilis 1423 -11530278 222688 yfif (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to transcriptional regulator (arac/xyls) (le:95647) (re:96591) (di:direct) BSUB0005 Z99108 g2633149 Bacillus subtilis 1423 -11530278 7500923518 yfif unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:9323) (re:10267) (di:direct) D50543 D50543 g1486248 Bacillus subtilis 1423 -11530278 6500726420 hypothetical protein:hypothetical transcriptional regulator in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiF yfiF Bacillus subtilis 1423 -11530278

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778022	3216	25372	477	158

Description

5000689159 hypothetical protein:hypothetical metabolite transport protein in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiG yfiG Bacillus subtilis 1423 -11530279 111943 yfig (de:hypothetical metabolite transport protein in glvbc 3'region) (db:swissprot) YFIG_BACSU P54723 BACILLUS SUBTILIS 1423 -11530279 7000687724 yfig metabolite transport protein homolog yfig (cl:glucose transport protein) (db:pir2.dat) B69803 B69803 Bacillus subtilis 1423 -11530279 222689 yfig (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to metabolite transport protein) (le:96766) (re:98214) (di:direct) BSUB0005 Z99108 g2633150 Bacillus subtilis 1423 -11530279 7500923521 yfig unknown (fn:unknown) (sr:bacillus subtilis (strain:168, haplotype:haploid) dna) (db:genpept-bct1) (de:bacillus subtilis dna for 76-degree region, complete cds.) (le:10442) (re:11890) (di:direct) D50543 D50543 g1486249 Bacillus subtilis 1423 -11530279 6500726421 hypothetical protein:hypothetical metabolite transport protein in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiG yfiG Bacillus subtilis 1423 -11530279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778040	3217	25373	348	116

Description

6500726422 hypothetical protein:hypothetical 34.8 kd protein in glvbc 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiH yfiH Bacillus subtilis 1423 -11530280 111945 yfih (de:hypothetical 34.8 kd protein in glvbc 3'region) (db:swissprot) YFIH_BACSU P54724 BACILLUS SUBTILIS 1423 -11530280 7000687727 yfih hypothetical protein yfih (db:pir2.dat) C69803 C69803 Bacillus subtilis 1423 -11530280 222805 yfih (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:98241) (re:99182) (di:direct) BSUB0005 Z99108 g2633151 Bacillus subtilis 1423 -11530280 7500923522 yfih (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:117) (re:1058) (di:direct) D78508 D78508 g1817532 Bacillus subtilis 1423 -11530280

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778053	3218	25374	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778054	3219	25375	432	143

Description

6500726423 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiI yfiI Bacillus subtilis 1423 -11530281 7000693276 yfii hypothetical protein yfii (db:pir2.dat) D69803 D69803 Bacillus subtilis 1423 -11530281 222806 yfii (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:99192) (re:100373) (di:direct) BSUB0005 Z99108 g2633152 Bacillus subtilis 1423 -11530281 7500964236 yfii (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:1068) (re:2249) (di:direct) D78508 D78508 g1817533 Bacillus subtilis 1423 -11530281

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778056	3220	25376	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778057	3221	25377	258	85

Description

6500726424 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiJ yfiJ Bacillus subtilis 1423 -11530282 7000694574 yfij two-component sensor histidine kinase yfij (db:pir2.dat) JC5358 JC5358 Bacillus subtilis 1423 -11530282 7500965426 yfij (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to two-component sensor histidine kinase) (le:100497) (re:101699) (di:direct) BSUB0005 Z99108 g2633153 Bacillus subtilis 1423 -11530282 222807 yfij (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:2373) (re:3575) (di:direct) D78508 D78508 g1817534 Bacillus subtilis 1423 -11530282 7000694573 yfij two-component sensor histidine kinase yfij (db:pir) JC5358 JC5358 Bacillus subtilis 1423 -11530282

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778063	3222	25378	552	183

Description

6500726425 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiK yfiK Bacillus subtilis 1423 -11530283 7000694490 yfik two-component regulator protein yfik (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) JC5359 JC5359 Bacillus subtilis 1423 -11530283 7500965384 yfik (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to two-component response regulator (yfij)) (le:101696) (re:102358) (di:direct) BSUB0005 Z99108 g2633154 Bacillus subtilis 1423 -11530283 222808 yfik (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:3572) (re:4234) (di:direct) D78508 D78508 g1817535 Bacillus subtilis 1423 -11530283 7000694489 yfik two-component regulator protein yfik (cl:response regulator homology) (db:pir) JC5359 JC5359 Bacillus subtilis 1423 -11530283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778064	3223	25379	183	60

Description

6500726426 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiL yfiL Bacillus subtilis 1423 -11530284 7000692082 yfil abc transporter atp-binding protein homolog yfil (cl:atp-binding cassette homology) (db:pir2.dat) G69803 G69803 Bacillus subtilis 1423 -11530284 222809 yfil (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:102502) (re:103437) (di:direct) BSUB0005 Z99108 g2633155 Bacillus subtilis 1423 -11530284 7500963321 yfil (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:4378) (re:5313) (di:direct) D78508 D78508 g1817536 Bacillus subtilis 1423 -11530284

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778083	3224	25380	1218	406

Description

GTC ORF with score 295 to: (db:genpept-bct1) (de:pseudomonas azelaica putative transcriptional activator
(hbpr),2,3-dihydroxybiphenyl-1,2-dioxygenase
(hbpc),2-hydroxybiphenyl-3-monooxygenase (hbpa)
and2-hydroxy-6-phenyl-6-oxo-2,4-dienoic acid hydrolase...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778096	3225	25381	627	209

Description

6500726427 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiM yfiM Bacillus subtilis 1423 -11530285 7000692083 yfim abc transporter atp-binding protein homolog yfim (db:pir2.dat) H69803 H69803 Bacillus subtilis 1423 -11530285 222810 yfim (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:103450) (re:104640) (di:direct) BSUB0005 Z99108 g2633156 Bacillus subtilis 1423 -11530285 7500963322 yfim (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:5326) (re:6516) (di:direct) D78508 D78508 g1817537 Bacillus subtilis 1423 -11530285

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778097	3226	25382	591	196

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778100	3227	25383	552	183

Description

6500726428 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiN yfiN Bacillus subtilis 1423 -11530286 7000692084 yfin abc transporter atp-binding protein homolog yfin (db:pir2.dat) A69804 A69804 Bacillus subtilis 1423 -11530286 222811 yfin (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:104654) (re:105811) (di:direct) BSUB0005 Z99108 g2633157 Bacillus subtilis 1423 -11530286 7500963323 yfin (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:6530) (re:7687) (di:direct) D78508 D78508 g1817538 Bacillus subtilis 1423 -11530286

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778102	3228	25384	372	123

Description

6500726429 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiO yfiO Bacillus subtilis 1423 -11530287 7000693277 yfio hypothetical protein yfio (db:pir2.dat) B69804 B69804 Bacillus subtilis 1423 -11530287 222812 yfio (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:105884) (re:106432) (di:complement) BSUB0005 Z99108 g2633158 Bacillus subtilis 1423 -11530287 7500964237 yfio (sr:bacillus subtilis (strain:ac327) dna) (db:genpept-bct1) (de:bacillus subtilis dna for yfio, yfip, yfin, yfim, yfil, yfik, yfij,yfii, yfih, complete cds.) (le:7760) (re:8308) (di:complement) D78508 D78508 g1817539 Bacillus subtilis 1423 -11530287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778112	3229	25385	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778119	3230	25386	948	315

Description

GTC ORF with score 679 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c10d6.) (nt:spcc10d6.04, unknown, len:660aa, similar eg. to) (le:21546:21635:21866:22154) (re:21587:21807:22102:23684) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778121	3231	25387	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778123	3232	25388	291	96

Description

6500726430 hypothetical protein:similar to surface adhesion (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiQ yfiQ Bacillus subtilis 1423 -11530288 7000694662 yfiq surface adhesion homolog yfiq (db:pir2.dat) C69804 C69804 Bacillus subtilis 1423 -11530288 7000694663 yfiq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to surface adhesion) (le:107526) (re:108614) (di:direct) BSUB0005 Z99108 g2633160 Bacillus subtilis 1423 -11530288 7500965244 yfiq (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:417) (re:1505) (di:direct) D85082 D85082 g2804521 Bacillus subtilis 1423 -11530288

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778134	3233	25389	630	209

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778164	3234	25390	528	175

Description

6500726431 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiR yfiR Bacillus subtilis 1423 -11530289 7000692489 yfir conserved hypothetical protein yfir (db:pir2.dat) D69804 D69804 Bacillus subtilis 1423 -11530289 7000692490 yfir (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:108650) (re:109267) (di:complement) BSUB0005 Z99108 g2633161 Bacillus subtilis 1423 -11530289 7500963635 yfir (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:1541) (re:2158) (di:complement) D85082 D85082 g2804522 Bacillus subtilis 1423 -11530289

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778167	3235	25391	363	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778179	3236	25392	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778180	3237	25393	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778184	3238	25394	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778186	3239	25395	525	174

Description

6500726432 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiS yfiS Bacillus subtilis 1423 -11530290 7000694241 yfis multidrug resistance protein homolog yfis (db:pir2.dat) E69804 E69804 Bacillus subtilis 1423 -11530290 7000694242 yfis (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to multidrug resistance protein) (le:109233) (re:110486) (di:complement) BSUB0005 Z99108 g2633162 Bacillus subtilis 1423 -11530290 7500964968 yfis (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:2124) (re:3377) (di:complement) D85082 D85082 g2804523 Bacillus subtilis 1423 -11530290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778192	3240	25396	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778198	3241	25397	435	145

Description

6500726433 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiT yfiT Bacillus subtilis 1423 -11530291 7000693278 yfit hypothetical protein yfit (db:pir2.dat) F69804 F69804 Bacillus subtilis 1423 -11530291 7000693279 yfit (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:110610) (re:111146) (di:direct) BSUB0005 Z99108 g2633163 Bacillus subtilis 1423 -11530291 7500964238 yfit (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:3501) (re:4037) (di:direct) D85082 D85082 g2804524 Bacillus subtilis 1423 -11530291

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778199	3242	25398	321	106

Description

6500726434 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiU yfiU Bacillus subtilis 1423 -11530292 7000694251 yfiu multidrug-efflux transporter homolog yfiu (cl:multidrug-efflux transporter) (db:pir2.dat) G69804 G69804 Bacillus subtilis 1423 -11530292 7000694252 yfiu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to multidrug-efflux transporter) (le:111143) (re:112699) (di:complement) BSUB0005 Z99108 g2633164 Bacillus subtilis 1423 -11530292 7500955416 yfiu (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:4034) (re:5590) (di:complement) D85082 D85082 g2804525 Bacillus subtilis 1423 -11530292

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778210	3243	25399	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778212	3244	25400	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778220	3245	25401	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778235	3246	25402	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778245	3247	25403	429	143

Description

6500726435 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiV yfiV Bacillus subtilis 1423 -11530293 7000694766 yfiv transcription regulator marr family homolog yfiv (cl:transcription regulator yfiv) (db:pir2.dat) H69804 H69804 Bacillus subtilis 1423 -11530293 7000694767 yfiv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to transcriptional regulator (marr family)) (le:112810) (re:113292) (di:complement) BSUB0005 Z99108 g2633165 Bacillus subtilis 1423 -11530293 7500955934 yfiv (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:5701) (re:6183) (di:complement) D85082 D85082 g2804526 Bacillus subtilis 1423 -11530293

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778258	3248	25404	360	119

Description

6500726436 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiW yfiW Bacillus subtilis 1423 -11530294 7000693280 yfiw hypothetical protein yfiw (db:pir2.dat) A69805 A69805 Bacillus subtilis 1423 -11530294 7000693281 yfiw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:113464) (re:114240) (di:direct) BSUB0005 Z99108 g2633166 Bacillus subtilis 1423 -11530294 7500964239 yfiw (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:6355) (re:7131) (di:direct) D85082 D85082 g2804527 Bacillus subtilis 1423 -11530294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778267	3249	25405	735	244

Description

6500726437 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiX yfiX Bacillus subtilis 1423 -11530295 7000692491 yfix conserved hypothetical protein yfix (db:pir2.dat) B69805 B69805 Bacillus subtilis 1423 -11530295 7500963636 yfix (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:114215) (re:116035) (di:direct) BSUB0005 Z99108 g2633167 Bacillus subtilis 1423 -11530295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778269	3250	25406	534	177

Description

GTC ORF with score 305 to: (sr:western european house mouse) (db:genpept-rod) (ec:1.1.1.14) (de:mus musculus sorbitol dehydrogenase precursor mrna, partial cds.) (nt:l-iditol:nad+ 2-oxidoreductase precursor) (le:<1) (re:1128) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778270	3251	25407	204	67

Description

6500726438 hypothetical protein:similar to iron:iii dicitrate transport permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiY yfiY Bacillus subtilis 1423 -11530296 7000694127 yfiy iron iii dicitrate transport permease homolog yfiy (cl:iron(iii) dicitrate transport protein) (db:pir2.dat) C69805 C69805 Bacillus subtilis 1423 -11530296 7000694128 yfiy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to iron(iii) dicitrate transport permease) (le:116053) (re:117030) (di:complement) BSUB0005 Z99108 g2633168 Bacillus subtilis 1423 -11530296 7500955813 yfiy (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:8944) (re:9921) (di:complement) D85082 D85082 g2804529 Bacillus subtilis 1423 -11530296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778273	3252	25408	246	81

Description

GTC ORF with score 164 to: (sr:fruit fly) (db:genpept) (de:drosophila melanogaster sorbitol dehydrogenase (sdh) gene, completecds.) (nt:medium chain alcohol dehydrogenase; sdh) (le:480:585:925:1454:1727) (re:533:618:1394:1672:1848) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778275	3253	25409	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778284	3254	25410	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778573	3255	25411	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778575	3256	25412	726	241

Description

6500726439 hypothetical protein:similar to iron:iii dicitrate transport permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfiZ yfiZ Bacillus subtilis 1423 -11530297 7000694129 yfiz iron iii dicitrate transport permease homolog yfiz (db:pir2.dat) D69805 D69805 Bacillus subtilis 1423 -11530297 7000694130 yfiz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to iron(iii) dicitrate transport permease) (le:117161) (re:118162) (di:direct) BSUB0005 Z99108 g2633169 Bacillus subtilis 1423 -11530297 7500964877 yfiz (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:10052) (re:11053) (di:direct) D85082 D85082 g2804530 Bacillus subtilis 1423 -11530297

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778587	3257	25413	219	72

Description

6500726440 hypothetical protein:similar to iron:iii dicitrate transport permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhA yfhA Bacillus subtilis 1423 -11530298 7000694125 yfha iron iii dicitrate transport permease homolog yfha (db:pir2.dat) B69800 B69800 Bacillus subtilis 1423 -11530298 7000694126 yfha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to iron(iii) dicitrate transport permease) (le:118159) (re:119190) (di:direct) BSUB0005 Z99108 g2633170 Bacillus subtilis 1423 -11530298 7500964876 yfha (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:11050) (re:12081) (di:direct) D85082 D85082 g2804531 Bacillus subtilis 1423 -11530298

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778593	3258	25414	453	150

Description

6500726441 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhB yfhB Bacillus subtilis 1423 -11530299 7000692483 yfhb conserved hypothetical protein yfhb (db:pir2.dat) C69800 C69800 Bacillus subtilis 1423 -11530299 7000692484 yfhb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:119305) (re:120186) (di:direct) BSUB0005 Z99108 g2633171 Bacillus subtilis 1423 -11530299 7500963632 yfhb (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:12196) (re:13077) (di:direct) D85082 D85082 g2804532 Bacillus subtilis 1423 -11530299

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778607	3259	25415	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778623	3260	25416	423	140

Description

6500726442 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhC yfhC Bacillus subtilis 1423 -11530300 7000692485 yfhc conserved hypothetical protein yfhc (db:pir2.dat) D69800 D69800 Bacillus subtilis 1423 -11530300 7000692486 yfhc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:120274) (re:120858) (di:direct) BSUB0005 Z99108 g2633172 Bacillus subtilis 1423 -11530300 7500963633 yfhc (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:13165) (re:13749) (di:direct) D85082 D85082 g2804533 Bacillus subtilis 1423 -11530300

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778629	3261	25417	540	180

Description

6500726443 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhD yfhD Bacillus subtilis 1423 -11530301 7000693259 yfhd hypothetical protein yfhd (db:pir2.dat) E69800 E69800 Bacillus subtilis 1423 -11530301 7000693260 yfhd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:120897) (re:121088) (di:complement) BSUB0005 Z99108 g2633173 Bacillus subtilis 1423 -11530301 7500964227 yfhd (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:13788) (re:13979) (di:complement) D85082 D85082 g2804534 Bacillus subtilis 1423 -11530301

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778633	3262	25418	417	138

Description

6500726444 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhE yfhE Bacillus subtilis 1423 -11530302 7000693261 yfhe hypothetical protein yfhe (db:pir2.dat) F69800 F69800 Bacillus subtilis 1423 -11530302 7000693262 yfhe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:121155) (re:121265) (di:complement) BSUB0005 Z99108 g2633174 Bacillus subtilis 1423 -11530302 7500964228 yfhe (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:14046) (re:14156) (di:complement) D85082 D85082 g2804535 Bacillus subtilis 1423 -11530302

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778636	3263	25419	561	186

Description

6500726445 hypothetical protein:similar to cell-division inhibitor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhF yfhF Bacillus subtilis 1423 -11530303 7000692343 yfhf cell-division inhibitor homolog yfhf (cl:cell division inhibitor yfhf) (db:pir2.dat) G69800 G69800 Bacillus subtilis 1423 -11530303 7000692344 yfhf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to cell-division inhibitor) (le:121320) (re:122231) (di:complement) BSUB0005 Z99108 g2633175 Bacillus subtilis 1423 -11530303 7500963510 yfhf (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:14211) (re:15122) (di:complement) D85082 D85082 g2804536 Bacillus subtilis 1423 -11530303

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778645	3264	25420	1011	336

Description

6500726446 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhG yfhG Bacillus subtilis 1423 -11530304 7000693263 yfhg hypothetical protein yfhg (db:pir2.dat) H69800 H69800 Bacillus subtilis 1423 -11530304 7000693264 yfhg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:122320) (re:123114) (di:direct) BSUB0005 Z99108 g2633176 Bacillus subtilis 1423 -11530304 7500964229 yfhg (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:15211) (re:16005) (di:direct) D85082 D85082 g2804537 Bacillus subtilis 1423 -11530304

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778660	3265	25421	663	220

Description

GTC ORF with score 152 to: (db:genpept-bct2) (de:mycobacterium smegmatis exochelin gene cluster, exit (exit) andfxbb (fxbb) genes, complete cds; and fxbc (fxbc) gene, partial cds.) (nt:abc transporter; this abc transporter probably) (le:489) (re:3857) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778661	3266	25422	1278	425

Description

6500726447 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhH yfhH Bacillus subtilis 1423 -11530305 7000693265 yfhh hypothetical protein yfhh (db:pir2.dat) A69801 A69801 Bacillus subtilis 1423 -11530305 7000693266 yfhh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:123116) (re:123430) (di:direct) BSUB0005 Z99108 g2633177 Bacillus subtilis 1423 -11530305 7500964230 yfhh (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:16007) (re:16321) (di:direct) D85082 D85082 g2804538 Bacillus subtilis 1423 -11530305

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778666	3267	25423	408	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778667	3268	25424	225	74

Description

6500726448 hypothetical protein:similar to antibiotic resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhI yfhI Bacillus subtilis 1423 -11530306 7000692215 yfhi chloramphenicol resistance protein homolog yfhi (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) B69801 B69801 Bacillus subtilis 1423 -11530306 7500963421 yfhi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to antibiotic resistance protein) (le:123573) (re:124766) (di:direct) BSUB0005 Z99108 g2633178 Bacillus subtilis 1423 -11530306

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778672	3269	25425	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778678	3270	25426	321	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778679	3271	25427	621	206

Description

6500726449 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhJ yfhJ Bacillus subtilis 1423 -11530307 7000693267 yfhj hypothetical protein yfhj (db:pir2.dat) C69801 C69801 Bacillus subtilis 1423 -11530307 7000693268 yfhj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:125076) (re:125345) (di:direct) BSUB0005 Z99108 g2633179 Bacillus subtilis 1423 -11530307 7500964231 yfhj (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:17967) (re:18236) (di:direct) D85082 D85082 g2804540 Bacillus subtilis 1423 -11530307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778680	3272	25428	483	160

Description

6500726450 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhK yfhK Bacillus subtilis 1423 -11530308 7000692487 yfhk conserved hypothetical protein yfhk (db:pir2.dat) D69801 D69801 Bacillus subtilis 1423 -11530308 7000692488 yfhk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins from b. subtilis) (le:125490) (re:126008) (di:direct) BSUB0005 Z99108 g2633180 Bacillus subtilis 1423 -11530308 7500963634 yfhk (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:18381) (re:18899) (di:direct) D85082 D85082 g2804541 Bacillus subtilis 1423 -11530308

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778687	3273	25429	210	69

Description

6500726451 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhL yfhL Bacillus subtilis 1423 -11530309 7000693269 yfhl hypothetical protein yfhl (db:pir2.dat) E69801 E69801 Bacillus subtilis 1423 -11530309 7000693270 yfhl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:126093) (re:126425) (di:direct) BSUB0005 Z99108 g2633181 Bacillus subtilis 1423 -11530309 7500964232 yfhl (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:18984) (re:19316) (di:direct) D85082 D85082 g2804542 Bacillus subtilis 1423 -11530309

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778689	3274	25430	1170	389

Description

6500726452 hypothetical protein:similar to epoxide hydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhM yfhM Bacillus subtilis 1423 -11530310 7000692968 yfhm epoxide hydrolase homolog yfhm (db:pir2.dat) F69801 F69801 Bacillus subtilis 1423 -11530310 7000692969 yfhm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to epoxide hydrolase) (le:126412) (re:127272) (di:direct) BSUB0005 Z99108 g2633182 Bacillus subtilis 1423 -11530310 7500963972 yfhm (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:19303) (re:20163) (di:direct) D85082 D85082 g2804543 Bacillus subtilis 1423 -11530310

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778690	3275	25431	1512	504

Description

6500726453 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhO yfhO Bacillus subtilis 1423 -11530311 7000693271 yfho hypothetical protein yfho (db:pir2.dat) G69801 G69801 Bacillus subtilis 1423 -11530311 7000693272 yfho (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:128691) (re:131150) (di:direct) BSUB0005 Z99108 g2633184 Bacillus subtilis 1423 -11530311 7500964233 yfho (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:21582) (re:24041) (di:direct) D85082 D85082 g2804545 Bacillus subtilis 1423 -11530311

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778709	3276	25432	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778737	3277	25433	1008	335

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778746	3278	25434	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778749	3279	25435	330	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778754	3280	25436	621	206

Description

6500726454 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhP yfhP Bacillus subtilis 1423 -11530312 7000693273 yfhp hypothetical protein yfhp (db:pir2.dat) H69801 H69801 Bacillus subtilis 1423 -11530312 7000693274 yfhp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:131143) (re:132126) (di:complement) BSUB0005 Z99108 g2633185 Bacillus subtilis 1423 -11530312 7500964234 yfhp (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:24034) (re:25017) (di:complement) D85082 D85082 g2804546 Bacillus subtilis 1423 -11530312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778778	3281	25437	423	140

Description

6500726455 hypothetical protein:similar to a/g-specific adenine glycosylase (gtcfc:14.1) (ec:3.2.2.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhQ yfhQ Bacillus subtilis 1423 -11530313 7000692072 yfhq a/g-specific adenine glycosylase homolog yfhq (db:pir2.dat) A69802 A69802 Bacillus subtilis 1423 -11530313 7000692073 yfhq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to a/g-specific adenine glycosylase) (le:132342) (re:133451) (di:direct) BSUB0005 Z99108 g2633186 Bacillus subtilis 1423 -11530313 7500963315 yfhq (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:25233) (re:26342) (di:direct) D85082 D85082 g2804547 Bacillus subtilis 1423 -11530313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778780	3282	25438	765	254

Description

6500726456 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhS yfhS Bacillus subtilis 1423 -11530314 7000693275 yfhs hypothetical protein yfhs (db:pir2.dat) C69802 C69802 Bacillus subtilis 1423 -11530314 7500964235 yfhs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:133459) (re:133683) (di:complement) BSUB0005 Z99108 g2633187 Bacillus subtilis 1423 -11530314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778791	3283	25439	342	113

Description

GTC ORF with score 224 to: (fn:converts 4-hydroxyphenylpyruvate to) (db:genpept-pln1) (ec:1.13.11.27) (de:mycosphaerella graminicola 4-hydroxyphenylpyruvate dioxygenase(hppd) gene, complete cds.) (nt:tyrosine catabolic pathway.) (le:1079) (re:2338) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778792	3284	25440	555	184

Description

GTC ORF with score 430 to: (sr:coccidioides immitis (individual_isolate c735) mycelial dna) (db:genpept-pln1) (de:coccidioides immitis t-cell reactive protein (trcp) gene exons 1-4,complete cds.) (nt:homology to 4-hydroxyphenylpyruvate dioxygenase and)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778796	3285	25441	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778797	3286	25442	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778801	3287	25443	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778812	3288	25444	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501778813	3289	25445	546	181

Description

6500726457 ygaa:yfhr hypothetical protein:similar to glucose 1-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yfhR yfhR Bacillus subtilis 1423 -11530315 7000693033 yfhr glucose 1-dehydrogenase homolog yfhr (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) B69802 B69802 Bacillus subtilis 1423 -11530315 220371 yfhr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: ygaa; similar to glucose) (le:133765) (re:134517) (di:direct) BSUB0005 Z99108 g2633188 Bacillus subtilis 1423 -11530315 7000693034 ygaa unidentfied dehydrogenase (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:615) (re:1367) (di:direct) BSZ82044 Z82044 g1673388 Bacillus subtilis 1423 -11530315 7500964015 yfhr (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis dna, genome sequence, 79 to 81 degree region.) (le:26656) (re:27408) (di:direct) D85082 D85082 g2804548 Bacillus subtilis 1423 -11530315

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779157	3290	25446	294	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779162	3291	25447	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779163	3292	25448	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779181	3293	25449	1494	498

Description

6500726458 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaB ygaB Bacillus subtilis 1423 -11530316 7000693313 ygab hypothetical protein ygab (db:pir2.dat) E69815 E69815 Bacillus subtilis 1423 -11530316 220373 ygab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:134929) (re:135273) (di:direct) BSUB0005 Z99108 g2633190 Bacillus subtilis 1423 -11530316 7500964269 ygab hypothetical 13.5 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:1779) (re:2123) (di:direct) BSZ82044 Z82044 g1673390 Bacillus subtilis 1423 -11530316

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779190	3294	25450	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779203	3295	25451	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779228	3296	25452	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779231	3297	25453	243	80

Description

6500726459 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaC ygaC Bacillus subtilis 1423 -11530317 7000693314 ygac hypothetical protein ygac (db:pir2.dat) F69815 F69815 Bacillus subtilis 1423 -11530317 220374 ygac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:135417) (re:135734) (di:direct) BSUB0005 Z99108 g2633191 Bacillus subtilis 1423 -11530317 7500964270 ygac hypothetical 12.2 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:2267) (re:2584) (di:direct) BSZ82044 Z82044 g1673391 Bacillus subtilis 1423 -11530317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779235	3298	25454	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779245	3299	25455	549	182

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779268	3300	25456	531	176

Description

6500726460 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaD ygaD Bacillus subtilis 1423 -11530318 7000692087 ygad abc transporter atp-binding protein homolog ygad (cl:atp-binding cassette homology) (db:pir2.dat) G69815 G69815 Bacillus subtilis 1423 -11530318 220375 ygad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:136007) (re:137776) (di:direct) BSUB0005 Z99108 g2633192 Bacillus subtilis 1423 -11530318 7500963326 ygad unidentified transporter-atp binding (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:2857) (re:4626) (di:direct) BSZ82044 Z82044 g1673392 Bacillus subtilis 1423 -11530318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779287	3301	25457	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779293	3302	25458	480	159

Description

6500726461 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaE ygaE Bacillus subtilis 1423 -11530319 7000693315 ygae hypothetical protein ygae (db:pir2.dat) H69815 H69815 Bacillus subtilis 1423 -11530319 220376 ygae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:137853) (re:138914) (di:complement) BSUB0005 Z99108 g2633193 Bacillus subtilis 1423 -11530319 7500964271 ygae hypothetical 40.7 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:4703) (re:5764) (di:complement) BSZ82044 Z82044 g1673393 Bacillus subtilis 1423 -11530319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779304	3303	25459	678	225

Description

6500726462 hypothetical protein:similar to thiol-specific antioxidant protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaF ygaF Bacillus subtilis 1423 -11530320 7000694677 ygaf thiol-specific antioxidant protein homolog ygaf (db:pir2.dat) A69816 A69816 Bacillus subtilis 1423 -11530320 220378 ygaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to thiol-specific antioxidant protein) (le:140576) (re:140818) (di:direct) BSUB0005 Z99108 g2633195 Bacillus subtilis 1423 -11530320 7500965262 ygaf hypothetical 9.1 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (nt:homology to thiol-specific antioxidant protein) (le:7426) (re:7668) (di:direct) BSZ82044 Z82044 g1673395 Bacillus subtilis 1423 -11530320

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779309	3304	25460	483	161

Description

6500726463 hypothetical protein:similar to transcriptional regulator:fur family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaG ygaG Bacillus subtilis 1423 -11530321 7502851652 ygag (de:ferric uptake regulation protein homolog 3) (db:swissprot) FUR3_BACSU P71086 BACILLUS SUBTILIS 1423 -11530321 7000694728 ygag transcription regulator fur family homolog ygag (cl:ferric uptake regulator) (db:pir2.dat) B69816 B69816 Bacillus subtilis 1423 -11530321 220379 ygag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to transcriptional regulator (fur family)) (le:141173) (re:141610) (di:direct) BSUB0005 Z99108 g2633196 Bacillus subtilis 1423 -11530321 7500965302 ygag hypothetical 16.4 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (nt:homology to ferric uptake regulation protein) (le:8023) (re:8460) (di:direct) BSZ82044 Z82044 g1673396 Bacillus subtilis 1423 -11530321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779310	3305	25461	216	71

Description

6500726464 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaH ygaH Bacillus subtilis 1423 -11530322 7000693316 ygah hypothetical protein ygah (db:pir2.dat) C69816 C69816 Bacillus subtilis 1423 -11530322 220380 ygah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:141851) (re:142183) (di:direct) BSUB0005 Z99108 g2633197 Bacillus subtilis 1423 -11530322 7500964272 ygah hypothetical 12.8 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:8701) (re:9033) (di:direct) BSZ82044 Z82044 g1673397 Bacillus subtilis 1423 -11530322

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779312	3306	25462	288	95

Description

GTC ORF with score 273 to: (or:Spinacia oleracea) (sr:spinacia oleracea (strain:dash) cdna to mrna) (db:genpept-pln1) (ec:3.2.1.20) (de:spinacia oleracea mrna for alpha-glucosidase precoursor, completecds.) (nt:putative) (le:19) (re:2730) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779316	3307	25463	816	271

Description

GTC ORF with score 224 to: (fn:unknown) (db:genpept-bct1) (de:streptomyces sp. c5 acyl carrier protein (daua(g)),glycosyltransferase (dauh), and aklaviketone reductase (daue)genes, complete cds.) (nt:orf1) (le:28) (re:891) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779320	3308	25464	957	318

Description

GTC ORF with score 371 to: (sr:rhizobium meliloti (strain 15-30) dna) (db:genpept-bct1) (de:rhizobium meliloti rhizopine biosynthesis and membrane proteins(mosa, mosb, and mosc) genes, complete cds's.) (le:1479) (re:2480) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779323	3309	25465	558	185

Description

5000689566 hypothetical protein:hypothetical 34.4 kd protein in rrnd 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygxA ygxA Bacillus subtilis 1423 -11530323 7500936622 ygxa (de:hypothetical 34.4 kd protein in rrnd 5'region) (db:swissprot) YGXA_BACSU Q04385 BACILLUS SUBTILIS 1423 -11530323 7000687881 ygxa conserved hypothetical protein ygxa (db:pir2.dat) E69817 E69817 Bacillus subtilis 1423 -11530323 220381 ygxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins from b. subtilis) (le:142207) (re:143091) (di:direct) BSUB0005 Z99108 g2633198 Bacillus subtilis 1423 -11530323 7502851653 ygxa hypothetical 34.4 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (nt:9925..15108 rrnd operon) (le:9057) (re:9941) (di:direct) BSZ82044 Z82044 g1673398 Bacillus subtilis 1423 -11530323 112538 ygxa (de:hypothetical 34.4 kd protein in rrnd 5'region) (db:swissprot) YGXA_BACSU Q04385 BACILLUS SUBTILIS 1423 -11530323 6500726465 hypothetical protein:hypothetical 34.4 kd protein in rrnd 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygxA ygxA Bacillus subtilis 1423 -11530323

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779324	3310	25466	348	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779338	3311	25467	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779355	3312	25468	267	88

Description

GTC ORF with score 194 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri3) (de:homo sapiens mrna for kiaa0017 protein, complete cds.) (nt:similar to human xeroderma pigmentosum groupe) (le:157) (re:3810) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779357	3313	25469	1260	419

Description

GTC ORF with score 1032 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri3) (de:homo sapiens mrna for kiaa0017 protein, complete cds.) (nt:similar to human xeroderma pigmentosum groupe) (le:157) (re:3810) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779361	3314	25470	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779363	3315	25471	1281	426

Description

6500726466 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaI ygaI Bacillus subtilis 1423 -11530324 7000693317 ygai hypothetical protein ygai (db:pir2.dat) D69816 D69816 Bacillus subtilis 1423 -11530324 220382 ygai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:150059) (re:150835) (di:complement) BSUB0005 Z99108 g2633199 Bacillus subtilis 1423 -11530324 7500964273 ygai hypothetical 29.7 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (le:16909) (re:17685) (di:complement) BSZ82044 Z82044 g1673399 Bacillus subtilis 1423 -11530324

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779373	3316	25472	414	137

Description

6500726467 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygzA ygzA Bacillus subtilis 1423 -11530325 7000693321 ygza hypothetical protein ygza (db:pir2.dat) G69817 G69817 Bacillus subtilis 1423 -11530325 7500964277 ygza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:150977) (re:151180) (di:direct) BSUB0005 Z99108 g2633200 Bacillus subtilis 1423 -11530325

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779375	3317	25473	564	188

Description

6500726468 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaJ ygaJ Bacillus subtilis 1423 -11530326 7000693318 ygaj hypothetical protein ygaj (db:pir2.dat) E69816 E69816 Bacillus subtilis 1423 -11530326 220383 ygaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:151577) (re:152332) (di:direct) BSUB0005 Z99108 g2633201 Bacillus subtilis 1423 -11530326 7500964274 ygaj hypothetical 28.3 kd protein (db:genpept-bct1) (de:b.subtilis 25 kb genomic dna segment (from sspe to kata).) (nt:homology to pepe) (le:18427) (re:19182) (di:direct) BSZ82044 Z82044 g1673400 Bacillus subtilis 1423 -11530326

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779376	3318	25474	810	269

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779383	3319	25475	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779402	3320	25476	543	180

Description

GTC ORF with score 479 to: (or:Aspergillus oryzae) (sr:aspergillus oryzae (strain:kbn616) dna) (db:genpept-pln1) (ec:3.2.1.4) (de:aspergillus oryzae cela gene for endo-1,4-beta-glucanase, completecds.) (le:501:1006:1301) (re:907:1238:1380) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779414	3321	25477	1320	440

Description

6500726469 hypothetical protein:similar to reticuline oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaK ygaK Bacillus subtilis 1423 -11530327 7000694505 ygak reticuline oxidase homolog ygak (db:pir2.dat) F69816 F69816 Bacillus subtilis 1423 -11530327 7500965143 ygak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to reticuline oxidase) (le:154393) (re:155496) (di:complement) BSUB0005 Z99108 g2633203 Bacillus subtilis 1423 -11530327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779420	3322	25478	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779430	3323	25479	705	235

Description

6500726470 hypothetical protein:similar to nitrate abc transporter:binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaL ygaL Bacillus subtilis 1423 -11530328 7502851654 ssub (de:putative aliphatic sulfonates transport atp-binding protein ssub) (db:swissprot) SSUB_BACSU P97027 BACILLUS SUBTILIS 1423 -11530328 7000694323 ygal nitrate abc transporter binding protein homolog ygal (cl:atp-binding cassette homology) (db:pir2.dat) G69816 G69816 Bacillus subtilis 1423 -11530328 308001 ygal (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to nitrate abc transporter (binding) (le:158026) (re:158850) (di:direct) BSUB0005 Z99108 g2633206 Bacillus subtilis 1423 -11530328 7500965020 ygal hypothetical 30.6 kd protein (db:genpept-bct1) (de:b.subtilis yga(l,m,n,o,p,q,r,s,t), yzdb and yze(a,c} genes.) (le:352) (re:1176) (di:direct) BSZ93102 Z93102 g1903038 Bacillus subtilis 1423 -11530328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779431	3324	25480	600	199

Description

5000688685 yzea:ygba hypothetical protein:hypothetical 36.3 kd lipoprotein precursor:orfk (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygbA ygbA Bacillus subtilis 1423 -11530329 117002 ssua (de:putative aliphatic sulfonates binding protein precursor) (db:swissprot) SSUA_BACSU P40400 BACILLUS SUBTILIS 1423 -11530329 7000688835 ygba abc transporter binding lipoprotein homolog ygba (db:pir2.dat) I39927 I39927 Bacillus subtilis 1423 -11530329 7500953076 (sr:bacillus subtilis (individual_isolate ms11) (library: tn91) (db:genpept-bct1) (de:bacillus subtilis orfk, orfl and orfm, complete cds's.) (nt:likely n-terminal signal sequence, followed by) (le:69) (re:1067) (di:direct) BACORFKLM L16808 g438472 Bacillus subtilis 1423 -11530329 216419 ygba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yzea; similar to abc) (le:158868) (re:159866) (di:direct) BSUB0005 Z99108 g2633207 Bacillus subtilis 1423 -11530329 308002 yzea hypothetical 36.3 kd lipoprotein precursor (db:genpept-bct1) (de:b.subtilis yga{l,m,n,o,p,q,r,s,t), yzdb and yze{a,c} genes.) (nt:homology to nitrate transport protein precursor) (le:1194) (re:2192) (di:direct) BSZ93102 Z93102 g1903039 Bacillus subtilis 1423 -11530329 170251 ygba abc transporter binding lipoprotein homolog ygba (db:pir) I39927 I39927 Bacillus subtilis 1423 -11530329 6500726471 yzea hypothetical protein:hypothetical 36.3 kd lipoprotein precursor:orfk (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygbA ygbA Bacillus subtilis 1423 -11530329

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779436	3325	25481	456	151

Description

5000689893 yzeb:ygam hypothetical protein:probable abc transporter permease protein:orfl (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaM ygaM Bacillus subtilis 1423 -11530330 117003 ssuc (de:putative aliphatic sulfonates transport permease protein ssuc) (db:swissprot) SSUC_BACSU P40401 BACILLUS SUBTILIS 1423 -11530330 7000688836 ygam nitrate transport protein nrtb homolog ygam (cl:synechococcus nitrate transport protein nrtb) (db:pir2.dat) I39928 I39928 Bacillus subtilis 1423 -11530330 7500924003 (sr:bacillus subtilis (individual_isolate ms11) (library: tn91) (db:genpept-bct1) (de:bacillus subtilis orfk, orfl and orfm, complete cds's.) (nt:protein is hydrophobic, with homology to e. coli) (le:1064) (re:1894) (di:direct) BACORFKLM L16808 g438473 Bacillus subtilis 1423 -11530330 216420 ygam (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yzeb; similar to abc) (le:159863) (re:160693) (di:direct) BSUB0005 Z99108 g2633208 Bacillus subtilis 1423 -11530330 308003 ygam hypothetical 30.2 kd protein (db:genpept-bct1) (de:b.subtilis yga(l,m,n,o,p,q,r,s,t), yzdb and yze(a,c} genes.) (nt:homology to nitrate permease protein) (le:2189) (re:3019) (di:direct) BSZ93102 Z93102 g1903040 Bacillus subtilis 1423 -11530330 170466 ygam abc transporter permease homolog ygam (cl:hypothetical protein b0934) (db:pir) I39928 I39928 Bacillus subtilis 1423 -11530330 6500726472 yzeb hypothetical protein:probable abc transporter permease protein:orfl (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaM ygaM Bacillus subtilis 1423 -11530330

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779445	3326	25482	510	170

Description

6500726473 yzec:ygca hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygcA ygcA Bacillus subtilis 1423 -11530331 7000692507 ygca sulfate starvation-induced protein 6 homolog ygca (db:pir2.dat) D69817 D69817 Bacillus subtilis 1423 -11530331 308004 ygca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yzec; similar to hypothetical) (le:160710) (re:161846) (di:direct) BSUB0005 Z99108 g2633209 Bacillus subtilis 1423 -11530331 7500963645 yzec hypothetical 42 kd protein (db:genpept-bct1) (de:b.subtilis yga(l,m,n,o,p,q,r,s,t), yzdb and yze(a,c} genes.) (le:3036) (re:4172) (di:direct) BSZ93102 Z93102 g1903041 Bacillus subtilis 1423 -11530331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779449	3327	25483	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779455	3328	25484	1107	368

Description

6500726474 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaN ygaN Bacillus subtilis 1423 -11530332 7000693319 ygan hypothetical protein ygan (db:pir2.dat) A69817 A69817 Bacillus subtilis 1423 -11530332 308005 ygan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:161950) (re:162486) (di:direct) BSUB0005 Z99108 g2633210 Bacillus subtilis 1423 -11530332 7500964275 ygan hypothetical 19.9 kd protein (db:genpept-bct1) (de:b.subtilis yga(l,m,n,o,p,q,r,s,t), yzdb and yze(a,c) genes.) (le:4276) (re:4812) (di:direct) BSZ93102 Z93102 g1903042 Bacillus subtilis 1423 -11530332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779462	3329	25485	327	108

Description

6500726475 hypothetical protein:similar to ribosomal protein s14 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhzA yhzA Bacillus subtilis 1423 -11530333 7000694534 yhza ribosomal protein s14 homolog yhza (cl:escherichia coli ribosomal protein s14) (db:pir2.dat) F69835 F69835 Bacillus subtilis 1423 -11530333 7500965159 yhza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to ribosomal protein s14) (le:162598) (re:162867) (di:direct) BSUB0005 Z99108 g2633211 Bacillus subtilis 1423 -11530333

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779749	3330	25486	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779756	3331	25487	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779758	3332	25488	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779761	3333	25489	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779763	3334	25490	351	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779770	3335	25491	681	226

Description

6500726476 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygaO ygaO Bacillus subtilis 1423 -11530334 7000693320 ygao hypothetical protein ygao (db:pir2.dat) B69817 B69817 Bacillus subtilis 1423 -11530334 308006 ygao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:162885) (re:163358) (di:complement) BSUB0005 Z99108 g2633212 Bacillus subtilis 1423 -11530334 7500964276 ygao hypothetical 17.8 kd protein (db:genpept-bct1) (de:b.subtilis yga(l,m,n,o,p,q,r,s,t), yzdb and yze(a,c) genes.) (le:5211) (re:5684) (di:complement) BSZ93102 Z93102 g1903043 Bacillus subtilis 1423 -11530334

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779795	3336	25492	300	99

Description

6500726477 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhzB yhzB Bacillus subtilis 1423 -11530335 7000693358 yhzb hypothetical protein yhzb (db:pir2.dat) G69835 G69835 Bacillus subtilis 1423 -11530335 7500964314 yhzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:163918) (re:164541) (di:complement) BSUB0005 Z99108 g2633213 Bacillus subtilis 1423 -11530335

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779805	3337	25493	498	165

Description

6500726478 ygap:yhba hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbA yhbA Bacillus subtilis 1423 -11530336 7000692515 yhba conserved hypothetical protein yhba (db:pir2.dat) E69820 E69820 Bacillus subtilis 1423 -11530336 308007 yhba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: ygap; similar to hypothetical) (le:164477) (re:165784) (di:direct) BSUB0005 Z99108 g2633214 Bacillus subtilis 1423 -11530336 7500963650 ygap hypothetical 48.5 kd protein (db:genpept-bct1) (de:b.subtilis yga(l,m,n,o,p,q,r,s,t), yzdb and yze(a,c) genes.) (le:6803) (re:8110) (di:direct) BSZ93102 Z93102 g1903044 Bacillus subtilis 1423 -11530336

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779823	3338	25494	525	174

Description

6500726479 ygaq:yhbb hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbB yhbB Bacillus subtilis 1423 -11530337 7000692516 yhbb conserved hypothetical protein yhbb (db:pir2.dat) F69820 F69820 Bacillus subtilis 1423 -11530337 7500963651 yhbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: ygaq; similar to hypothetical) (le:165851) (re:166786) (di:direct) BSUB0005 Z99108 g2633215 Bacillus subtilis 1423 -11530337

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779831	3339	25495	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779835	3340	25496	900	299

Description

GTC ORF with score 118 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c27a2.) (nt:similar to histidine acid phosphotase family) (le:3498:3822:4165) (re:3779:3971:4302) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779850	3341	25497	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779869	3342	25498	369	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779891	3343	25499	939	312

Description

6500726480 ygas:yhbd hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbD yhbD Bacillus subtilis 1423 -11530338 7000692517 yhbd conserved hypothetical protein yhbd (db:pir2.dat) G69820 G69820 Bacillus subtilis 1423 -11530338 308010 yhbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: ygas; similar to hypothetical) (le:167356) (re:168072) (di:direct) BSUB0005 Z99108 g2633217 Bacillus subtilis 1423 -11530338 7500963652 ygas hypothetical 27 kd protein (db:genpept-bct1) (de:b.subtilis yga{l,m,n,o,p,q,r,s,t), yzdb and yze{a,c} genes.) (le:9682) (re:10398) (di:direct) BSZ93102 Z93102 g1903047 Bacillus subtilis 1423 -11530338

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779908	3344	25500	588	196

Description

6500726481 yzda:ygat:yhbe hypothetical protein:hypothetical 24.7 kd protein in prka 5region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbE yhbE Bacillus subtilis 1423 -11530339 116997 yhbe (de:hypothetical 24.7 kd protein in prka 5'region (orf1)) (db:swissprot) YHBE_BACSU P39132 BACILLUS SUBTILIS 1423 -11530339 7000687898 yhbe conserved hypothetical protein yhbe (cl:conserved hypothetical protein yhbf) (db:pir2.dat) H69820 H69820 Bacillus subtilis 1423 -11530339 308011 yhbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yzda, ygat; similar to) (le:168063) (re:168776) (di:direct) BSUB0005 Z99108 g2633218 Bacillus subtilis 1423 -11530339 7500936769 ygat hypothetical 24.7 kd protein (db:genpept-bct1) (de:b.subtilis yga(l,m,n,o,p,q,r,s,t), yzdb and yze(a,c) genes.) (le:10389) (re:11102) (di:direct) BSZ93102 Z93102 g1903048 Bacillus subtilis 1423 -11530339

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779928	3345	25501	1218	406

Description

6500726482 yzdb:yhbf hypothetical protein:hypothetical 25.1 kd protein in prka 5region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbF yhbF Bacillus subtilis 1423 -11530340 7500963653 yhbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yzdb; similar to hypothetical) (le:168788) (re:169495) (di:direct) BSUB0005 Z99108 g2633219 Bacillus subtilis 1423 -11530340 7000692518 yhbf conserved hypothetical protein yhbf (db:pir) A69821 A69821 Bacillus subtilis 1423 -11530340

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779938	3346	25502	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779956	3347	25503	939	312

Description

6500726483 yzdc:yhbh hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbH yhbH Bacillus subtilis 1423 -11530341 7502851655 yhbh (de:hypothetical 45.3 kd protein in prka-cspb intergenic region (orf4)) (db:swissprot) YHBH_BACSU P45742 BACILLUS SUBTILIS 1423 -11530341 7000692519 yhbh conserved hypothetical protein yhbh (db:pir2.dat) B69821 B69821 Bacillus subtilis 1423 -11530341 7500963654 yhbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:alternate gene name: yzdc; similar to hypothetical) (le:171920) (re:173098) (di:direct) BSUB0005 Z99108 g2633221 Bacillus subtilis 1423 -11530341

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779958	3348	25504	1035	344

Description

6500726484 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbI yhbI Bacillus subtilis 1423 -11530342 7000694768 yhbi transcription regulator marr family homolog yhbi (db:pir2.dat) C69821 C69821 Bacillus subtilis 1423 -11530342 7500965335 yhbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to transcriptional regulator (marr family)) (le:173258) (re:173722) (di:direct) BSUB0005 Z99108 g2633222 Bacillus subtilis 1423 -11530342

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501779965	3349	25505	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780354	3350	25506	426	141

Description

6500726485 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhbJ yhbJ Bacillus subtilis 1423 -11530343 7000693331 yhbj hypothetical protein yhbj (db:pir2.dat) D69821 D69821 Bacillus subtilis 1423 -11530343 7500964287 yhbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:173758) (re:174423) (di:direct) BSUB0005 Z99108 g2633223 Bacillus subtilis 1423 -11530343

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780360	3351	25507	537	179

Description

6500726486 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcA yhcA Bacillus subtilis 1423 -11530344 7502851656 yhca (de:hypothetical 58.3 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCA_BACSU P54585 BACILLUS SUBTILIS 1423 -11530344 7000694244 yhca multidrug resistance protein homolog yhca (db:pir2.dat) E69821 E69821 Bacillus subtilis 1423 -11530344 7500964970 yhca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to multidrug resistance protein) (le:174464) (re:176062) (di:direct) BSUB0005 Z99108 g2633224 Bacillus subtilis 1423 -11530344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780362	3352	25508	1359	453

Description

GTC ORF with score 286 to: (db:genpept) (de:fusarium solani f. sp. pisi histidine kinase fik (fik) gene,complete cds.) (nt:similar to neurospora nik-1, genbank accession) (le:718:1689:2571:2885) (re:1549:2515:2837:4384) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780373	3353	25509	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780375	3354	25510	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780376	3355	25511	984	327

Description

5000689162 hypothetical protein:hypothetical 19.0 kd protein in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcB yhcB Bacillus subtilis 1423 -11530345 218964 yhcb (de:hypothetical 19.0 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCB_BACSU P54586 BACILLUS SUBTILIS 1423 -11530345 7000687915 yhcb flavodoxin homolog yhcb (cl:conserved hypothetical protein ycr004c) (db:pir2.dat) F69821 F69821 Bacillus subtilis 1423 -11530345 6500726487 yhcb hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to trp repressor-binding protein wrba) (le:279) (re:809) (di:direct) BS75DGREG X96983 g1239977 Bacillus subtilis 1423 -11530345 308480 yhcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to flavodoxin) (le:176085) (re:176615) (di:direct) BSUB0005 Z99108 g2633225 Bacillus subtilis 1423 -11530345 112665 yhcb (de:hypothetical 19.0 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCB_BACSU P54586 BACILLUS SUBTILIS 1423 -11530345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780382	3356	25512	816	271

Description

5000689163 hypothetical protein:hypothetical 14.0 kd protein in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcC yhcC Bacillus subtilis 1423 -11530346 218965 yhcc (de:hypothetical 14.0 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCC_BACSU P54587 BACILLUS SUBTILIS 1423 -11530346 7000687917 yhcc hypothetical protein yhcc (db:pir2.dat) G69821 G69821 Bacillus subtilis 1423 -11530346 6500726488 yhcc hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (le:822) (re:1196) (di:direct) BS75DGREG X96983 g1239978 Bacillus subtilis 1423 -11530346 308481 yhcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:176628) (re:177002) (di:direct) BSUB0005 Z99108 g2633226 Bacillus subtilis 1423 -11530346 112668 yhcc (de:hypothetical 14.0 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCC_BACSU P54587 BACILLUS SUBTILIS 1423 -11530346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780388	3357	25513	540	179

Description

5000689164 hypothetical protein:hypothetical 6.0 kd protein in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcD yhcD Bacillus subtilis 1423 -11530347 218966 yhcd (de:hypothetical 6.0 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCD_BACSU P54588 BACILLUS SUBTILIS 1423 -11530347 7000687918 yhcd hypothetical protein yhcd (db:pir2.dat) H69821 H69821 Bacillus subtilis 1423 -11530347 6500726489 yhcd hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (le:1196) (re:1351) (di:direct) BS75DGREG X96983 g1239979 Bacillus subtilis 1423 -11530347 308482 yhcd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:177002) (re:177157) (di:direct) BSUB0005 Z99108 g2633227 Bacillus subtilis 1423 -11530347 112670 yhcd (de:hypothetical 6.0 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCD_BACSU P54588 BACILLUS SUBTILIS 1423 -11530347

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780390	3358	25514	396	131

Description

5000689165 hypothetical protein:hypothetical 29.5 kd protein in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcE yhcE Bacillus subtilis 1423 -11530348 218967 yhce (de:hypothetical 29.5 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCE_BACSU P54589 BACILLUS SUBTILIS 1423 -11530348 7000687920 yhce hypothetical protein yhce (db:pir2.dat) A69822 A69822 Bacillus subtilis 1423 -11530348 6500726490 yhce hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (le:1356) (re:2117) (di:direct) BS75DGREG X96983 g1239980 Bacillus subtilis 1423 -11530348 308483 yhce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:177162) (re:177923) (di:direct) BSUB0005 Z99108 g2633228 Bacillus subtilis 1423 -11530348 112672 yhce (de:hypothetical 29.5 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCE_BACSU P54589 BACILLUS SUBTILIS 1423 -11530348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780392	3359	25515	486	161

Description

5000689166 hypothetical protein:hypothetical transcriptional regulator in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcF yhcF Bacillus subtilis 1423 -11530349 218968 yhcf (de:hypothetical transcriptional regulator in prka-cspb intergenic region) (db:swissprot) YHCF_BACSU P54590 BACILLUS SUBTILIS 1423 -11530349 7000687921 yhcf transcription regulator gntr family homolog yhcf (db:pir2.dat) B69822 B69822 Bacillus subtilis 1423 -11530349 6500726491 yhcf hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to members of the gntr regulator family) (le:2120) (re:2485) (di:direct) BS75DGREG X96983 g1239981 Bacillus subtilis 1423 -11530349 308484 yhcf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to transcriptional regulator (gntr family)) (le:177926) (re:178291) (di:direct) BSUB0005 Z99108 g2633229 Bacillus subtilis 1423 -11530349 112674 yhcf (de:hypothetical transcriptional regulator in prka-cspb intergenic region) (db:swissprot) YHCF_BACSU P54590 BACILLUS SUBTILIS 1423 -11530349

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780408	3360	25516	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780409	3361	25517	435	144

Description

5000689167 hypothetical protein:hypothetical abc transporter atp-binding protein 1 in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcG yhcG Bacillus subtilis 1423 -11530350 218969 yhcg (de:intergenic region) (db:swissprot) YHCG_BACSU P54591 BACILLUS SUBTILIS 1423 -11530350 7000687923 yhcg glycine betaine/l-proline transport homolog yhcg (cl:atp-binding cassette homology) (db:pir2.dat) C69822 C69822 Bacillus subtilis 1423 -11530350 6500726492 yhcg hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to abc transporters like the sulfate) (le:2487) (re:3185) (di:direct) BS75DGREG X96983 g1239982 Bacillus subtilis 1423 -11530350 308485 yhcg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to glycine betaine/l-proline transport) (le:178293) (re:178991) (di:direct) BSUB0005 Z99108 g2633230 Bacillus subtilis 1423 -11530350 112676 yhcg (de:intergenic region) (db:swissprot) YHCG_BACSU P54591 BACILLUS SUBTILIS 1423 -11530350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780410	3362	25518	615	204

Description

5000689168 hypothetical protein:hypothetical abc transporter atp-binding protein 2 in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcH yhcH Bacillus subtilis 1423 -11530351 218970 yhch (de:intergenic region) (db:swissprot) YHCH_BACSU P54592 BACILLUS SUBTILIS 1423 -11530351 7000687925 yhch abc transporter atp-binding protein homolog yhch (cl:atp-binding cassette homology) (db:pir2.dat) D69822 D69822 Bacillus subtilis 1423 -11530351 6500726493 yhch hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to abc transporters like the copper) (le:3202) (re:4119) (di:direct) BS75DGREG X96983 g1239983 Bacillus subtilis 1423 -11530351 308486 yhch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (atp-binding protein)) (le:179008) (re:179925) (di:direct) BSUB0005 Z99108 g2633231 Bacillus subtilis 1423 -11530351 112678 yhch (de:intergenic region) (db:swissprot) YHCH_BACSU P54592 BACILLUS SUBTILIS 1423 -11530351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780413	3363	25519	762	253

Description

GTC ORF with score 569 to: (fn:catalyzes the first methylation step from pe to) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe phosphatidylethanolaminemethyltransferase (cho2+) gene, complete cds.) (nt:cho2p) (le:1018) (re:3348) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780418	3364	25520	699	232

Description

5000689169 hypothetical protein:hypothetical 34.9 kd protein in glpd-cspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcI yhcI Bacillus subtilis 1423 -11530352 218971 yhci (de:hypothetical 34.9 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCI_BACSU P54593 BACILLUS SUBTILIS 1423 -11530352 7000687927 yhci hypothetical protein yhci (db:pir2.dat) E69822 E69822 Bacillus subtilis 1423 -11530352 6500726494 yhci hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to the membrane protein nosy from) (le:4112) (re:5053) (di:direct) BS75DGREG X96983 g1239984 Bacillus subtilis 1423 -11530352 308487 yhci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:179918) (re:180859) (di:direct) BSUB0005 Z99108 g2633232 Bacillus subtilis 1423 -11530352 112681 yhci (de:hypothetical 34.9 kd protein in glpd-cspb intergenic region) (db:swissprot) YHCI_BACSU P54593 BACILLUS SUBTILIS 1423 -11530352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780461	3365	25521	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780462	3366	25522	303	100

Description

5000689170 hypothetical protein:hypothetical 29.2 kd lipoprotein in cspb-glpp intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcJ yhcJ Bacillus subtilis 1423 -11530353 218973 yhcj (de:precursor) (db:swissprot) YHCJ_BACSU P54594 BACILLUS SUBTILIS 1423 -11530353 7000687929 yhcj abc transporter binding lipoprotein homolog yhcj (db:pir2.dat) F69822 F69822 Bacillus subtilis 1423 -11530353 6500726495 yhcj hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to lipoprotein-28 precursor nlpa from) (le:5784) (re:6575) (di:direct) BS75DGREG X96983 g1239986 Bacillus subtilis 1423 -11530353 308489 yhcj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to abc transporter (binding lipoprotein)) (le:181590) (re:182381) (di:direct) BSUB0005 Z99108 g2633234 Bacillus subtilis 1423 -11530353 112684 yhcj (de:precursor) (db:swissprot) YHCJ_BACSU P54594 BACILLUS SUBTILIS 1423 -11530353

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780465	3367	25523	798	265

Description

5000689171 hypothetical protein:hypothetical 40.7 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcK yhcK Bacillus subtilis 1423 -11530354 218974 yhck (de:hypothetical 40.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCK_BACSU P54595 BACILLUS SUBTILIS 1423 -11530354 7000687931 yhck conserved hypothetical protein yhck (db:pir2.dat) G69822 G69822 Bacillus subtilis 1423 -11530354 6500726496 yhck hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to hypothetical proteins from) (le:6616) (re:7695) (di:complement) BS75DGREG X96983 g1239987 Bacillus subtilis 1423 -11530354 308490 yhck (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:182422) (re:183501) (di:complement) BSUB0005 Z99108 g2633235 Bacillus subtilis 1423 -11530354 112686 yhck (de:hypothetical 40.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCK_BACSU P54595 BACILLUS SUBTILIS 1423 -11530354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780479	3368	25524	480	159

Description

5000689172 hypothetical protein:hypothetical 49.0 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcL yhcL Bacillus subtilis 1423 -11530355 218975 yhcl (de:hypothetical 49.0 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCL_BACSU P54596 BACILLUS SUBTILIS 1423 -11530355 7000687933 yhcl sodium-glutamate symporter homolog yhcl (cl:bacillus subtilis sodium-glutamate symporter homolog yhcl) (db:pir2.dat) H69822 H69822 Bacillus subtilis 1423 -11530355 6500726497 yhcl hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to the proton/sodium-glutamate symport) (le:7868) (re:9259) (di:direct) BS75DGREG X96983 g1239988 Bacillus subtilis 1423 -11530355 308491 yhcl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to sodium-glutamate symporter) (le:183674) (re:185065) (di:direct) BSUB0005 Z99108 g2633236 Bacillus subtilis 1423 -11530355 112688 yhcl (de:hypothetical 49.0 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCL_BACSU P54596 BACILLUS SUBTILIS 1423 -11530355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780484	3369	25525	723	240

Description

5000689173 hypothetical protein:hypothetical 17.0 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcM yhcM Bacillus subtilis 1423 -11530356 218976 yhcm (de:hypothetical 17.0 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCM_BACSU P54597 BACILLUS SUBTILIS 1423 -11530356 7000687935 yhcm hypothetical protein yhcm (db:pir2.dat) A69823 A69823 Bacillus subtilis 1423 -11530356 6500726498 yhcm hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:glutamine-rich protein.) (le:9299) (re:9754) (di:complement) BS75DGREG X96983 g1239989 Bacillus subtilis 1423 -11530356 308492 yhcm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:185105) (re:185560) (di:complement) BSUB0005 Z99108 g2633237 Bacillus subtilis 1423 -11530356 112690 yhcm (de:hypothetical 17.0 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCM_BACSU P54597 BACILLUS SUBTILIS 1423 -11530356

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780492	3370	25526	372	123

Description

5000689174 hypothetical protein:hypothetical 21.0 kd lipoprotein in cspb-glpp intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcN yhcN Bacillus subtilis 1423 -11530357 218977 yhcn (de:precursor) (db:swissprot) YHCN_BACSU P54598 BACILLUS SUBTILIS 1423 -11530357 7000687937 yhcn conserved hypothetical protein yhcn (db:pir2.dat) B69823 B69823 Bacillus subtilis 1423 -11530357 6500726499 yhcn hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:asparagine-rich protein. similarity to cs3 pili) (le:9904) (re:10473) (di:direct) BS75DGREG X96983 g1239990 Bacillus subtilis 1423 -11530357 308493 yhcn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:185710) (re:186279) (di:direct) BSUB0005 Z99108 g2633238 Bacillus subtilis 1423 -11530357 112692 yhcn (de:precursor) (db:swissprot) YHCN_BACSU P54598 BACILLUS SUBTILIS 1423 -11530357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780493	3371	25527	225	74

Description

5000689175 hypothetical protein:hypothetical 11.4 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcO yhcO Bacillus subtilis 1423 -11530358 218978 yhco (de:hypothetical 11.4 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCO_BACSU P54599 BACILLUS SUBTILIS 1423 -11530358 7000687939 yhco hypothetical protein yhco (db:pir2.dat) C69823 C69823 Bacillus subtilis 1423 -11530358 6500726500 yhco hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (le:10653) (re:10952) (di:direct) BS75DGREG X96983 g1239991 Bacillus subtilis 1423 -11530358 308494 yhco (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:186459) (re:186758) (di:direct) BSUB0005 Z99108 g2633239 Bacillus subtilis 1423 -11530358 112694 yhco (de:hypothetical 11.4 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCO_BACSU P54599 BACILLUS SUBTILIS 1423 -11530358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780494	3372	25528	711	236

Description

5000689176 hypothetical protein:hypothetical 24.1 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcP yhcP Bacillus subtilis 1423 -11530359 218979 yhcp (de:hypothetical 24.1 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCP_BACSU P54600 BACILLUS SUBTILIS 1423 -11530359 7000687941 yhcp hypothetical protein yhcp (db:pir2.dat) D69823 D69823 Bacillus subtilis 1423 -11530359 6500726501 yhcp hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (le:10943) (re:11560) (di:direct) BS75DGREG X96983 g1239992 Bacillus subtilis 1423 -11530359 308495 yhcp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:186749) (re:187366) (di:direct) BSUB0005 Z99108 g2633240 Bacillus subtilis 1423 -11530359 112696 yhcp (de:hypothetical 24.1 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCP_BACSU P54600 BACILLUS SUBTILIS 1423 -11530359

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780516	3373	25529	978	326

Description

5000689177 hypothetical protein:hypothetical 24.8 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcQ yhcQ Bacillus subtilis 1423 -11530360 218980 yhcq (de:hypothetical 24.8 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCQ_BACSU P54601 BACILLUS SUBTILIS 1423 -11530360 7000687943 yhcq conserved hypothetical protein yhcq (db:pir2.dat) E69823 E69823 Bacillus subtilis 1423 -11530360 6500726502 yhcq hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to spore coat protein f (cotf) from) (le:11492) (re:12145) (di:complement) BS75DGREG X96983 g1239993 Bacillus subtilis 1423 -11530360 308496 yhcq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins from b. subtilis) (le:187298) (re:187951) (di:complement) BSUB0005 Z99108 g2633241 Bacillus subtilis 1423 -11530360 112698 yhcq (de:hypothetical 24.8 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCQ_BACSU P54601 BACILLUS SUBTILIS 1423 -11530360

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780520	3374	25530	525	174

Description

5000689178 hypothetical protein:hypothetical 132.7 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcR yhcR Bacillus subtilis 1423 -11530361 218981 yhcr (de:hypothetical 132.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCR_BACSU P54602 BACILLUS SUBTILIS 1423 -11530361 7000687945 yhcr probable phosphoesterase:yhcr:5-nucleotidase homolog yhcr (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) F69823 F69823 Bacillus subtilis 1423 -11530361 6500726503 yhcr hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity (c-terminal half) to udp-sugar hydrolase) (le:12228) (re:15881) (di:direct) BS75DGREG X96983 g1239994 Bacillus subtilis 1423 -11530361 308497 yhcr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to 5'-nucleotidase) (le:188034) (re:191687) (di:direct) BSUB0005 Z99108 g2633242 Bacillus subtilis 1423 -11530361 112700 yhcr (de:hypothetical 132.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCR_BACSU P54602 BACILLUS SUBTILIS 1423 -11530361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780522	3375	25531	723	240

Description

5000689179 hypothetical protein:hypothetical 22.0 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcS yhcS Bacillus subtilis 1423 -11530362 218982 yhcs (de:hypothetical 22.0 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCS_BACSU P54603 BACILLUS SUBTILIS 1423 -11530362 7000687947 yhcs hypothetical protein yhcs (db:pir2.dat) G69823 G69823 Bacillus subtilis 1423 -11530362 6500726504 yhcs hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (le:15878) (re:16474) (di:direct) BS75DGREG X96983 g1239995 Bacillus subtilis 1423 -11530362 308498 yhcs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:191684) (re:192280) (di:direct) BSUB0005 Z99108 g2633243 Bacillus subtilis 1423 -11530362 112702 yhcs (de:hypothetical 22.0 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCS_BACSU P54603 BACILLUS SUBTILIS 1423 -11530362

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780532	3376	25532	924	307

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780543	3377	25533	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780565	3378	25534	510	169

Description

GTC ORF with score 142 to: (db:genpept-bct2) (de:acinetobacter calcoaceticus benzaldehyde dehydrogenase ii (xylc)and benzyl alcohol dehydrogenase (xylb) genes, complete cds.) (nt:ec_number=1.2.1.28) (le:328) (re:1782) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780566	3379	25535	612	203

Description

5000689180 hypothetical protein:hypothetical 33.7 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcT yhcT Bacillus subtilis 1423 -11530363 218983 yhct (de:hypothetical 33.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCT_BACSU P54604 BACILLUS SUBTILIS 1423 -11530363 7000687949 yhct conserved hypothetical protein yhct (cl:conserved hypothetical protein hi0176) (db:pir2.dat) H69823 H69823 Bacillus subtilis 1423 -11530363 6500726505 yhct hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to drap deaminase from saccharomyces) (le:16504) (re:17412) (di:complement) BS75DGREG X96983 g1239996 Bacillus subtilis 1423 -11530363 308499 yhct (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:192310) (re:193218) (di:complement) BSUB0005 Z99108 g2633244 Bacillus subtilis 1423 -11530363 112705 yhct (de:hypothetical 33.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCT_BACSU P54604 BACILLUS SUBTILIS 1423 -11530363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780569	3380	25536	633	210

Description

5000689181 hypothetical protein:hypothetical 15.3 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcU yhcU Bacillus subtilis 1423 -11530364 218984 yhcu (de:hypothetical 15.3 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCU_BACSU P54605 BACILLUS SUBTILIS 1423 -11530364 7000687950 yhcu hypothetical protein yhcu (db:pir2.dat) A69824 A69824 Bacillus subtilis 1423 -11530364 6500726506 yhcu hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (le:17523) (re:17918) (di:direct) BS75DGREG X96983 g1239997 Bacillus subtilis 1423 -11530364 308500 yhcu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:193329) (re:193724) (di:direct) BSUB0005 Z99108 g2633245 Bacillus subtilis 1423 -11530364 112706 yhcu (de:hypothetical 15.3 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCU_BACSU P54605 BACILLUS SUBTILIS 1423 -11530364

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780573	3381	25537	618	205

Description

5000689183 hypothetical protein:hypothetical 24.7 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcW yhcW Bacillus subtilis 1423 -11530365 218986 yhcw (de:hypothetical 24.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCW_BACSU P54607 BACILLUS SUBTILIS 1423 -11530365 7000687952 yhcw phosphoglycolate phosphatase homolog yhcw (cl:hypothetical protein b2690) (db:pir2.dat) C69824 C69824 Bacillus subtilis 1423 -11530365 6500726507 yhcw hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to phosphoglycolate phosphatase from) (le:18604) (re:19266) (di:direct) BS75DGREG X96983 g1239999 Bacillus subtilis 1423 -11530365 308502 yhcw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to phosphoglycolate phosphatase) (le:194410) (re:195072) (di:direct) BSUB0005 Z99108 g2633247 Bacillus subtilis 1423 -11530365 112708 yhcw (de:hypothetical 24.7 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCW_BACSU P54607 BACILLUS SUBTILIS 1423 -11530365

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780577	3382	25538	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780585	3383	25539	1722	574

Description

5000689184 hypothetical protein:hypothetical 60.2 kd protein in cspb-glpp intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcX yhcX Bacillus subtilis 1423 -11530366 218987 yhcx (de:hypothetical 60.2 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCX_BACSU P54608 BACILLUS SUBTILIS 1423 -11530366 7000687953 yhcx conserved hypothetical protein yhcx (db:pir2.dat) D69824 D69824 Bacillus subtilis 1423 -11530366 6500726508 yhcx hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna (region 75 degrees: cspb upstream ofglppfkd operon).) (nt:similarity to nitrilase 2 from arabidopsis thaliana) (le:19282) (re:20823) (di:direct) BS75DGREG X96983 g1240000 Bacillus subtilis 1423 -11530366 308503 yhcx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:195088) (re:196629) (di:direct) BSUB0005 Z99108 g2633248 Bacillus subtilis 1423 -11530366 112709 yhcx (de:hypothetical 60.2 kd protein in cspb-glpp intergenic region) (db:swissprot) YHCX_BACSU P54608 BACILLUS SUBTILIS 1423 -11530366

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780594	3384	25540	810	269

Description

6500726509 hypothetical protein:putative aminotransferase yhxa (gtcfc:14.1) (ec:2.6.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhxA yhxA Bacillus subtilis 1423 -11530367 113042 yhxa (ec:2.6.-.-) (de:probable aminotransferase yhxa,) (db:swissprot) YHXA_BACSU P33189 BACILLUS SUBTILIS 1423 -11530367 7000688003 yhxa adenosylmethionine-8-amino-7-oxononanoate homolog yhxa (cl:beta-alanine--pyruvate transaminase) (db:pir2.dat) B69835 B69835 Bacillus subtilis 1423 -11530367 4000714553 yhxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to) (le:197049) (re:198401) (di:direct) BSUB0005 Z99108 g2633249 Bacillus subtilis 1423 -11530367 6000690449 yhxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to) (le:369) (re:1721) (di:direct) BSUB0006 Z99109 g2633261 Bacillus subtilis 1423 -11530367 7500937201 yhxa hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:similarity to dapa aminotransferase (bioa) from) (le:17) (re:1369) (di:direct) BSY14079 Y14079 g2226134 Bacillus subtilis 1423 -11530367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780625	3385	25541	258	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780631	3386	25542	1389	463

Description

6500726510 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcY yhcY Bacillus subtilis 1423 -11530368 7000694874 yhcy two-component sensor histidine kinase homolog yhcy (db:pir2.dat) E69824 E69824 Bacillus subtilis 1423 -11530368 4000714555 yhcy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to two-component sensor histidine kinase) (le:205305) (re:206444) (di:direct) BSUB0005 Z99108 g2633255 Bacillus subtilis 1423 -11530368 6000690453 yhcy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to two-component sensor histidine kinase) (le:8625) (re:9764) (di:direct) BSUB0006 Z99109 g2633267 Bacillus subtilis 1423 -11530368 7500965411 yhcy hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:similarity to the sensory transduction kinase degs) (le:8273) (re:9412) (di:direct) BSY14079 Y14079 g2226140 Bacillus subtilis 1423 -11530368

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780644	3387	25543	228	75

Description

6500726511 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhcZ yhcZ Bacillus subtilis 1423 -11530369 7000694845 yhcz two-component response regulator yhcy homolog yhcz) (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) F69824 F69824 Bacillus subtilis 1423 -11530369 4000714556 yhcz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to two-component response regulator (yhcy)) (le:206441) (re:207085) (di:direct) BSUB0005 Z99108 g2633256 Bacillus subtilis 1423 -11530369 6000690455 yhcz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to two-component response regulator (yhcy)) (le:9761) (re:10405) (di:direct) BSUB0006 Z99109 g2633268 Bacillus subtilis 1423 -11530369 7500965394 yhcz hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:similarity to the transcriptional regulator degu) (le:9409) (re:10053) (di:direct) BSY14079 Y14079 g2226141 Bacillus subtilis 1423 -11530369

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780654	3388	25544	765	254

Description

GTC ORF with score 273 to: (sr:thale cress) (db:genpept-pln2) (de:genomic sequence for arabidopsis thaliana bac f20n2, completesequence.) (nt:similar to beta transducin isolog (ac002333);) (le:63736:64009:64568:65002) (re:63873:64205:64895:65093) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780669	3389	25545	669	222

Description

6500726512 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdA yhdA Bacillus subtilis 1423 -11530370 7000692520 yhda conserved hypothetical protein yhda (db:pir2.dat) G69824 G69824 Bacillus subtilis 1423 -11530370 4000714557 yhda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (nt:similar to hypothetical proteins) (le:207082) (re:207606) (di:direct) BSUB0005 Z99108 g2633257 Bacillus subtilis 1423 -11530370 6000690457 yhda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:10402) (re:10926) (di:direct) BSUB0006 Z99109 g2633269 Bacillus subtilis 1423 -11530370 7500963655 yhda hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:similarity to the hypothetical protein yief from) (le:10050) (re:10574) (di:direct) BSY14079 Y14079 g2226142 Bacillus subtilis 1423 -11530370

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501780673	3390	25546	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781052	3391	25547	525	174

Description

6500726513 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdB yhdB Bacillus subtilis 1423 -11530371 7000693332 yhdb hypothetical protein yhdb (db:pir2.dat) H69824 H69824 Bacillus subtilis 1423 -11530371 4000714558 yhdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:207621) (re:207863) (di:complement) BSUB0005 Z99108 g2633258 Bacillus subtilis 1423 -11530371 6000690459 yhdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:10941) (re:11183) (di:complement) BSUB0006 Z99109 g2633270 Bacillus subtilis 1423 -11530371 7500964288 yhdb hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (le:10589) (re:10831) (di:complement) BSY14079 Y14079 g2226143 Bacillus subtilis 1423 -11530371

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781055	3392	25548	546	181

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781057	3393	25549	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781079	3394	25550	813	270

Description

GTC ORF with score 108 to: (sr:pisum sativum (strain alaska) (clone: na481-5) (clone library) (db:genpept-pln1) (de:pisum sativum l. (clone na-481-5) mrna, complete cds.) (nt:protein localized in the nucleoli of pea nuclei;) (le:75) (re:1910) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781089	3395	25551	315	105

Description

6500726514 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdC yhdC Bacillus subtilis 1423 -11530372 7000693333 yhdc hypothetical protein yhdc (db:pir2.dat) A69825 A69825 Bacillus subtilis 1423 -11530372 4000714559 yhdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.) (le:208064) (re:208387) (di:direct) BSUB0005 Z99108 g2633259 Bacillus subtilis 1423 -11530372 6000690461 yhdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:11384) (re:11707) (di:direct) BSUB0006 Z99109 g2633271 Bacillus subtilis 1423 -11530372 7500964289 yhdc hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (le:11032) (re:11355) (di:direct) BSY14079 Y14079 g2226144 Bacillus subtilis 1423 -11530372

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781097	3396	25552	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781107	3397	25553	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781112	3398	25554	636	212

Description

GTC ORF with score 135 to: (sr:soybean) (db:genpept-pln1) (ec:2.7.7.6) (de:soybean rpb1-b1 gene for the largest subunit of rna polymerase ii(ec 2.7.7.6).) (nt:largest subunit of rna polymerase ii) (le:<1:2062:2196) (re:1736:2133:2265) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781118	3399	25555	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781133	3400	25556	396	131

Description

GTC ORF with score 102 to: (db:genpept-bct2) (de:salmonella typhimurium (g30k) gene, partial cds; and 50s ribosomalprotein l32 (rpmf), plsx (plsx), 3-oxoacyl-acyl carrier proteinsynthase iii (fabh), malonyl coa-acyl carrier protein transacylase(fabd), ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781136	3401	25557	417	138

Description

6500726515 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdE yhdE Bacillus subtilis 1423 -11530373 7000692521 yhde conserved hypothetical protein yhde (cl:hypothetical protein b2531) (db:pir2.dat) C69825 C69825 Bacillus subtilis 1423 -11530373 4000714603 yhde (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:13367) (re:13807) (di:complement) BSUB0006 Z99109 g2633273 Bacillus subtilis 1423 -11530373 7500955872 yhde hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to the hypothetical protein yjeb from) (le:15) (re:455) (di:complement) BSY14082 Y14082 g2226194 Bacillus subtilis 1423 -11530373

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781137	3402	25558	312	103

Description

6500726516 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ygxB ygxB Bacillus subtilis 1423 -11530374 7500936623 ygxb (de:hypothetical 60.0 kd protein in glpd-spovr intergenic region (orf1)) (db:swissprot) YGXB_BACSU P37874 BACILLUS SUBTILIS 1423 -11530374 7000692508 ygxb conserved hypothetical protein ygxb:hypothetical protein sp0vb 3region (db:pir2.dat) F69817 F69817 Bacillus subtilis 1423 -11530374 7500936625 ygxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:13910) (re:15568) (di:complement) BSUB0006 Z99109 g2633274 Bacillus subtilis 1423 -11530374 4000714604 ygxb hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:see subtilist bg10181, embl 126337 and swiss prot) (le:558) (re:2216) (di:complement) BSY14082 Y14082 g2226195 Bacillus subtilis 1423 -11530374

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781163	3403	25559	561	187

Description

GTC ORF with score 134 to: (db:genpept-syn) (de:cloning vector tlf97-1, lambda phage lacz translational fusionvector, complete sequence.) (nt:ecori site normally present at the 3' end of lacz) (le:20812) (re:23859) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781164	3404	25560	1341	446

Description

6500726517 hypothetical protein:similar to glucose 1-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdF yhdF Bacillus subtilis 1423 -11530375 7500936833 yhdf (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YHDF_BACSU O07575 BACILLUS SUBTILIS 1423 -11530375 7000693035 yhdf glucose 1-dehydrogenase homolog yhdf (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D69825 D69825 Bacillus subtilis 1423 -11530375 7500936835 yhdf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to glucose 1-dehydrogenase) (le:22211) (re:23080) (di:direct) BSUB0006 Z99109 g2633280 Bacillus subtilis 1423 -11530375 4000714606 yhdf hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to glucose and ribitol dehydrogenase) (le:8859) (re:9728) (di:direct) BSY14082 Y14082 g2226201 Bacillus subtilis 1423 -11530375

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781189	3405	25561	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781205	3406	25562	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781206	3407	25563	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781208	3408	25564	648	215

Description

6500726518 hypothetical protein:similar to amino acid transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdG yhdG Bacillus subtilis 1423 -11530376 7000692202 yhdg amino acid transporter homolog yhdg (cl:arginine permease) (db:pir2.dat) E69825 E69825 Bacillus subtilis 1423 -11530376 4000714607 yhdg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to amino acid transporter) (le:23330) (re:24727) (di:direct) BSUB0006 Z99109 g2633281 Bacillus subtilis 1423 -11530376 7500963410 yhdg hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to human retroviral receptor (pir) (le:9978) (re:11375) (di:direct) BSY14082 Y14082 g2226202 Bacillus subtilis 1423 -11530376

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781210	3409	25565	1137	378

Description

6500726519 hypothetical protein:similar to sodium-dependent transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdH yhdH Bacillus subtilis 1423 -11530377 7000694593 yhdh sodium-dependent transporter homolog yhdh (cl:gamma-aminobutyric acid transporter) (db:pir2.dat) F69825 F69825 Bacillus subtilis 1423 -11530377 4000714608 yhdh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to sodium-dependent transporter) (le:24845) (re:26200) (di:direct) BSUB0006 Z99109 g2633282 Bacillus subtilis 1423 -11530377 7500965192 yhdh hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to sodium dependent transporters;) (le:11493) (re:12848) (di:direct) BSY14082 Y14082 g2226203 Bacillus subtilis 1423 -11530377

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781212	3410	25566	189	62

Description

6500726520 hypothetical protein:similar to transcriptional regulator:gntr family / aminotransferase:mocr-like (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdI yhdI Bacillus subtilis 1423 -11530378 7000694733 yhdi transcription regulator gntr family homolog yhdi (cl:hypothetical protein b1439) (db:pir2.dat) G69825 G69825 Bacillus subtilis 1423 -11530378 4000714609 yhdi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to transcriptional regulator (gntr family)) (le:26235) (re:27644) (di:complement) BSUB0006 Z99109 g2633283 Bacillus subtilis 1423 -11530378 7500965307 yhdi hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to mocr from rhizobium meliloti,) (le:12883) (re:14292) (di:complement) BSY14082 Y14082 g2226204 Bacillus subtilis 1423 -11530378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781214	3411	25567	375	124

Description

6500726521 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdJ yhdJ Bacillus subtilis 1423 -11530379 7000693334 yhdj hypothetical protein yhdj (db:pir2.dat) H69825 H69825 Bacillus subtilis 1423 -11530379 4000714610 yhdj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:27754) (re:28182) (di:direct) BSUB0006 Z99109 g2633284 Bacillus subtilis 1423 -11530379 7500964290 yhdj hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to phno from e.coli, regulator of) (le:14402) (re:14830) (di:direct) BSY14082 Y14082 g2226205 Bacillus subtilis 1423 -11530379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781215	3412	25568	240	79

Description

6500726522 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdK yhdK Bacillus subtilis 1423 -11530380 7000693335 yhdk hypothetical protein yhdk (db:pir2.dat) A69826 A69826 Bacillus subtilis 1423 -11530380 4000714611 yhdk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:28213) (re:28503) (di:complement) BSUB0006 Z99109 g2633285 Bacillus subtilis 1423 -11530380 7500964291 yhdk hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:no similarities.) (le:14861) (re:15151) (di:complement) BSY14082 Y14082 g2226206 Bacillus subtilis 1423 -11530380

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781224	3413	25569	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781233	3414	25570	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781242	3415	25571	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781263	3416	25572	561	186

Description

6500726523 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdL yhdL Bacillus subtilis 1423 -11530381 7000693336 yhdl hypothetical protein yhdl (db:pir2.dat) B69826 B69826 Bacillus subtilis 1423 -11530381 4000714612 yhdl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:28491) (re:29567) (di:complement) BSUB0006 Z99109 g2633286 Bacillus subtilis 1423 -11530381 7500964292 yhdl hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:no similarities.) (le:15139) (re:16215) (di:complement) BSY14082 Y14082 g2226207 Bacillus subtilis 1423 -11530381

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781268	3417	25573	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781269	3418	25574	297	98

Description

6500726524 hypothetical protein:similar to rna polymerase ecf-type sigma factor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdM yhdM Bacillus subtilis 1423 -11530382 7000694554 yhdm rna polymerase ecf-type sigma factor homolog yhdm (db:pir2.dat) C69826 C69826 Bacillus subtilis 1423 -11530382 4000714613 yhdm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to rna polymerase ecf-type sigma factor) (le:29557) (re:30048) (di:complement) BSUB0006 Z99109 g2633287 Bacillus subtilis 1423 -11530382 7500965166 yhdm hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to ybbl from b.subtilis, putative ecf) (le:16205) (re:16696) (di:complement) BSY14082 Y14082 g2226208 Bacillus subtilis 1423 -11530382

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781278	3419	25575	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781281	3420	25576	513	170

Description

GTC ORF with score 98 to: (sr:saccharomyces cerevisiae (clone: plg1) (clone library: hieter yeas) (db:genpept-pln2) (de:saccharomyces cerevisiae nucleoporin (rat7/nup159) gene, completecds.) (nt:rat7p or nup159p) (le:313) (re:4695) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781282	3421	25577	372	124

Description

GTC ORF with score 324 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c17g10.) (nt:similar to alcohol dehydrogenase/ribitol) (le:35008:35306:35576) (re:35261:35529:35789) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781288	3422	25578	1800	600

Description

6500726525 hypothetical protein:similar to aldo/keto reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdN yhdN Bacillus subtilis 1423 -11530383 7500882777 yhdn (de:general stress protein 69 (gsp69)) (db:swissprot) GS69_BACSU P80874 BACILLUS SUBTILIS 1423 -11530383 7000692171 yhdn aldo/keto reductase homolog yhdn (cl:conserved hypothetical protein ypl088w) (db:pir2.dat) D69826 D69826 Bacillus subtilis 1423 -11530383 7500882779 yhdn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to aldo/keto reductase) (le:30245) (re:31240) (di:direct) BSUB0006 Z99109 g2633288 Bacillus subtilis 1423 -11530383 4000714614 yhdn hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to yxbf from b.subtilis, swiss prot) (le:16893) (re:17888) (di:direct) BSY14082 Y14082 g2226209 Bacillus subtilis 1423 -11530383

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781302	3423	25579	285	94

Description

6500726526 hypothetical protein:similar to 1-acylglycerol-3-phosphate o-acyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdO yhdO Bacillus subtilis 1423 -11530384 7000692032 yhdo 1-acylglycerol-3-phosphate o-acyltransfera homolog yhdo (db:pir2.dat) E69826 E69826 Bacillus subtilis 1423 -11530384 4000714615 yhdo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to 1-acylglycerol-3-phosphate) (le:31375) (re:31974) (di:direct) BSUB0006 Z99109 g2633289 Bacillus subtilis 1423 -11530384 7500963285 yhdo hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to a hypothetical protein from) (le:18023) (re:18622) (di:direct) BSY14082 Y14082 g2226210 Bacillus subtilis 1423 -11530384

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781310	3424	25580	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781315	3425	25581	333	110

Description

6500726527 hypothetical protein:similar to hemolysin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdP yhdP Bacillus subtilis 1423 -11530385 7500936845 yhdp (de:hypothetical 49.9 kd protein in cita-sspb intergenic region) (db:swissprot) YHDP_BACSU O07585 BACILLUS SUBTILIS 1423 -11530385 7000693088 yhdp hemolysin homolog yhdp (cl:hypothetical protein hi0107) (db:pir2.dat) F69826 F69826 Bacillus subtilis 1423 -11530385 7500936847 yhdp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hemolysin) (le:32043) (re:33377) (di:complement) BSUB0006 Z99109 g2633290 Bacillus subtilis 1423 -11530385 4000714616 yhdp hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to yhdt, this submission, and to) (le:18691) (re:20025) (di:complement) BSY14082 Y14082 g2226211 Bacillus subtilis 1423 -11530385

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781320	3426	25582	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781326	3427	25583	528	176

Description

GTC ORF with score 404 to: (sr:fruit fly) (db:genpept) (de:drosophila melanogaster sorbitol dehydrogenase (sdh) gene, completecds.) (nt:medium chain alcohol dehydrogenase; sdh) (le:480:585:925:1454:1727) (re:533:618:1394:1672:1848) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781328	3428	25584	195	64

Description

6500726528 hypothetical protein:similar to transcriptional regulator:merr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdQ yhdQ Bacillus subtilis 1423 -11530386 7000694776 yhdq transcription regulator merr family homolog yhdq (db:pir2.dat) G69826 G69826 Bacillus subtilis 1423 -11530386 4000714617 yhdq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to transcriptional regulator (merr family)) (le:33438) (re:33869) (di:complement) BSUB0006 Z99109 g2633291 Bacillus subtilis 1423 -11530386 7500965339 yhdq hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to hi1623 from haemophilus influenzae,) (le:20086) (re:20517) (di:complement) BSY14082 Y14082 g2226212 Bacillus subtilis 1423 -11530386

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781330	3429	25585	225	75

Description

6500726529 hypothetical protein:similar to aspartate aminotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdR yhdR Bacillus subtilis 1423 -11530387 7000692236 yhdr aspartate aminotransferase homolog yhdr (db:pir2.dat) H69826 H69826 Bacillus subtilis 1423 -11530387 4000714618 yhdr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to aspartate aminotransferase) (le:34026) (re:35207) (di:direct) BSUB0006 Z99109 g2633292 Bacillus subtilis 1423 -11530387 7500963434 yhdr hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to aspartate aminotransferase from) (le:20674) (re:21855) (di:direct) BSY14082 Y14082 g2226213 Bacillus subtilis 1423 -11530387

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781335	3430	25586	1029	343

Description

6500726530 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdS yhdS Bacillus subtilis 1423 -11530388 7000693337 yhds hypothetical protein yhds (db:pir2.dat) A69827 A69827 Bacillus subtilis 1423 -11530388 4000714619 yhds (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:35347) (re:35457) (di:complement) BSUB0006 Z99109 g2633293 Bacillus subtilis 1423 -11530388 7500964293 yhds hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to a hypothetical protein,yf18, from) (le:21995) (re:22105) (di:complement) BSY14082 Y14082 g2226214 Bacillus subtilis 1423 -11530388

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781340	3431	25587	822	273

Description

6500726531 hypothetical protein:similar to hemolysin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdT yhdT Bacillus subtilis 1423 -11530389 7500936853 yhdt (de:hypothetical 51.5 kd protein in cita-sspb intergenic region) (db:swissprot) YHDT_BACSU O07589 BACILLUS SUBTILIS 1423 -11530389 7000693089 yhdt hemolysin homolog yhdt (cl:hypothetical protein hi0107) (db:pir2.dat) B69827 B69827 Bacillus subtilis 1423 -11530389 7500936855 yhdt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hemolysin) (le:35534) (re:36919) (di:direct) BSUB0006 Z99109 g2633294 Bacillus subtilis 1423 -11530389 4000714620 yhdt hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to yhdp, this submission, and to) (le:22182) (re:23567) (di:direct) BSY14082 Y14082 g2226215 Bacillus subtilis 1423 -11530389

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781341	3432	25588	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781345	3433	25589	651	217

Description

6500726532 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdU yhdU Bacillus subtilis 1423 -11530390 7000693338 yhdu hypothetical protein yhdu (db:pir2.dat) C69827 C69827 Bacillus subtilis 1423 -11530390 4000714621 yhdu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:36933) (re:37289) (di:complement) BSUB0006 Z99109 g2633295 Bacillus subtilis 1423 -11530390 7500964294 yhdu hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to internal part of nadh-plastoquinone) (le:23581) (re:23937) (di:complement) BSY14082 Y14082 g2226216 Bacillus subtilis 1423 -11530390

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781346	3434	25590	252	83

Description

6500726533 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdV yhdV Bacillus subtilis 1423 -11530391 7000693339 yhdv hypothetical protein yhdv (cl:hypothetical protein mj1523) (db:pir2.dat) D69827 D69827 Bacillus subtilis 1423 -11530391 4000714622 yhdv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:37286) (re:37681) (di:complement) BSUB0006 Z99109 g2633296 Bacillus subtilis 1423 -11530391 7500964295 yhdv hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:no similarities.) (le:23934) (re:24329) (di:complement) BSY14082 Y14082 g2226217 Bacillus subtilis 1423 -11530391

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781347	3435	25591	255	84

Description

6500726534 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdX yhdX Bacillus subtilis 1423 -11530392 7000693340 yhdx hypothetical protein yhdx (db:pir2.dat) F69827 F69827 Bacillus subtilis 1423 -11530392 4000714624 yhdx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:38633) (re:38740) (di:direct) BSUB0006 Z99109 g2633298 Bacillus subtilis 1423 -11530392 7500964296 yhdx hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to human transposon 11.1 with a base) (le:25281) (re:25388) (di:direct) BSY14082 Y14082 g2226219 Bacillus subtilis 1423 -11530392

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781348	3436	25592	795	265

Description

6500726535 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdY yhdY Bacillus subtilis 1423 -11530393 7000692522 yhdy conserved hypothetical protein yhdy (cl:conserved hypothetical protein mj0170) (db:pir2.dat) G69827 G69827 Bacillus subtilis 1423 -11530393 4000714625 yhdy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:38889) (re:40004) (di:direct) BSUB0006 Z99109 g2633299 Bacillus subtilis 1423 -11530393 7500963656 yhdy hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to yggb from e.coli (swiss prot p11666) (le:25537) (re:26652) (di:direct) BSY14082 Y14082 g2226220 Bacillus subtilis 1423 -11530393

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781704	3437	25593	1335	444

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781711	3438	25594	249	82

Description

6500726536 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdZ yhdZ Bacillus subtilis 1423 -11530394 7000692523 yhdz conserved hypothetical protein yhdz (db:pir2.dat) H69827 H69827 Bacillus subtilis 1423 -11530394 4000714626 yhdz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:40074) (re:40817) (di:direct) BSUB0006 Z99109 g2633300 Bacillus subtilis 1423 -11530394 7500963657 yhdz hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to lac repressor lacr from) (le:26722) (re:27465) (di:direct) BSY14082 Y14082 g2226221 Bacillus subtilis 1423 -11530394

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781712	3439	25595	369	123

Description

6500726537 hypothetical protein:similar to endo-1:4-beta-xylanase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheN yheN Bacillus subtilis 1423 -11530395 7000692961 yhen endo-1:4-beta-xylanase homolog yhen (cl:nodb homology) (db:pir2.dat) F69829 F69829 Bacillus subtilis 1423 -11530395 4000714627 yhen (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to endo-1,4-beta-xylanase) (le:40841) (re:41689) (di:complement) BSUB0006 Z99109 g2633301 Bacillus subtilis 1423 -11530395 7500963967 yhen hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 72 to 75 degrees: spovrto sspb.) (nt:similarity to hypothetical protein yfu2 from) (le:27489) (re:28337) (di:complement) BSY14082 Y14082 g2226222 Bacillus subtilis 1423 -11530395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781720	3440	25596	402	133

Description

6500726538 hypothetical protein:similar to na+/h+ antiporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheL yheL Bacillus subtilis 1423 -11530396 7000694292 yhel na+/h+ antiporter homolog yhel (cl:na+/h+-exchanging protein) (db:pir2.dat) D69829 D69829 Bacillus subtilis 1423 -11530396 4000714582 yhel (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to na+/h+ antiporter) (le:42865) (re:44226) (di:complement) BSUB0006 Z99109 g2633303 Bacillus subtilis 1423 -11530396 7500965001 yhel hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:similarity to na(+)/h(+) antiporter from bacillus) (le:17504) (re:18865) (di:direct) BSY14080 Y14080 g2226169 Bacillus subtilis 1423 -11530396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781724	3441	25597	315	104

Description

6500726539 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheK yheK Bacillus subtilis 1423 -11530397 7000692526 yhek conserved hypothetical protein yhek (db:pir2.dat) C69829 C69829 Bacillus subtilis 1423 -11530397 4000714581 yhek (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:44353) (re:44907) (di:complement) BSUB0006 Z99109 g2633304 Bacillus subtilis 1423 -11530397 7500963660 yhek hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:similarity to a hypothetical protein yxie from) (le:16823) (re:17377) (di:direct) BSY14080 Y14080 g2226168 Bacillus subtilis 1423 -11530397

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781725	3442	25598	336	111

Description

6500726540 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheJ yheJ Bacillus subtilis 1423 -11530398 7000693345 yhej hypothetical protein yhej (db:pir2.dat) B69829 B69829 Bacillus subtilis 1423 -11530398 4000714580 yhej (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:45017) (re:45178) (di:direct) BSUB0006 Z99109 g2633305 Bacillus subtilis 1423 -11530398 7500964301 yhej hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:16552) (re:16713) (di:complement) BSY14080 Y14080 g2226167 Bacillus subtilis 1423 -11530398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781739	3443	25599	927	308

Description

6500726541 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheI yheI Bacillus subtilis 1423 -11530399 7000692090 yhei abc transporter atp-binding protein homolog yhei (cl:atp-binding cassette homology) (db:pir2.dat) A69829 A69829 Bacillus subtilis 1423 -11530399 4000714579 yhei (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to abc transporter (atp-binding protein)) (le:45298) (re:47055) (di:direct) BSUB0006 Z99109 g2633306 Bacillus subtilis 1423 -11530399 7500963329 yhei hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:similarity to multidrug resistance-like atp binding) (le:14675) (re:16432) (di:complement) BSY14080 Y14080 g2226166 Bacillus subtilis 1423 -11530399

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781740	3444	25600	237	78

Description

6500726542 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheH yheH Bacillus subtilis 1423 -11530400 7000692089 yheh abc transporter atp-binding protein homolog yheh (cl:atp-binding cassette homology) (db:pir2.dat) H69828 H69828 Bacillus subtilis 1423 -11530400 4000714578 yheh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to abc transporter (atp-binding protein)) (le:47052) (re:49073) (di:direct) BSUB0006 Z99109 g2633307 Bacillus subtilis 1423 -11530400 7500963328 yheh hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:similarity to multidrug resistance-like atp binding) (le:12657) (re:14678) (di:complement) BSY14080 Y14080 g2226165 Bacillus subtilis 1423 -11530400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781749	3445	25601	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781757	3446	25602	417	138

Description

6500726543 hypothetical protein:similar to calcium-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheG yheG Bacillus subtilis 1423 -11530401 7000692302 yheg calcium-binding protein homolog yheg (db:pir2.dat) G69828 G69828 Bacillus subtilis 1423 -11530401 4000714577 yheg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to calcium-binding protein) (le:49122) (re:49742) (di:complement) BSUB0006 Z99109 g2633308 Bacillus subtilis 1423 -11530401 7500963471 yheg hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:similarity to bovine flavin reductase (pid =) (le:11988) (re:12608) (di:direct) BSY14080 Y14080 g2226164 Bacillus subtilis 1423 -11530401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781761	3447	25603	339	112

Description

6500726544 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheF yheF Bacillus subtilis 1423 -11530402 7000693344 yhef hypothetical protein yhef (db:pir2.dat) F69828 F69828 Bacillus subtilis 1423 -11530402 4000714576 yhef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:49781) (re:49906) (di:complement) BSUB0006 Z99109 g2633309 Bacillus subtilis 1423 -11530402 7500964300 yhef hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:11824) (re:11949) (di:direct) BSY14080 Y14080 g2226163 Bacillus subtilis 1423 -11530402

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781762	3448	25604	570	189

Description

6500726545 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheE yheE Bacillus subtilis 1423 -11530403 7000693343 yhee hypothetical protein yhee (db:pir2.dat) E69828 E69828 Bacillus subtilis 1423 -11530403 4000714575 yhee (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:50423) (re:50641) (di:complement) BSUB0006 Z99109 g2633311 Bacillus subtilis 1423 -11530403 7500964299 yhee hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:11089) (re:11307) (di:direct) BSY14080 Y14080 g2226161 Bacillus subtilis 1423 -11530403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781768	3449	25605	696	231

Description

GTC ORF with score 149 to: (fn:catalyzesf the conversion of sterigmatocystin) (sr:aspergillus parasiticus (strain srrc 143) (library: un1-zap) cdn) (db:genpept-pln1) (de:aspergillus parastieus o-methyltrasferase (omt-1) mrna, completecds.) (le:12) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781775	3450	25606	204	67

Description

6500726546 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheD yheD Bacillus subtilis 1423 -11530404 7000692525 yhed conserved hypothetical protein yhed (db:pir2.dat) D69828 D69828 Bacillus subtilis 1423 -11530404 4000714574 yhed (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:50791) (re:52152) (di:complement) BSUB0006 Z99109 g2633312 Bacillus subtilis 1423 -11530404 7500963659 yhed hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:9578) (re:10939) (di:direct) BSY14080 Y14080 g2226160 Bacillus subtilis 1423 -11530404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781777	3451	25607	219	73

Description

6500726547 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheC yheC Bacillus subtilis 1423 -11530405 7000692524 yhec conserved hypothetical protein yhec (db:pir2.dat) C69828 C69828 Bacillus subtilis 1423 -11530405 4000714573 yhec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:52142) (re:53233) (di:complement) BSUB0006 Z99109 g2633313 Bacillus subtilis 1423 -11530405 7500963658 yhec hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:8497) (re:9588) (di:direct) BSY14080 Y14080 g2226159 Bacillus subtilis 1423 -11530405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781780	3452	25608	207	68

Description

6500726548 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheB yheB Bacillus subtilis 1423 -11530406 7000693342 yheb hypothetical protein yheb (db:pir2.dat) B69828 B69828 Bacillus subtilis 1423 -11530406 4000714572 yheb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:53500) (re:54633) (di:direct) BSUB0006 Z99109 g2633314 Bacillus subtilis 1423 -11530406 7500964298 yheb hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:7097) (re:8230) (di:complement) BSY14080 Y14080 g2226158 Bacillus subtilis 1423 -11530406

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781782	3453	25609	462	153

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781784	3454	25610	510	169

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781797	3455	25611	1461	486

Description

6500726549 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yheA yheA Bacillus subtilis 1423 -11530407 7000693341 yhea hypothetical protein yhea (db:pir2.dat) A69828 A69828 Bacillus subtilis 1423 -11530407 4000714571 yhea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:54726) (re:55079) (di:direct) BSUB0006 Z99109 g2633315 Bacillus subtilis 1423 -11530407 7500964297 yhea hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:6651) (re:7004) (di:complement) BSY14080 Y14080 g2226157 Bacillus subtilis 1423 -11530407

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781800	3456	25612	942	313

Description

6500726550 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaZ yhaZ Bacillus subtilis 1423 -11530408 7000693330 yhaz hypothetical protein yhaz (db:pir2.dat) D69820 D69820 Bacillus subtilis 1423 -11530408 4000714570 yhaz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:55123) (re:56196) (di:complement) BSUB0006 Z99109 g2633316 Bacillus subtilis 1423 -11530408 7500964286 yhaz hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:5534) (re:6607) (di:direct) BSY14080 Y14080 g2226156 Bacillus subtilis 1423 -11530408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781811	3457	25613	297	98

Description

GTC ORF with score 162 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781812	3458	25614	495	164

Description

GTC ORF with score 101 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781814	3459	25615	711	237

Description

GTC ORF with score 138 to: (sr:bacillus licheniformis (strain:atcc 10716) dna) (db:genpept) (de:bacillus licheniformis genes for bacitracin synthetase 2 (ba2),bacitracin synthetase 1 (ba1), partial cds.) (le:1618) (re:>2859) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781825	3460	25616	204	67

Description

GTC ORF with score 170 to: (fn:membrane protein mediating transport of) (db:genpept-pln1) (de:candida albicans oligopeptide transporter (opt1) gene, completecds.) (nt:oligopeptide transporter) (le:482:2166) (re:2107:2891) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781826	3461	25617	252	83

Description

GTC ORF with score 145 to: (sr:schizosaccharomyces pombe (strain:972h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:fission yeast dna for isp4, peptidyl-prolyl cis-trans isomerase,atf1, chromosome ii cosmid 1228 sequence.) (nt:5' sequence for the ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781827	3462	25618	285	94

Description

6500726551 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaY yhaY Bacillus subtilis 1423 -11530409 7000693329 yhay hypothetical protein yhay (db:pir2.dat) C69820 C69820 Bacillus subtilis 1423 -11530409 4000714569 yhay (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:56389) (re:56640) (di:complement) BSUB0006 Z99109 g2633317 Bacillus subtilis 1423 -11530409 7500964285 yhay hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:5090) (re:5341) (di:direct) BSY14080 Y14080 g2226155 Bacillus subtilis 1423 -11530409

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781833	3463	25619	543	180

Description

6500726552 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaX yhaX Bacillus subtilis 1423 -11530410 7000692514 yhax conserved hypothetical protein yhax (db:pir2.dat) B69820 B69820 Bacillus subtilis 1423 -11530410 4000714568 yhax (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:56683) (re:57480) (di:direct) BSUB0006 Z99109 g2633318 Bacillus subtilis 1423 -11530410 7500963649 yhax hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:similarity to the yida/yigl (escherichia coli) and) (le:4250) (re:5047) (di:complement) BSY14080 Y14080 g2226154 Bacillus subtilis 1423 -11530410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781834	3464	25620	279	92

Description

6500726553 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaW yhaW Bacillus subtilis 1423 -11530411 7000693328 yhaw hypothetical protein yhaw (db:pir2.dat) A69820 A69820 Bacillus subtilis 1423 -11530411 4000714567 yhaw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:57660) (re:58160) (di:direct) BSUB0006 Z99109 g2633319 Bacillus subtilis 1423 -11530411 7500964284 yhaw hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:3570) (re:4070) (di:complement) BSY14080 Y14080 g2226153 Bacillus subtilis 1423 -11530411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781859	3465	25621	1329	443

Description

6500726554 hypothetical protein:similar to coproporphyrinogen iii oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaV yhaV Bacillus subtilis 1423 -11530412 7000692881 yhav coproporphyrinogen iii oxidase homolog yhav (db:pir2.dat) H69819 H69819 Bacillus subtilis 1423 -11530412 7500963911 yhav (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to coproporphyrinogen iii oxidase) (le:58292) (re:59164) (di:direct) BSUB0006 Z99109 g2633320 Bacillus subtilis 1423 -11530412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781869	3466	25622	1209	402

Description

6500726555 hypothetical protein:similar to na+/h+ antiporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaU yhaU Bacillus subtilis 1423 -11530413 7000694291 yhau na+/h+ antiporter homolog yhau (db:pir2.dat) G69819 G69819 Bacillus subtilis 1423 -11530413 4000714565 yhau (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to na+/h+ antiporter) (le:59182) (re:60408) (di:complement) BSUB0006 Z99109 g2633321 Bacillus subtilis 1423 -11530413 7500965000 yhau hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (nt:similarity to na(+)/h(+) antiporter from) (le:1322) (re:2548) (di:direct) BSY14080 Y14080 g2226151 Bacillus subtilis 1423 -11530413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781889	3467	25623	771	256

Description

6500726556 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaT yhaT Bacillus subtilis 1423 -11530414 7000692513 yhat conserved hypothetical protein yhat (db:pir2.dat) F69819 F69819 Bacillus subtilis 1423 -11530414 4000714564 yhat (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:60405) (re:60902) (di:complement) BSUB0006 Z99109 g2633322 Bacillus subtilis 1423 -11530414 7500963648 yhat hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:828) (re:1325) (di:direct) BSY14080 Y14080 g2226150 Bacillus subtilis 1423 -11530414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781906	3468	25624	747	248

Description

GTC ORF with score 254 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1483.) (nt:similar to saccharomyces cerevisiae orf ygr205w,) (le:138) (re:971) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781907	3469	25625	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781911	3470	25626	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781928	3471	25627	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781941	3472	25628	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781951	3473	25629	186	62

Description

GTC ORF with score 95 to: (fn:regulatory protein) (db:genpept-bct1) (de:pseudomonas fluorescens putative sensor kinase (apda) gene,complete cds.) (nt:putative sensor kinase; regulatory protein for) (le:209) (re:2962) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781953	3474	25630	1215	404

Description

6500726557 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaS yhaS Bacillus subtilis 1423 -11530415 7000693327 yhas hypothetical protein yhas (db:pir2.dat) E69819 E69819 Bacillus subtilis 1423 -11530415 4000714563 yhas (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:60966) (re:61304) (di:complement) BSUB0006 Z99109 g2633323 Bacillus subtilis 1423 -11530415 7500964283 yhas hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: sspb upstreamof glyb.) (le:426) (re:764) (di:direct) BSY14080 Y14080 g2226149 Bacillus subtilis 1423 -11530415

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781971	3475	25631	258	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781983	3476	25632	486	161

Description

6500726558 hypothetical protein:similar to 3-hydroxbutyryl-coa dehydratase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaR yhaR Bacillus subtilis 1423 -11530416 7000692041 yhar 3-hydroxbutyryl-coa dehydratase homolog yhar (cl:enoyl-coa hydratase homology) (db:pir2.dat) D69819 D69819 Bacillus subtilis 1423 -11530416 7500963293 yhar (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to 3-hydroxbutyryl-coa dehydratase) (le:61469) (re:62296) (di:direct) BSUB0006 Z99109 g2633324 Bacillus subtilis 1423 -11530416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501781989	3477	25633	699	232

Description

6500726559 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaQ yhaQ Bacillus subtilis 1423 -11530417 7000692088 yhaq abc transporter atp-binding protein homolog yhaq (cl:atp-binding cassette homology) (db:pir2.dat) C69819 C69819 Bacillus subtilis 1423 -11530417 4000714551 yhaq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to abc transporter (atp-binding protein)) (le:62567) (re:63463) (di:direct) BSUB0006 Z99109 g2633325 Bacillus subtilis 1423 -11530417 7500963327 yhaq hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 8.7 kb chromosomal dna: downstream glyb-prsaregion.) (nt:similarity to atp-dependent abc-transporter from) (le:6877) (re:7773) (di:complement) BSY14078 Y14078 g2226131 Bacillus subtilis 1423 -11530417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782000	3478	25634	300	99

Description

6500726560 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaP yhaP Bacillus subtilis 1423 -11530418 7500936754 yhap (de:hypothetical 45.4 kd protein in sspb-prsa intergenic region) (db:swissprot) YHAP_BACSU O07523 BACILLUS SUBTILIS 1423 -11530418 7000692512 yhap conserved hypothetical protein yhap (db:pir2.dat) B69819 B69819 Bacillus subtilis 1423 -11530418 7500936756 yhap (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:63456) (re:64715) (di:direct) BSUB0006 Z99109 g2633326 Bacillus subtilis 1423 -11530418 4000714550 yhap hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 8.7 kb chromosomal dna: downstream glyb-prsaregion.) (nt:aa 1-147 show similarity to putative) (le:5625) (re:6884) (di:complement) BSY14078 Y14078 g2226130 Bacillus subtilis 1423 -11530418

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782005	3479	25635	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782017	3480	25636	801	266

Description

6500726561 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaO yhaO Bacillus subtilis 1423 -11530419 7000692511 yhao probable phosphoesterase:yhao (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) A69819 A69819 Bacillus subtilis 1423 -11530419 4000714549 yhao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:64822) (re:66048) (di:direct) BSUB0006 Z99109 g2633327 Bacillus subtilis 1423 -11530419 7500954197 yhao hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 8.7 kb chromosomal dna: downstream glyb-prsaregion.) (nt:similarity to exonuclease sbcd from escherichia) (le:4292) (re:5518) (di:complement) BSY14078 Y14078 g2226129 Bacillus subtilis 1423 -11530419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782019	3481	25637	192	63

Description

GTC ORF with score 102 to: (sr:human) (db:genpept-pri2) (de:homo sapiens dna sequence from pac 127d3 on chromosome 1q23-25.contains fmo2 and fmo3 genes for flavin-containing monooxygenase 2and flavin-containing monooxygenase 3 ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782362	3482	25638	339	112

Description

6500726562 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaN yhaN Bacillus subtilis 1423 -11530420 7000692510 yhan conserved hypothetical protein yhan (db:pir2.dat) H69818 H69818 Bacillus subtilis 1423 -11530420 4000714548 yhan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:66053) (re:68944) (di:direct) BSUB0006 Z99109 g2633328 Bacillus subtilis 1423 -11530420 7500963647 yhan hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 8.7 kb chromosomal dna: downstream glyb-prsaregion.) (nt:similarity to orfx from staphylococcus aureus) (le:1396) (re:4287) (di:complement) BSY14078 Y14078 g2226128 Bacillus subtilis 1423 -11530420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782373	3483	25639	837	278

Description

6500726563 hypothetical protein:similar to cmp-binding factor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaM yhaM Bacillus subtilis 1423 -11530421 7000692378 yham cmp-binding factor homolog yham (db:pir2.dat) G69818 G69818 Bacillus subtilis 1423 -11530421 4000714547 yham (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to cmp-binding factor) (le:69018) (re:69962) (di:direct) BSUB0006 Z99109 g2633329 Bacillus subtilis 1423 -11530421 7500963540 yham hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 8.7 kb chromosomal dna: downstream glyb-prsaregion.) (nt:similarity to cmp-binding-factor-1 (cbf1) from) (le:378) (re:1322) (di:complement) BSY14078 Y14078 g2226127 Bacillus subtilis 1423 -11530421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782381	3484	25640	588	195

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782391	3485	25641	288	95

Description

GTC ORF with score 132 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome i bac f14j9 genomic sequencecontains phya marker, complete sequence.) (nt:highly similar to cinnamyl alcohol dehydrogenase,) (le:50999:51232:51547:51833) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782394	3486	25642	594	197

Description

6500726564 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaL yhaL Bacillus subtilis 1423 -11530422 7000693326 yhal hypothetical protein yhal (db:pir2.dat) F69818 F69818 Bacillus subtilis 1423 -11530422 4000714546 yhal (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:70087) (re:70299) (di:direct) BSUB0006 Z99109 g2633330 Bacillus subtilis 1423 -11530422 7500964282 yhal hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 8.7 kb chromosomal dna: downstream glyb-prsaregion.) (le:41) (re:253) (di:complement) BSY14078 Y14078 g2226126 Bacillus subtilis 1423 -11530422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782400	3487	25643	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782406	3488	25644	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782408	3489	25645	615	204

Description

6500726565 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaK yhaK Bacillus subtilis 1423 -11530423 7000693325 yhak hypothetical protein yhak (db:pir2.dat) E69818 E69818 Bacillus subtilis 1423 -11530423 4000714545 yhak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:72018) (re:72272) (di:complement) BSUB0006 Z99109 g2633332 Bacillus subtilis 1423 -11530423 7500964281 yhak hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (le:8641) (re:8895) (di:direct) BSY14077 Y14077 g2226123 Bacillus subtilis 1423 -11530423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782414	3490	25646	864	288

Description

GTC ORF with score 305 to: (or:Homo sapiens) (sr:homo sapiens male myeloblast cell-line kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0073 gene, partial cds.) (nt:the ha1539 protein is related to cyclophilin.) (le:<1) (re:1939) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782417	3491	25647	747	248

Description

6500726566 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaJ yhaJ Bacillus subtilis 1423 -11530424 7000693324 yhaj hypothetical protein yhaj (db:pir2.dat) D69818 D69818 Bacillus subtilis 1423 -11530424 4000714544 yhaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:72296) (re:72535) (di:complement) BSUB0006 Z99109 g2633333 Bacillus subtilis 1423 -11530424 7500964280 yhaj hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (le:8378) (re:8617) (di:direct) BSY14077 Y14077 g2226122 Bacillus subtilis 1423 -11530424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782418	3492	25648	435	144

Description

6500726567 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaI yhaI Bacillus subtilis 1423 -11530425 7000693323 yhai hypothetical protein yhai (db:pir2.dat) C69818 C69818 Bacillus subtilis 1423 -11530425 4000714543 yhai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:72743) (re:73084) (di:direct) BSUB0006 Z99109 g2633334 Bacillus subtilis 1423 -11530425 7500964279 yhai hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (le:7829) (re:8170) (di:complement) BSY14077 Y14077 g2226121 Bacillus subtilis 1423 -11530425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782422	3493	25649	822	273

Description

6500726568 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaH yhaH Bacillus subtilis 1423 -11530426 7000692509 yhah conserved hypothetical protein yhah (db:pir2.dat) B69818 B69818 Bacillus subtilis 1423 -11530426 4000714542 yhah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:73870) (re:74226) (di:complement) BSUB0006 Z99109 g2633336 Bacillus subtilis 1423 -11530426 7500963646 yhah hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (le:6687) (re:7043) (di:direct) BSY14077 Y14077 g2226119 Bacillus subtilis 1423 -11530426

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782432	3494	25650	1269	422

Description

GTC ORF with score 458 to: (sr:human) (db:genpept-pri3) (de:homo sapiens lysosomal pepstatin insensitive protease (cln2) gene,complete cds.) (nt:deficient in late-infantile neuronal ceroid) (le:1329:1462:1814:2938) (re:1345:1533:1953:3088) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782444	3495	25651	486	161

Description

6500726569 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaG yhaG Bacillus subtilis 1423 -11530427 7000693322 yhag hypothetical protein yhag (db:pir2.dat) A69818 A69818 Bacillus subtilis 1423 -11530427 4000714541 yhag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:74619) (re:75137) (di:complement) BSUB0006 Z99109 g2633337 Bacillus subtilis 1423 -11530427 7500964278 yhag hypothetical protein (db:genpept-bct1) (de:bacillus subitlis 10.6 kb chromosomal dna: glyb-prsa region.) (nt:similarity to prow from e.coli (swiss prot p14176)) (le:5776) (re:6294) (di:direct) BSY14077 Y14077 g2226118 Bacillus subtilis 1423 -11530427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782446	3496	25652	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782447	3497	25653	420	139

Description

6500726570 hypothetical protein:similar to aminoacylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhaA yhaA Bacillus subtilis 1423 -11530428 7000692204 yhaa aminoacylase homolog yhaa (cl:hippurate hydrolase) (db:pir2.dat) H69817 H69817 Bacillus subtilis 1423 -11530428 7500963412 yhaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to aminoacylase) (le:80123) (re:81313) (di:complement) BSUB0006 Z99109 g2633343 Bacillus subtilis 1423 -11530428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782449	3498	25654	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782451	3499	25655	1161	386

Description

6500726571 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfA yhfA Bacillus subtilis 1423 -11530429 7000693346 yhfa hypothetical protein yhfa (db:pir2.dat) G69829 G69829 Bacillus subtilis 1423 -11530429 4000714630 yhfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:81386) (re:82777) (di:complement) BSUB0006 Z99109 g2633344 Bacillus subtilis 1423 -11530429 7500964302 yhfa hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:low similarity to dcuc protein from escherichia) (le:1245) (re:2636) (di:complement) BSY14083 Y14083 g2226226 Bacillus subtilis 1423 -11530429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782455	3500	25656	1245	415

Description

6500726572 yixb:yhgb hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhgB yhgB Bacillus subtilis 1423 -11530430 7500936924 yhgb (de:hypothetical 12.0 kd protein in ecsc-pbpf intergenic region) (db:swissprot) YHGB_BACSU P38048 BACILLUS SUBTILIS 1423 -11530430 7000692533 yhgb conserved hypothetical protein yhgb:hypothetical protein y pbpf 5 region (db:pir2.dat) E69832 E69832 Bacillus subtilis 1423 -11530430 7500936926 yhgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yixb; similar to hypothetical) (le:82843) (re:83157) (di:complement) BSUB0006 Z99109 g2633345 Bacillus subtilis 1423 -11530430 4000714631 yixb hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p38048; yixb_bacsu) (le:2702) (re:3016) (di:complement) BSY14083 Y14083 g2226227 Bacillus subtilis 1423 -11530430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782468	3501	25657	285	95

Description

GTC ORF with score 102 to: (sr:rice) (db:genpept-pln1) (de:oryza sativa putative adp-glucose pyrophosphorylase subunit sh2 andputative nadph-dependent reductase a1 genes, complete cds.) (nt:similar to maize a1 protein encoded by genbank) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782479	3502	25658	486	161

Description

GTC ORF with score 193 to: (sr:baker's yeast) (db:genpept) (de:saccharomyces cerevisiae adp-ribosylation factor-like protein 1(arp1) gene, complete cds.) (nt:small gtpase; has gtp binding activity) (le:349) (re:945) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782480	3503	25659	189	62

Description

GTC ORF with score 138 to: (sr:baker's yeast) (db:genpept) (de:saccharomyces cerevisiae adp-ribosylation factor-like protein 1(arp1) gene, complete cds.) (nt:small gtpase; has gtp binding activity) (le:349) (re:945) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782505	3504	25660	360	120

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782509	3505	25661	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782515	3506	25662	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782520	3507	25663	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782532	3508	25664	513	170

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782551	3509	25665	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782567	3510	25666	1374	458

Description

GTC ORF with score 445 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c2f3.) (nt:spac2f3.15, putative cell division protein kinase,) (le:32056:33050:33207:33937) (re:33003:33140:33885:34000) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782568	3511	25667	1251	416

Description

5000689571 yixc:yhgc hypothetical protein:hypothetical 18.8 kd protein in pbpf 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhgC yhgC Bacillus subtilis 1423 -11530431 113507 yhgc (de:hypothetical 18.8 kd protein in ecsc-pbpf intergenic region) (db:swissprot) YHGC_BACSU P38049 BACILLUS SUBTILIS 1423 -11530431 7000688058 yhgc conserved hypothetical protein yhgc:hypothetical protein x pbpf 5 region (db:pir2.dat) B40614 B40614 Bacillus subtilis 1423 -11530431 7500936928 (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis penicillin-binding protein (pbpf) gene, 5' end.) (nt:product unknown) (le:247) (re:747) (di:complement) BACPBPF L10630 g304160 Bacillus subtilis 1423 -11530431 216436 yhgc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yixc; similar to hypothetical) (le:83202) (re:83702) (di:complement) BSUB0006 Z99109 g2633346 Bacillus subtilis 1423 -11530431 4000707460 yixc hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p38049; yixc_bacsu) (le:3061) (re:3561) (di:complement) BSY14083 Y14083 g2226228 Bacillus subtilis 1423 -11530431 170259 yhgc conserved hypothetical protein yhgc:hypothetical protein x pbpf 5 region (db:pir) B40614 B40614 Bacillus subtilis 1423 -11530431 6500726573 yixc hypothetical protein:hypothetical 18.8 kd protein in pbpf 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhgC yhgC Bacillus subtilis 1423 -11530431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782583	3512	25668	501	166

Description

5000688925 yixd:yhgd hypothetical protein:hypothetical transcriptional regulator in hemy 3region:orfa (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhgD yhgD Bacillus subtilis 1423 -11530432 113508 yhgd (de:(orfa)) (db:swissprot) YHGD_BACSU P32398 BACILLUS SUBTILIS 1423 -11530432 7000688059 yhgd transcription regulator tetr/acrr family homolog yhgd:orfa 3 of hemy (db:pir2.dat) E47045 E47045 Bacillus subtilis 1423 -11530432 7500936929 (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis penicillin binding protein 1a (pona) gene;uroporphyrinogen decarboxylase (heme) gene; ferrochelatase (hemh)gene complete cds, (hemy) gene, complete cds; orfa, complete cds... BACHEMEHY M97208 g143046 Bacillus subtilis 1423 -11530432 215833 yhgd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yixd; similar to) (le:89728) (re:90303) (di:direct) BSUB0006 Z99109 g2633351 Bacillus subtilis 1423 -11530432 4000707461 yixd hypothetical transcriptional regulator (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p32398; yixd_bacsu.) (le:9587) (re:10162) (di:direct) BSY14083 Y14083 g2226233 Bacillus subtilis 1423 -11530432 170403 yhgd transcriptional regulator tetr/acrr family homolog yhgd:orfa 3 of hemy (db:pir) E47045 E47045 Bacillus subtilis 1423 -11530432 6500726574 yixd hypothetical protein:hypothetical transcriptional regulator in hemy 3region:orfa (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhgD yhgD Bacillus subtilis 1423 -11530432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782584	3513	25669	324	107

Description

6500726575 yixe:yhge hypothetical protein:similar to phage infection protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhgE yhgE Bacillus subtilis 1423 -11530433 7500936930 yhge (de:hypothetical 84.1 kd protein in hemy-gltt intergenic region (orfb)) (db:swissprot) YHGE_BACSU P32399 BACILLUS SUBTILIS 1423 -11530433 7000694365 yhge phage infection protein homolog yhge (db:pir2.dat) H69832 H69832 Bacillus subtilis 1423 -11530433 7500936932 yhge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yixe; similar to phage) (le:90374) (re:92701) (di:direct) BSUB0006 Z99109 g2633352 Bacillus subtilis 1423 -11530433 4000714632 yixe hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:see swiss prot p32399; yixe_bacsu. this databank) (le:10233) (re:12560) (di:direct) BSY14083 Y14083 g2226234 Bacillus subtilis 1423 -11530433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782587	3514	25670	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782602	3515	25671	579	192

Description

6500726576 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfC yhfC Bacillus subtilis 1423 -11530434 7000693347 yhfc hypothetical protein yhfc (db:pir2.dat) A69830 A69830 Bacillus subtilis 1423 -11530434 4000714634 yhfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:93846) (re:94622) (di:direct) BSUB0006 Z99109 g2633354 Bacillus subtilis 1423 -11530434 7500964303 yhfc hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (le:13705) (re:14481) (di:direct) BSY14083 Y14083 g2226236 Bacillus subtilis 1423 -11530434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782604	3516	25672	507	168

Description

6500726577 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfD yhfD Bacillus subtilis 1423 -11530435 7000693348 yhfd hypothetical protein yhfd (db:pir2.dat) B69830 B69830 Bacillus subtilis 1423 -11530435 4000714635 yhfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:94713) (re:94916) (di:complement) BSUB0006 Z99109 g2633355 Bacillus subtilis 1423 -11530435 7500964304 yhfd hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:low similarity to methallothionein isoform ia from) (le:14572) (re:14775) (di:complement) BSY14083 Y14083 g2226237 Bacillus subtilis 1423 -11530435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782612	3517	25673	561	186

Description

6500726578 hypothetical protein:similar to glucanase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfE yhfE Bacillus subtilis 1423 -11530436 7000693027 yhfe glucanase homolog yhfe (db:pir2.dat) C69830 C69830 Bacillus subtilis 1423 -11530436 4000714636 yhfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to glucanase) (le:95035) (re:96075) (di:direct) BSUB0006 Z99109 g2633356 Bacillus subtilis 1423 -11530436 7500964008 yhfe hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to endoglucanase celm from clostridium) (le:14894) (re:15934) (di:direct) BSY14083 Y14083 g2226238 Bacillus subtilis 1423 -11530436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782613	3518	25674	519	172

Description

6500726579 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfF yhfF Bacillus subtilis 1423 -11530437 7000693349 yhff hypothetical protein yhff (db:pir2.dat) D69830 D69830 Bacillus subtilis 1423 -11530437 4000714637 yhff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:96088) (re:96495) (di:direct) BSUB0006 Z99109 g2633357 Bacillus subtilis 1423 -11530437 7500964305 yhff hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to part of late embryogenesis abundant) (le:15947) (re:16354) (di:direct) BSY14083 Y14083 g2226239 Bacillus subtilis 1423 -11530437

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782616	3519	25675	1389	462

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782626	3520	25676	516	171

Description

GTC ORF with score 117 to: (db:genpept-bct2) (de:pseudomonas aeruginosa wzz (rol) (wzz (rol)) gene, partial cds,wbpa (wbpb), wbpb (wbpb), wbpc (wbpc), wbpd (wbpd), wbpe (wbpe),wzy (rfc) (wzy (rfc)), wzx (wzx), hish (hish), hisf (hisf), wbpg(wbpg), wbph...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782631	3521	25677	414	137

Description

6500726580 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfH yhfH Bacillus subtilis 1423 -11530438 7000693350 yhfh hypothetical protein yhfh (db:pir2.dat) E69830 E69830 Bacillus subtilis 1423 -11530438 4000714639 yhfh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:98092) (re:98232) (di:complement) BSUB0006 Z99109 g2633359 Bacillus subtilis 1423 -11530438 7500964306 yhfh hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:low similarity to several zinc-finger proteins;) (le:17951) (re:18091) (di:complement) BSY14083 Y14083 g2226241 Bacillus subtilis 1423 -11530438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782640	3522	25678	252	83

Description

6500726581 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfI yhfI Bacillus subtilis 1423 -11530439 7000692527 yhfi conserved hypothetical protein yhfi (db:pir2.dat) F69830 F69830 Bacillus subtilis 1423 -11530439 4000714640 yhfi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:98384) (re:99118) (di:direct) BSUB0006 Z99109 g2633360 Bacillus subtilis 1423 -11530439 7500963661 yhfi hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to arylsulphatase precursor 'ats' from) (le:18243) (re:18977) (di:direct) BSY14083 Y14083 g2226242 Bacillus subtilis 1423 -11530439

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782641	3523	25679	453	150

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782642	3524	25680	588	195

Description

6500726582 hypothetical protein:similar to lipoate-protein ligase (gtcfc:14.1) (ec:6.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfJ yhfJ Bacillus subtilis 1423 -11530440 7000694166 yhfj lipoate-protein ligase homolog yhfj (cl:lipoate-protein ligase) (db:pir2.dat) G69830 G69830 Bacillus subtilis 1423 -11530440 4000714641 yhfj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to lipoate-protein ligase) (le:99131) (re:100126) (di:direct) BSUB0006 Z99109 g2633361 Bacillus subtilis 1423 -11530440 7500954499 yhfj hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to several lipoate-protein ligases) (le:18990) (re:19985) (di:direct) BSY14083 Y14083 g2226243 Bacillus subtilis 1423 -11530440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782657	3525	25681	189	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782977	3526	25682	1398	465

Description

6500726583 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfK yhfK Bacillus subtilis 1423 -11530441 7000692528 yhfk conserved hypothetical protein yhfk (cl:hypothetical protein ymr090w) (db:pir2.dat) H69830 H69830 Bacillus subtilis 1423 -11530441 4000714642 yhfk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:100191) (re:100835) (di:direct) BSUB0006 Z99109 g2633362 Bacillus subtilis 1423 -11530441 7500963662 yhfk hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to several hypothetical proteins, from) (le:20050) (re:20694) (di:direct) BSY14083 Y14083 g2226244 Bacillus subtilis 1423 -11530441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782979	3527	25683	441	146

Description

6500726584 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfM yhfM Bacillus subtilis 1423 -11530442 7000693351 yhfm hypothetical protein yhfm (db:pir2.dat) B69831 B69831 Bacillus subtilis 1423 -11530442 4000714644 yhfm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:102532) (re:102927) (di:complement) BSUB0006 Z99109 g2633364 Bacillus subtilis 1423 -11530442 7500964307 yhfm hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (le:22391) (re:22786) (di:complement) BSY14083 Y14083 g2226246 Bacillus subtilis 1423 -11530442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782980	3528	25684	741	246

Description

6500726585 yzoa:yhfn hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfN yhfN Bacillus subtilis 1423 -11530443 7000692529 yhfn conserved hypothetical protein yhfn (db:pir2.dat) C69831 C69831 Bacillus subtilis 1423 -11530443 4000714645 yhfn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yzoa; similar to hypothetical) (le:103076) (re:104356) (di:direct) BSUB0006 Z99109 g2633365 Bacillus subtilis 1423 -11530443 7500963663 yhfn hypothetical protein (db:genpept-bct2) (de:bacillus subtilis chromosomal dna, region 76-78 degrees: betweenglyb-apre.) (nt:similarity to several hypothetical proteins, from) (le:22935) (re:24215) (di:direct) BSY14083 Y14083 g2226247 Bacillus subtilis 1423 -11530443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501782997	3529	25685	231	76

Description

6500726586 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfO yhfO Bacillus subtilis 1423 -11530444 7000692530 yhfo conserved hypothetical protein yhfo (db:pir2.dat) D69831 D69831 Bacillus subtilis 1423 -11530444 4000714648 yhfo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:105975) (re:106424) (di:direct) BSUB0006 Z99109 g2633367 Bacillus subtilis 1423 -11530444 7500963664 yhfo hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to several hypothetical proteins, from) (le:403) (re:852) (di:direct) BSY14084 Y14084 g2226251 Bacillus subtilis 1423 -11530444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783010	3530	25686	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783015	3531	25687	966	321

Description

GTC ORF with score 1534 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completecds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783025	3532	25688	354	117

Description

6500726587 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfP yhfP Bacillus subtilis 1423 -11530445 7000692531 yhfp conserved hypothetical protein yhfp (cl:bacillus subtilis conserved hypothetical protein yhfp) (db:pir2.dat) E69831 E69831 Bacillus subtilis 1423 -11530445 4000714649 yhfp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:106496) (re:107488) (di:direct) BSUB0006 Z99109 g2633368 Bacillus subtilis 1423 -11530445 7500963665 yhfp hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:high similarity to yhdh from e.coli (swiss prot) (le:924) (re:1916) (di:direct) BSY14084 Y14084 g2226252 Bacillus subtilis 1423 -11530445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783027	3533	25689	804	267

Description

6500726588 hypothetical protein:similar to iron:iii dicitrate-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfQ yhfQ Bacillus subtilis 1423 -11530446 7000694132 yhfq iron iii dicitrate-binding protein homolog yhfq (cl:iron(iii) dicitrate transport protein) (db:pir2.dat) F69831 F69831 Bacillus subtilis 1423 -11530446 4000714650 yhfq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to iron(iii) dicitrate-binding protein) (le:107630) (re:108676) (di:direct) BSUB0006 Z99109 g2633369 Bacillus subtilis 1423 -11530446 7500955812 yhfq hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to citrate-dependent iron transport) (le:2058) (re:3104) (di:direct) BSY14084 Y14084 g2226253 Bacillus subtilis 1423 -11530446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783028	3534	25690	603	200

Description

6500726589 hypothetical protein:similar to acetyl-coa c-acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfS yhfS Bacillus subtilis 1423 -11530447 7000692136 yhfs acetyl-coa c-acetyltransferase homolog yhfs (db:pir2.dat) H69831 H69831 Bacillus subtilis 1423 -11530447 4000714652 yhfs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to acetyl-coa c-acetyltransferase) (le:109360) (re:110454) (di:complement) BSUB0006 Z99109 g2633371 Bacillus subtilis 1423 -11530447 7500963368 yhfs hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to acetyl-coauacetyltransferases (thil,) (le:3788) (re:4882) (di:complement) BSY14084 Y14084 g2226255 Bacillus subtilis 1423 -11530447

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783032	3535	25691	411	136

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783044	3536	25692	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783047	3537	25693	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783056	3538	25694	753	251

Description

6500726590 hypothetical protein:similar to biotin biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfU yhfU Bacillus subtilis 1423 -11530448 7000692286 yhfu biotin biosynthesis homolog yhfu (db:pir2.dat) B69832 B69832 Bacillus subtilis 1423 -11530448 4000714654 yhfu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to biotin biosynthesis) (le:111897) (re:112457) (di:complement) BSUB0006 Z99109 g2633373 Bacillus subtilis 1423 -11530448 7500963457 yhfu hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to bioy from bacillus sphaericus (swiss) (le:6325) (re:6885) (di:complement) BSY14084 Y14084 g2226257 Bacillus subtilis 1423 -11530448

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783063	3539	25695	258	85

Description

6500726591 hypothetical protein:similar to methyl-accepting chemotaxis protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfV yhfV Bacillus subtilis 1423 -11530449 7000694214 yhfv methyl-accepting chemotaxis protein homolog yhfv (db:pir2.dat) C69832 C69832 Bacillus subtilis 1423 -11530449 4000714655 yhfv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to methyl-accepting chemotaxis protein) (le:112592) (re:113890) (di:complement) BSUB0006 Z99109 g2633374 Bacillus subtilis 1423 -11530449 7500964939 yhfv hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to methyl-accepting chemotaxis proteins,) (le:7020) (re:8318) (di:complement) BSY14084 Y14084 g2226258 Bacillus subtilis 1423 -11530449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783064	3540	25696	714	237

Description

6500726592 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhfW yhfW Bacillus subtilis 1423 -11530450 7000692532 yhfw conserved hypothetical protein yhfw (db:pir2.dat) D69832 D69832 Bacillus subtilis 1423 -11530450 4000714656 yhfw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:114029) (re:115558) (di:complement) BSUB0006 Z99109 g2633375 Bacillus subtilis 1423 -11530450 7500963666 yhfw hypothetical protein (db:genpept-bct1) (de:b.subtilis chromosomal dna, region 78-80 degrees: apre to comk.) (nt:similarity to oxidoreductase ordl from e.coli) (le:8457) (re:9986) (di:complement) BSY14084 Y14084 g2226259 Bacillus subtilis 1423 -11530450

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783109	3541	25697	618	206

Description

6500726593 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhzC yhzC Bacillus subtilis 1423 -11530451 7000693359 yhzc hypothetical protein yhzc (db:pir2.dat) H69835 H69835 Bacillus subtilis 1423 -11530451 7500964315 yhzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:116555) (re:116788) (di:complement) BSUB0006 Z99109 g2633377 Bacillus subtilis 1423 -11530451

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783124	3542	25698	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783129	3543	25699	381	126

Description

6500726594 hypothetical protein:similar to ribitol dehydrogenase (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhxD yhxD Bacillus subtilis 1423 -11530452 7500937210 yhxd (ec:1.-.-.-) (de:(ec 1.-.-.-) (orfy)) (db:swissprot) YHXD_BACSU P40398 BACILLUS SUBTILIS 1423 -11530452 7000694510 yhxd ribitol dehydrogenase homolog yhxd (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) E69835 E69835 Bacillus subtilis 1423 -11530452 7500937212 yhxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to ribitol dehydrogenase) (le:117706) (re:118605) (di:complement) BSUB0006 Z99109 g2633379 Bacillus subtilis 1423 -11530452 4000714584 yhxd hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:bp 1-501 overlaps with bp 1525-1947 (end) from embl) (le:1) (re:900) (di:complement) BSY14081 Y14081 g2226172 Bacillus subtilis 1423 -11530452 7502851657 yhxd hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:bp 1-501 overlaps with bp 1525-1947 (end) from embl) (le:1) (re:900) (di:complement) BSY14081 Y14081 g2226172 Bacillus subtilis 1423 -11530452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783133	3544	25700	450	149

Description

6500726595 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjA yhjA Bacillus subtilis 1423 -11530453 7000693352 yhja hypothetical protein yhja (db:pir2.dat) A69833 A69833 Bacillus subtilis 1423 -11530453 4000714585 yhja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:118822) (re:119091) (di:direct) BSUB0006 Z99109 g2633380 Bacillus subtilis 1423 -11530453 7500964308 yhja hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (le:1117) (re:1386) (di:direct) BSY14081 Y14081 g2226173 Bacillus subtilis 1423 -11530453 7502851658 yhja hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (le:1117) (re:1386) (di:direct) BSY14081 Y14081 g2226173 Bacillus subtilis 1423 -11530453

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783152	3545	25701	249	82

Description

6500726596 hypothetical protein:similar to metabolite permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjB yhjB Bacillus subtilis 1423 -11530454 7000694203 yhjb metabolite permease homolog yhjb (cl:proline carrier protein) (db:pir2.dat) B69833 B69833 Bacillus subtilis 1423 -11530454 4000714586 yhjb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to metabolite permease) (le:119134) (re:120603) (di:complement) BSUB0006 Z99109 g2633381 Bacillus subtilis 1423 -11530454 7500964930 yhjb hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to proline permease (putp) from) (le:1429) (re:2898) (di:complement) BSY14081 Y14081 g2226174 Bacillus subtilis 1423 -11530454 7502851659 yhjb hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to proline permease (putp) from) (le:1429) (re:2898) (di:complement) BSY14081 Y14081 g2226174 Bacillus subtilis 1423 -11530454

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783153	3546	25702	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783154	3547	25703	366	121

Description

6500726597 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjC yhjC Bacillus subtilis 1423 -11530455 7000693353 yhjc hypothetical protein yhjc (db:pir2.dat) C69833 C69833 Bacillus subtilis 1423 -11530455 4000714587 yhjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:120600) (re:120800) (di:complement) BSUB0006 Z99109 g2633382 Bacillus subtilis 1423 -11530455 7500964309 yhjc hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (le:2895) (re:3095) (di:complement) BSY14081 Y14081 g2226175 Bacillus subtilis 1423 -11530455 7502851660 yhjc hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (le:2895) (re:3095) (di:complement) BSY14081 Y14081 g2226175 Bacillus subtilis 1423 -11530455

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783162	3548	25704	537	178

Description

6500726598 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjD yhjD Bacillus subtilis 1423 -11530456 7000693354 yhjd hypothetical protein yhjd (db:pir2.dat) D69833 D69833 Bacillus subtilis 1423 -11530456 4000714588 yhjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:121008) (re:121370) (di:complement) BSUB0006 Z99109 g2633383 Bacillus subtilis 1423 -11530456 7500964310 yhjd hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (le:3303) (re:3665) (di:complement) BSY14081 Y14081 g2226176 Bacillus subtilis 1423 -11530456 7502851661 yhjd hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (le:3303) (re:3665) (di:complement) BSY14081 Y14081 g2226176 Bacillus subtilis 1423 -11530456

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783170	3549	25705	282	93

Description

6500726599 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjE yhjE Bacillus subtilis 1423 -11530457 7000692534 yhje conserved hypothetical protein yhje (db:pir2.dat) E69833 E69833 Bacillus subtilis 1423 -11530457 4000714589 yhje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:121523) (re:122146) (di:direct) BSUB0006 Z99109 g2633384 Bacillus subtilis 1423 -11530457 7500963667 yhje hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to hypothetical protein yqed from) (le:3818) (re:4441) (di:direct) BSY14081 Y14081 g2226177 Bacillus subtilis 1423 -11530457 7502851662 yhje hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to hypothetical protein yqed from) (le:3818) (re:4441) (di:direct) BSY14081 Y14081 g2226177 Bacillus subtilis 1423 -11530457

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783171	3550	25706	243	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783179	3551	25707	405	134

Description

6500726600 hypothetical protein:similar to monooxygenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjG yhjG Bacillus subtilis 1423 -11530458 7000694235 yhjg monooxygenase homolog yhjg (db:pir2.dat) F69833 F69833 Bacillus subtilis 1423 -11530458 4000714591 yhjg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to monooxygenase) (le:122834) (re:124333) (di:direct) BSUB0006 Z99109 g2633386 Bacillus subtilis 1423 -11530458 7500964962 yhjg hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to fad dependent polyketide hydroxylases) (le:5129) (re:6628) (di:direct) BSY14081 Y14081 g2226179 Bacillus subtilis 1423 -11530458 7502851663 yhjg hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to fad dependent polyketide hydroxylases) (le:5129) (re:6628) (di:direct) BSY14081 Y14081 g2226179 Bacillus subtilis 1423 -11530458

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783181	3552	25708	828	275

Description

GTC ORF with score 214 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783198	3553	25709	1026	341

Description

6500726601 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjH yhjH Bacillus subtilis 1423 -11530459 7000692535 yhjh conserved hypothetical protein yhjh (cl:hypothetical protein yhjh) (db:pir2.dat) G69833 G69833 Bacillus subtilis 1423 -11530459 4000714592 yhjh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:124410) (re:124937) (di:direct) BSUB0006 Z99109 g2633387 Bacillus subtilis 1423 -11530459 7500955932 yhjh hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to hypothetical protein yzha from) (le:6705) (re:7232) (di:direct) BSY14081 Y14081 g2226180 Bacillus subtilis 1423 -11530459 7502851664 yhjh hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to hypothetical protein yzha from) (le:6705) (re:7232) (di:direct) BSY14081 Y14081 g2226180 Bacillus subtilis 1423 -11530459

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783228	3554	25710	210	69

Description

6500726602 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjI yhjI Bacillus subtilis 1423 -11530460 7000692536 yhji conserved hypothetical protein yhji (db:pir2.dat) H69833 H69833 Bacillus subtilis 1423 -11530460 4000714593 yhji (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:125095) (re:126300) (di:complement) BSUB0006 Z99109 g2633388 Bacillus subtilis 1423 -11530460 7000692537 yhji hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to a family of possible integral) (le:7390) (re:8595) (di:complement) BSY14081 Y14081 g2226181 Bacillus subtilis 1423 -11530460 7500963668 glct1 glucose transporter (db:genpept-bct2) (de:bacillus subtilis glucose transporter (glct1) and yhza homologgenes, complete cds.) (nt:glct1) (le:736) (re:1941) (di:direct) AF002191 AF002191 g2828808 Bacillus subtilis 1423 -11530460 7502851665 yhji hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to a family of possible integral) (le:7390) (re:8595) (di:complement) BSY14081 Y14081 g2226181 Bacillus subtilis 1423 -11530460

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783230	3555	25711	321	106

Description

6500726603 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjJ yhjJ Bacillus subtilis 1423 -11530461 7000692538 yhjj conserved hypothetical protein yhjj (db:pir2.dat) A69834 A69834 Bacillus subtilis 1423 -11530461 4000714594 yhjj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:126372) (re:127424) (di:complement) BSUB0006 Z99109 g2633389 Bacillus subtilis 1423 -11530461 7500963669 yhjj hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to myo-inositol 2-dehydrogenase (idh)) (le:8667) (re:9719) (di:complement) BSY14081 Y14081 g2226182 Bacillus subtilis 1423 -11530461 7502851666 yhjj hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to myo-inositol 2-dehydrogenase (idh)) (le:8667) (re:9719) (di:complement) BSY14081 Y14081 g2226182 Bacillus subtilis 1423 -11530461

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783231	3556	25712	480	159

Description

6500726604 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjK yhjK Bacillus subtilis 1423 -11530462 7000692539 yhjk conserved hypothetical protein yhjk (db:pir2.dat) B69834 B69834 Bacillus subtilis 1423 -11530462 4000714595 yhjk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:127427) (re:128287) (di:complement) BSUB0006 Z99109 g2633390 Bacillus subtilis 1423 -11530462 7500963670 yhjk hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to a large family of hypothetical) (le:9722) (re:10582) (di:complement) BSY14081 Y14081 g2226183 Bacillus subtilis 1423 -11530462 7502851667 yhjk hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to a large family of hypothetical) (le:9722) (re:10582) (di:complement) BSY14081 Y14081 g2226183 Bacillus subtilis 1423 -11530462

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783235	3557	25713	711	237

Description

6500726605 hypothetical protein:similar to sensory transduction pleiotropic regulatory protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjL yhjL Bacillus subtilis 1423 -11530463 7000694576 yhjl sensory transduction pleiotropic regulator homolog yhjl (cl:erythromycin resistance protein) (db:pir2.dat) C69834 C69834 Bacillus subtilis 1423 -11530463 4000714596 yhjl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to sensory transduction pleiotropic) (le:128259) (re:129584) (di:complement) BSUB0006 Z99109 g2633391 Bacillus subtilis 1423 -11530463 7500965175 yhjl hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to sensory transduction/ pleiotropic) (le:10554) (re:11879) (di:complement) BSY14081 Y14081 g2226184 Bacillus subtilis 1423 -11530463 7502851668 yhjl hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to sensory transduction/ pleiotropic) (le:10554) (re:11879) (di:complement) BSY14081 Y14081 g2226184 Bacillus subtilis 1423 -11530463

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783236	3558	25714	507	168

Description

6500726606 hypothetical protein:similar to transcriptional regulator:laci family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjM yhjM Bacillus subtilis 1423 -11530464 7000694745 yhjm transcription regulator laci family homolog yhjm (cl:lac repressor) (db:pir2.dat) D69834 D69834 Bacillus subtilis 1423 -11530464 4000714597 yhjm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to transcriptional regulator (laci family)) (le:129688) (re:130677) (di:direct) BSUB0006 Z99109 g2633392 Bacillus subtilis 1423 -11530464 7500965317 yhjm hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to repressors of the laci family; like) (le:11983) (re:12972) (di:direct) BSY14081 Y14081 g2226185 Bacillus subtilis 1423 -11530464 7502851669 yhjm hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to repressors of the laci family; like) (le:11983) (re:12972) (di:direct) BSY14081 Y14081 g2226185 Bacillus subtilis 1423 -11530464

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783237	3559	25715	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783241	3560	25716	837	278

Description

6500726607 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjN yhjN Bacillus subtilis 1423 -11530465 7000693355 yhjn hypothetical protein yhjn (db:pir2.dat) E69834 E69834 Bacillus subtilis 1423 -11530465 4000714598 yhjn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:130891) (re:132045) (di:complement) BSUB0006 Z99109 g2633393 Bacillus subtilis 1423 -11530465 7500964311 yhjn hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; similarity to a hypothetical protein) (le:13186) (re:14340) (di:complement) BSY14081 Y14081 g2226186 Bacillus subtilis 1423 -11530465 7502851670 yhjn hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; similarity to a hypothetical protein) (le:13186) (re:14340) (di:complement) BSY14081 Y14081 g2226186 Bacillus subtilis 1423 -11530465

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783631	3561	25717	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783666	3562	25718	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783676	3563	25719	1167	388

Description

6500726608 hypothetical protein:similar to multidrug-efflux transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjO yhjO Bacillus subtilis 1423 -11530466 7000694255 yhjo multidrug-efflux transporter homolog yhjo (db:pir2.dat) F69834 F69834 Bacillus subtilis 1423 -11530466 4000714599 yhjo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to multidrug-efflux transporter) (le:132152) (re:133357) (di:complement) BSUB0006 Z99109 g2633394 Bacillus subtilis 1423 -11530466 7500964977 yhjo hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to hypothetical protein yqjv from) (le:14447) (re:15652) (di:complement) BSY14081 Y14081 g2226187 Bacillus subtilis 1423 -11530466 7502851671 yhjo hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to hypothetical protein yqjv from) (le:14447) (re:15652) (di:complement) BSY14081 Y14081 g2226187 Bacillus subtilis 1423 -11530466

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783692	3564	25720	1680	559

Description

6500726609 hypothetical protein:similar to transporter binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjP yhjP Bacillus subtilis 1423 -11530467 7000694813 yhjp transporter binding protein homolog yhjp (db:pir2.dat) G69834 G69834 Bacillus subtilis 1423 -11530467 4000714600 yhjp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to transporter binding protein) (le:133471) (re:135198) (di:direct) BSUB0006 Z99109 g2633395 Bacillus subtilis 1423 -11530467 7500965367 yhjp hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; similarity to hypothetical proteins yabn) (le:15766) (re:17493) (di:direct) BSY14081 Y14081 g2226188 Bacillus subtilis 1423 -11530467 7502851672 yhjp hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; similarity to hypothetical proteins yabn) (le:15766) (re:17493) (di:direct) BSY14081 Y14081 g2226188 Bacillus subtilis 1423 -11530467

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783701	3565	25721	672	223

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783714	3566	25722	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783716	3567	25723	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783718	3568	25724	240	79

Description

6500726610 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjQ yhjQ Bacillus subtilis 1423 -11530468 7000693356 yhjq hypothetical protein yhjq (db:pir2.dat) H69834 H69834 Bacillus subtilis 1423 -11530468 4000714601 yhjq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:135228) (re:135554) (di:complement) BSUB0006 Z99109 g2633396 Bacillus subtilis 1423 -11530468 7500964312 yhjq hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to poly-ferredoxin from methanococcus) (le:17523) (re:17849) (di:complement) BSY14081 Y14081 g2226189 Bacillus subtilis 1423 -11530468 7502851673 yhjq hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:similarity to poly-ferredoxin from methanococcus) (le:17523) (re:17849) (di:complement) BSY14081 Y14081 g2226189 Bacillus subtilis 1423 -11530468

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783720	3569	25725	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783724	3570	25726	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783730	3571	25727	375	125

Description

6500726611 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhjR yhjR Bacillus subtilis 1423 -11530469 7000693357 yhjr hypothetical protein yhjr (db:pir2.dat) A69835 A69835 Bacillus subtilis 1423 -11530469 4000714602 yhjr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:135672) (re:136109) (di:complement) BSUB0006 Z99109 g2633397 Bacillus subtilis 1423 -11530469 7500964313 yhjr hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; similarity to nigerythrin from) (le:17967) (re:18404) (di:complement) BSY14081 Y14081 g2226190 Bacillus subtilis 1423 -11530469 7502851674 yhjr hypothetical protein (db:genpept) (de:bacillus subtilis chromosomal dna, region 92 degrees: regionbetween comk and addab.) (nt:ttg start; similarity to nigerythrin from) (le:17967) (re:18404) (di:complement) BSY14081 Y14081 g2226190 Bacillus subtilis 1423 -11530469

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783737	3572	25728	573	190

Description

6500726612 hypothetical protein:similar to dna exonuclease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yirY yirY Bacillus subtilis 1423 -11530470 7000692927 yiry dna exonuclease homolog yiry (db:pir2.dat) A69836 A69836 Bacillus subtilis 1423 -11530470 7500963944 yiry (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to dna exonuclease) (le:144721) (re:148113) (di:direct) BSUB0006 Z99109 g2633401 Bacillus subtilis 1423 -11530470

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783745	3573	25729	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783758	3574	25730	1083	360

Description

6500726613 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisB yisB Bacillus subtilis 1423 -11530471 7000693360 yisb hypothetical protein yisb (db:pir2.dat) B69836 B69836 Bacillus subtilis 1423 -11530471 3000694785 yisb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:148127) (re:148429) (di:direct) BSUB0006 Z99109 g2633402 Bacillus subtilis 1423 -11530471 7500964316 yisb (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:5353) (re:5655) (di:direct) BSY09476 Y09476 g2145367 Bacillus subtilis 1423 -11530471

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783759	3575	25731	297	98

Description

6500726614 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisC yisC Bacillus subtilis 1423 -11530472 7000692540 yisc conserved hypothetical protein yisc (cl:bacillus subtilis conserved hypothetical protein yish) (db:pir2.dat) C69836 C69836 Bacillus subtilis 1423 -11530472 3000694786 yisc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:148466) (re:148693) (di:complement) BSUB0006 Z99109 g2633403 Bacillus subtilis 1423 -11530472 7500963671 yisc (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:5692) (re:5919) (di:complement) BSY09476 Y09476 g2145368 Bacillus subtilis 1423 -11530472

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783775	3576	25732	963	320

Description

6500726615 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisD yisD Bacillus subtilis 1423 -11530473 7000693361 yisd hypothetical protein yisd (db:pir2.dat) D69836 D69836 Bacillus subtilis 1423 -11530473 3000694787 yisd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:148716) (re:149117) (di:complement) BSUB0006 Z99109 g2633404 Bacillus subtilis 1423 -11530473 7500964317 yisd (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:5942) (re:6343) (di:complement) BSY09476 Y09476 g2145369 Bacillus subtilis 1423 -11530473

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783785	3577	25733	600	199

Description

6500726616 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisE yisE Bacillus subtilis 1423 -11530474 7000693362 yise hypothetical protein yise (db:pir2.dat) E69836 E69836 Bacillus subtilis 1423 -11530474 3000694788 yise (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:149117) (re:149293) (di:complement) BSUB0006 Z99109 g2633405 Bacillus subtilis 1423 -11530474 7500964318 yise (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:6343) (re:6519) (di:complement) BSY09476 Y09476 g2145370 Bacillus subtilis 1423 -11530474

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783797	3578	25734	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783802	3579	25735	873	291

Description

6500726617 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisF yisF Bacillus subtilis 1423 -11530475 7000693363 yisf hypothetical protein yisf (db:pir2.dat) F69836 F69836 Bacillus subtilis 1423 -11530475 3000694789 yisf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:149290) (re:149907) (di:complement) BSUB0006 Z99109 g2633406 Bacillus subtilis 1423 -11530475 7500964319 yisf (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:6516) (re:7133) (di:complement) BSY09476 Y09476 g2145371 Bacillus subtilis 1423 -11530475

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783808	3580	25736	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783816	3581	25737	846	281

Description

6500726618 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisG yisG Bacillus subtilis 1423 -11530476 7000693364 yisg hypothetical protein yisg (db:pir2.dat) G69836 G69836 Bacillus subtilis 1423 -11530476 7500964320 yisg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:149930) (re:150172) (di:complement) BSUB0006 Z99109 g2633407 Bacillus subtilis 1423 -11530476

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783818	3582	25738	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783852	3583	25739	990	330

Description

6500726619 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisH yisH Bacillus subtilis 1423 -11530477 7000692541 yish conserved hypothetical protein yish (cl:bacillus subtilis conserved hypothetical protein yish) (db:pir2.dat) H69836 H69836 Bacillus subtilis 1423 -11530477 3000694791 yish (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:150178) (re:150399) (di:complement) BSUB0006 Z99109 g2633408 Bacillus subtilis 1423 -11530477 7500963672 yish (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:7404) (re:7625) (di:complement) BSY09476 Y09476 g2145373 Bacillus subtilis 1423 -11530477

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783891	3584	25740	189	62

Description

GTC ORF with score 101 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k03a1.) (nt:coded for by c. elegans cdna yk52e10.5; coded for) (le:25059:25231:25587) (re:25184:25387:25896) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783895	3585	25741	210	69

Description

6500726620 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisI yisI Bacillus subtilis 1423 -11530478 7000693365 yisi hypothetical protein yisi (db:pir2.dat) A69837 A69837 Bacillus subtilis 1423 -11530478 3000694792 yisi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:150822) (re:150992) (di:complement) BSUB0006 Z99109 g2633409 Bacillus subtilis 1423 -11530478 7500964321 yisi (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:8048) (re:8218) (di:complement) BSY09476 Y09476 g2145374 Bacillus subtilis 1423 -11530478

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783897	3586	25742	207	68

Description

6500726621 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisJ yisJ Bacillus subtilis 1423 -11530479 7000693366 yisj hypothetical protein yisj (db:pir2.dat) B69837 B69837 Bacillus subtilis 1423 -11530479 3000694793 yisj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:151138) (re:152061) (di:complement) BSUB0006 Z99109 g2633410 Bacillus subtilis 1423 -11530479 7500964322 yisj (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:8364) (re:9287) (di:complement) BSY09476 Y09476 g2145375 Bacillus subtilis 1423 -11530479

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783898	3587	25743	369	122

Description

6500726622 hypothetical protein:similar to 5-oxo-1:2:5-tricarboxilic-3-penten acid decarboxylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisK yisK Bacillus subtilis 1423 -11530480 7000692068 yisk 5-oxo-1:2:5-tricarboxilic-3-penten acid de homolog yisk (cl:2-hydroxyhepta-2,4-diene-1,7-dioate isomerase) (db:pir2.dat) C69837 C69837 Bacillus subtilis 1423 -11530480 3000694794 yisk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to 5-oxo-1,2,5-tricarboxilic-3-penten acid) (le:152216) (re:153121) (di:direct) BSUB0006 Z99109 g2633411 Bacillus subtilis 1423 -11530480 7500963312 yisk (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - homology with oxo-tricarboxilic-pentene) (le:9442) (re:10347) (di:direct) BSY09476 Y09476 g2145376 Bacillus subtilis 1423 -11530480

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783906	3588	25744	402	134

Description

6500726623 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisL yisL Bacillus subtilis 1423 -11530481 7000693367 yisl hypothetical protein yisl (db:pir2.dat) D69837 D69837 Bacillus subtilis 1423 -11530481 3000694795 yisl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:153237) (re:153593) (di:direct) BSUB0006 Z99109 g2633412 Bacillus subtilis 1423 -11530481 7500964323 yisl (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:10463) (re:10819) (di:direct) BSY09476 Y09476 g2145377 Bacillus subtilis 1423 -11530481

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783911	3589	25745	510	169

Description

GTC ORF with score 394 to: (sr:thale cress c24) (db:genpept-pln1) (de:glycine-rich protein {clone atgrp-1} (arabidopsis thaliana, c24,mrna partial, 740 nt).) (nt:this sequence comes from fig. 3a; atgrp) (le:1) (re:634) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783923	3590	25746	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783925	3591	25747	969	323

Description

6500726624 yuca:yisn hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisN yisN Bacillus subtilis 1423 -11530482 7000692542 yisn conserved hypothetical protein yisn (db:pir2.dat) E69837 E69837 Bacillus subtilis 1423 -11530482 3000694797 yisn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yuca; similar to hypothetical) (le:156476) (re:157063) (di:complement) BSUB0006 Z99109 g2633414 Bacillus subtilis 1423 -11530482 7500963673 yisn (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:13702) (re:14289) (di:complement) BSY09476 Y09476 g2145379 Bacillus subtilis 1423 -11530482

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783936	3592	25748	426	142

Description

6500726625 yucb:yiso hypothetical protein:similar to asparagine synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisO yisO Bacillus subtilis 1423 -11530483 7000692234 yiso asparagine synthase homolog yiso (db:pir2.dat) F69837 F69837 Bacillus subtilis 1423 -11530483 3000694798 yiso (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yucb; similar to asparagine) (le:157278) (re:159053) (di:direct) BSUB0006 Z99109 g2633415 Bacillus subtilis 1423 -11530483 7500963432 yiso (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - homology with x91388) (le:14504) (re:16279) (di:direct) BSY09476 Y09476 g2145380 Bacillus subtilis 1423 -11530483

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783942	3593	25749	432	143

Description

6500726626 yucd:yisp hypothetical protein:similar to phytoene synthase (gtcfc:14.1) (ec:2.5.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisP yisP Bacillus subtilis 1423 -11530484 7000694426 yisp phytoene synthase homolog yisp (db:pir2.dat) G69837 G69837 Bacillus subtilis 1423 -11530484 3000694799 yisp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yucd; similar to phytoene) (le:159895) (re:160719) (di:direct) BSUB0006 Z99109 g2633416 Bacillus subtilis 1423 -11530484 7500965082 yisp (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:17121) (re:17945) (di:direct) BSY09476 Y09476 g2145381 Bacillus subtilis 1423 -11530484

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783944	3594	25750	219	72

Description

6500726627 yuce:yisq hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisQ yisQ Bacillus subtilis 1423 -11530485 7000692543 yisq conserved hypothetical protein yisq (db:pir2.dat) H69837 H69837 Bacillus subtilis 1423 -11530485 1500694339 yisq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yuce; similar to hypothetical) (le:160749) (re:162116) (di:complement) BSUB0006 Z99109 g2633417 Bacillus subtilis 1423 -11530485 3500684478 yisq (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:17975) (re:19342) (di:complement) BSY09476 Y09476 g2145382 Bacillus subtilis 1423 -11530485 7500963674 yuce unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuca to yuch.) (le:4030) (re:5397) (di:complement) BSZ93940 Z93940 g1934838 Bacillus subtilis 1423 -11530485

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783945	3595	25751	246	81

Description

6500726628 yuxc:yucf:yisr hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisR yisR Bacillus subtilis 1423 -11530486 7500937642 yisr (de:hypothetical transcriptional regulator in wpra-dega intergenic region) (db:swissprot) YISR_BACSU P40331 BACILLUS SUBTILIS 1423 -11530486 7000694717 yisr transcription regulator arac/xyls family homolog yisr (db:pir2.dat) A69838 A69838 Bacillus subtilis 1423 -11530486 3500684479 yisr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yuxc, yucf; similar to) (le:162240) (re:163103) (di:direct) BSUB0006 Z99109 g2633418 Bacillus subtilis 1423 -11530486 7500937644 yisr (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:19466) (re:20329) (di:direct) BSY09476 Y09476 g2145383 Bacillus subtilis 1423 -11530486 1500694340 yucf unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuca to yuch.) (nt:yucf is yuxc in subtilist 1995) (le:5521) (re:6384) (di:direct) BSZ93940 Z93940 g1934839 Bacillus subtilis 1423 -11530486

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783953	3596	25752	927	309

Description

6500726629 yuxd:yucg:yiss hypothetical protein:similar to myo-inositol 2-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisS yisS Bacillus subtilis 1423 -11530487 7500937646 yiss (de:hypothetical 37.5 kd protein in dega-nprb intergenic region) (db:swissprot) YISS_BACSU P40332 BACILLUS SUBTILIS 1423 -11530487 7000694272 yiss myo-inositol 2-dehydrogenase homolog yiss:dega 3-region hypothetical protein (cl:streptomyces griseus stri protein) (db:pir2.dat) B69838 B69838 Bacillus subtilis 1423 -11530487 3500684480 yiss (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yuxd, yucg; similar to) (le:164343) (re:165371) (di:direct) BSUB0006 Z99109 g2633420 Bacillus subtilis 1423 -11530487 7500937648 yiss (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - some homology with moca (r. meliloti)) (le:21569) (re:22597) (di:direct) BSY09476 Y09476 g2145385 Bacillus subtilis 1423 -11530487 1500694341 yucg unknown (db:genpept-bct1) (de:b.subtilis genomic dna fragment from yuca to yuch.) (nt:part of this gene is in subtilist as yuxd) (le:7623) (re:8651) (di:direct) BSZ93940 Z93940 g1934841 Bacillus subtilis 1423 -11530487

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783955	3597	25753	282	93

Description

6500726630 yuch:yist hypothetical protein:hypothetical 19.5 kd protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisT yisT Bacillus subtilis 1423 -11530488 7000694329 yist nuclease inhibitor homolog yist (cl:nuclease inhibitor dinb) (db:pir2.dat) C69838 C69838 Bacillus subtilis 1423 -11530488 7500955875 yist (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yuch; similar to nuclease) (le:165422) (re:165937) (di:complement) BSUB0006 Z99109 g2633421 Bacillus subtilis 1423 -11530488

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783958	3598	25754	573	190

Description

6500726631 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisU yisU Bacillus subtilis 1423 -11530489 7000692544 yisu conserved hypothetical protein yisu (db:pir2.dat) D69838 D69838 Bacillus subtilis 1423 -11530489 3000694801 yisu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:165981) (re:166643) (di:complement) BSUB0006 Z99109 g2633422 Bacillus subtilis 1423 -11530489 7500963675 yisu (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:23207) (re:23869) (di:complement) BSY09476 Y09476 g2145387 Bacillus subtilis 1423 -11530489

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783969	3599	25755	435	144

Description

6500726632 hypothetical protein:similar to transcriptional regulator:gntr family / aminotransferase:mocr-like (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisV yisV Bacillus subtilis 1423 -11530490 7000694734 yisv transcription regulator gntr family homolog yisv (db:pir2.dat) E69838 E69838 Bacillus subtilis 1423 -11530490 3000694802 yisv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to transcriptional regulator (gntr family)) (le:166710) (re:167423) (di:direct) BSUB0006 Z99109 g2633423 Bacillus subtilis 1423 -11530490 7500965308 yisv (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:23936) (re:24649) (di:direct) BSY09476 Y09476 g2145388 Bacillus subtilis 1423 -11530490

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783973	3600	25756	348	115

Description

6500726633 hypothetical protein:similar to opine aminotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisW yisW Bacillus subtilis 1423 -11530491 7000694341 yisw opine aminotransferase homolog yisw (db:pir2.dat) F69838 F69838 Bacillus subtilis 1423 -11530491 3000694803 yisw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to opine aminotransferase) (le:167524) (re:168165) (di:direct) BSUB0006 Z99109 g2633424 Bacillus subtilis 1423 -11530491 7500965031 yisw (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:24750) (re:25391) (di:direct) BSY09476 Y09476 g2145389 Bacillus subtilis 1423 -11530491

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Attorney Docket Number: 2...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501783976	3601	25757	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784276	3602	25758	486	161

Description

6500726634 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisX yisX Bacillus subtilis 1423 -11530492 7000693368 yisx hypothetical protein yisx (db:pir2.dat) G69838 G69838 Bacillus subtilis 1423 -11530492 3000694804 yisx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:168173) (re:168811) (di:complement) BSUB0006 Z99109 g2633425 Bacillus subtilis 1423 -11530492 7500964324 yisx (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:25399) (re:26037) (di:complement) BSY09476 Y09476 g2145390 Bacillus subtilis 1423 -11530492

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784287	3603	25759	846	282

Description

6500726635 hypothetical protein:similar to chloride peroxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yisY yisY Bacillus subtilis 1423 -11530493 7000692365 yisy chloride peroxidase homolog yisy (db:pir2.dat) H69838 H69838 Bacillus subtilis 1423 -11530493 3000694805 yisy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to chloride peroxidase) (le:169017) (re:169823) (di:direct) BSUB0006 Z99109 g2633426 Bacillus subtilis 1423 -11530493 7500963528 yisy (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - probable esterase) (le:26243) (re:27049) (di:direct) BSY09476 Y09476 g2145391 Bacillus subtilis 1423 -11530493

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784292	3604	25760	882	293

Description

6500726636 hypothetical protein:similar to phospho-adenylylsulfate sulfotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitB yitB Bacillus subtilis 1423 -11530494 7500879853 yitb (ec:1.8.99.4) (de:phosphoadenylylsulfate reductase) (paps sulfotransferase)) (db:swissprot) CYH2_BACSU O06737 BACILLUS SUBTILIS 1423 -11530494 7000694403 yitb 3-phosphoadenosine 5-phosphosulfate reductase homolog yitb (db:pir2.dat) C69839 C69839 Bacillus subtilis 1423 -11530494 7500879855 yitb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to phospho-adenylylsulfate) (le:171729) (re:172319) (di:complement) BSUB0006 Z99109 g2633429 Bacillus subtilis 1423 -11530494 3000694808 yitb (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - possible phosphoadenylyl) (le:28955) (re:29545) (di:complement) BSY09476 Y09476 g2145394 Bacillus subtilis 1423 -11530494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784306	3605	25761	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784318	3606	25762	699	233

Description

6500726637 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitC yitC Bacillus subtilis 1423 -11530495 7000692545 yitc conserved hypothetical protein yitc (db:pir2.dat) D69839 D69839 Bacillus subtilis 1423 -11530495 3000694809 yitc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:172624) (re:173310) (di:direct) BSUB0006 Z99109 g2633430 Bacillus subtilis 1423 -11530495 7500963676 yitc (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:29850) (re:30536) (di:direct) BSY09476 Y09476 g2145395 Bacillus subtilis 1423 -11530495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784319	3607	25763	507	168

Description

6500726638 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitD yitD Bacillus subtilis 1423 -11530496 7000692546 yitd conserved hypothetical protein yitd (cl:hypothetical protein yitd) (db:pir2.dat) E69839 E69839 Bacillus subtilis 1423 -11530496 3000694810 yitd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:173307) (re:174065) (di:direct) BSUB0006 Z99109 g2633431 Bacillus subtilis 1423 -11530496 7500955897 yitd (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:30533) (re:31291) (di:direct) BSY09476 Y09476 g2145396 Bacillus subtilis 1423 -11530496

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784320	3608	25764	462	153

Description

6500726639 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitE yitE Bacillus subtilis 1423 -11530497 7000692547 yite conserved hypothetical protein yite (cl:conserved hypothetical protein yitt) (db:pir2.dat) F69839 F69839 Bacillus subtilis 1423 -11530497 3000694811 yite (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:174110) (re:174739) (di:complement) BSUB0006 Z99109 g2633432 Bacillus subtilis 1423 -11530497 7500963677 yite (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:31336) (re:31965) (di:complement) BSY09476 Y09476 g2145397 Bacillus subtilis 1423 -11530497

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784326	3609	25765	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784335	3610	25766	600	199

Description

GTC ORF with score 133 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f52e4.) (nt:weak similarity to s. cerevisiae intracellular) (le:25893:26194:26744) (re:26144:26292:26868) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784340	3611	25767	1104	368

Description

6500726640 hypothetical protein:similar to mandelate racemase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitF yitF Bacillus subtilis 1423 -11530498 7000694195 yitf mandelate racemase homolog yitf (db:pir2.dat) G69839 G69839 Bacillus subtilis 1423 -11530498 3000694812 yitf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to mandelate racemase) (le:174835) (re:175950) (di:complement) BSUB0006 Z99109 g2633433 Bacillus subtilis 1423 -11530498 7500964922 yitf (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:32061) (re:33176) (di:complement) BSY09476 Y09476 g2145398 Bacillus subtilis 1423 -11530498

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784341	3612	25768	429	142

Description

6500726641 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitG yitG Bacillus subtilis 1423 -11530499 7000694245 yitg multidrug resistance protein homolog yitg (db:pir2.dat) H69839 H69839 Bacillus subtilis 1423 -11530499 7500964971 yitg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to multidrug resistance protein) (le:175959) (re:177227) (di:complement) BSUB0006 Z99109 g2633434 Bacillus subtilis 1423 -11530499

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784345	3613	25769	996	331

Description

6500726642 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitH yitH Bacillus subtilis 1423 -11530500 7000693369 yith hypothetical protein yith (db:pir2.dat) A69840 A69840 Bacillus subtilis 1423 -11530500 3000694814 yith (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:177339) (re:178187) (di:complement) BSUB0006 Z99109 g2633435 Bacillus subtilis 1423 -11530500 7500964325 yith (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:34565) (re:35413) (di:complement) BSY09476 Y09476 g2145400 Bacillus subtilis 1423 -11530500

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784347	3614	25770	414	137

Description

6500726643 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitI yitI Bacillus subtilis 1423 -11530501 7000692548 yiti conserved hypothetical protein yiti (db:pir2.dat) B69840 B69840 Bacillus subtilis 1423 -11530501 7500963678 yiti (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:178192) (re:178656) (di:complement) BSUB0006 Z99109 g2633436 Bacillus subtilis 1423 -11530501

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784348	3615	25771	828	275

Description

6500726644 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitJ yitJ Bacillus subtilis 1423 -11530502 7000692549 yitj conserved hypothetical protein yitj (db:pir2.dat) C69840 C69840 Bacillus subtilis 1423 -11530502 3000694816 yitj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:178731) (re:180569) (di:complement) BSUB0006 Z99109 g2633437 Bacillus subtilis 1423 -11530502 7500963679 yitj (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - some homology with meth2 (s. cerevisae)) (le:35957) (re:37795) (di:complement) BSY09476 Y09476 g2145402 Bacillus subtilis 1423 -11530502

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784355	3616	25772	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784358	3617	25773	315	104

Description

6500726645 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitK yitK Bacillus subtilis 1423 -11530503 7000692550 yitk conserved hypothetical protein yitk (cl:hypothetical protein b0426) (db:pir2.dat) D69840 D69840 Bacillus subtilis 1423 -11530503 3000694817 yitk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:180883) (re:181374) (di:complement) BSUB0006 Z99109 g2633438 Bacillus subtilis 1423 -11530503 7500955890 yitk (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative - some homology with hi1034 (h.) (le:38109) (re:38600) (di:complement) BSY09476 Y09476 g2145403 Bacillus subtilis 1423 -11530503

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784360	3618	25774	294	97

Description

6500726646 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitL yitL Bacillus subtilis 1423 -11530504 7000693370 yitl hypothetical protein yitl (db:pir2.dat) E69840 E69840 Bacillus subtilis 1423 -11530504 7500964326 yitl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:181473) (re:182369) (di:direct) BSUB0006 Z99109 g2633439 Bacillus subtilis 1423 -11530504

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784362	3619	25775	639	212

Description

6500726647 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitM yitM Bacillus subtilis 1423 -11530505 7000692551 yitm conserved hypothetical protein yitm (db:pir2.dat) F69840 F69840 Bacillus subtilis 1423 -11530505 3000694819 yitm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:182422) (re:183006) (di:complement) BSUB0006 Z99109 g2633440 Bacillus subtilis 1423 -11530505 7500963680 yitm (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative) (le:39648) (re:40232) (di:complement) BSY09476 Y09476 g2145405 Bacillus subtilis 1423 -11530505

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784373	3620	25776	435	144

Description

6500726648 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitN yitN Bacillus subtilis 1423 -11530506 7000692552 yitn conserved hypothetical protein yitn (db:pir2.dat) G69840 G69840 Bacillus subtilis 1423 -11530506 3000694820 yitn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:183003) (re:183371) (di:complement) BSUB0006 Z99109 g2633441 Bacillus subtilis 1423 -11530506 7500963681 yitn (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:40229) (re:40597) (di:complement) BSY09476 Y09476 g2145406 Bacillus subtilis 1423 -11530506

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784376	3621	25777	264	87

Description

6500726649 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitO yitO Bacillus subtilis 1423 -11530507 7000692553 yito conserved hypothetical protein yito (db:pir2.dat) H69840 H69840 Bacillus subtilis 1423 -11530507 3000694821 yito (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins from b. subtilis) (le:183503) (re:183715) (di:complement) BSUB0006 Z99109 g2633442 Bacillus subtilis 1423 -11530507 7500963682 yito (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:40729) (re:40941) (di:complement) BSY09476 Y09476 g2145407 Bacillus subtilis 1423 -11530507

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784377	3622	25778	243	80

Description

6500726650 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitP yitP Bacillus subtilis 1423 -11530508 7000692554 yitp conserved hypothetical protein yitp (db:pir2.dat) A69841 A69841 Bacillus subtilis 1423 -11530508 3000694822 yitp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:183916) (re:184452) (di:complement) BSUB0006 Z99109 g2633443 Bacillus subtilis 1423 -11530508 7500963683 yitp (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:41142) (re:41678) (di:complement) BSY09476 Y09476 g2145408 Bacillus subtilis 1423 -11530508

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784383	3623	25779	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784391	3624	25780	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784411	3625	25781	468	155

Description

GTC ORF with score 501 to: (sr:aspergillus kawachii (strain:ifo4308) dna) (db:genpept-pln1) (de:aspergillus kawachii dna for beta-d-glucosidase, complete cds.) (le:789:938:1130:1229:1333) (re:845:1080:1174:1281:2524) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784412	3626	25782	234	77

Description

GTC ORF with score 332 to: (or:Aspergillus aculeatus) (sr:aspergillus aculeatus (isolate:no.f-50) cdna to mrna, clone:pagb7) (db:genpept-pln1) (ec:3.2.1.21) (de:aspergillus aculeatus mrna for beta-glucosidase, complete cds.) (le:111) (re:2693) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784424	3627	25783	1809	602

Description

6500726651 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitQ yitQ Bacillus subtilis 1423 -11530509 7000693371 yitq hypothetical protein yitq (db:pir2.dat) B69841 B69841 Bacillus subtilis 1423 -11530509 3000694823 yitq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:184824) (re:185561) (di:direct) BSUB0006 Z99109 g2633444 Bacillus subtilis 1423 -11530509 7500964327 yitq (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:42050) (re:42787) (di:direct) BSY09476 Y09476 g2145409 Bacillus subtilis 1423 -11530509

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784431	3628	25784	1260	419

Description

6500726652 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitR yitR Bacillus subtilis 1423 -11530510 7000693372 yitr hypothetical protein yitr (db:pir2.dat) C69841 C69841 Bacillus subtilis 1423 -11530510 3000694824 yitr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:185581) (re:185874) (di:direct) BSUB0006 Z99109 g2633445 Bacillus subtilis 1423 -11530510 7500964328 yitr (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:42807) (re:43100) (di:direct) BSY09476 Y09476 g2145410 Bacillus subtilis 1423 -11530510

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784432	3629	25785	201	66

Description

6500726653 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitS yitS Bacillus subtilis 1423 -11530511 7000693373 yits hypothetical protein yits (db:pir2.dat) D69841 D69841 Bacillus subtilis 1423 -11530511 218945 putative::orf (fn:unknown) (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:1702) (re:2553) (di:complement) BS168NPRB Z79580 g1620923 Bacillus subtilis 1423 -11530511 304065 yits (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:187673) (re:188524) (di:complement) BSUB0006 Z99109 g2633447 Bacillus subtilis 1423 -11530511 3500684468 yits (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:44899) (re:45750) (di:complement) BSY09476 Y09476 g2145412 Bacillus subtilis 1423 -11530511

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784433	3630	25786	291	96

Description

6500726654 yuxa:yitt hypothetical protein:hypothetical 30.5 kd protein in ipi 5region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitT yitT Bacillus subtilis 1423 -11530512 218946 putative::orf (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:2691) (re:3533) (di:direct) BS168NPRB Z79580 g1620924 Bacillus subtilis 1423 -11530512 304066 yitt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yuxa; similar to hypothetical) (le:188662) (re:189504) (di:direct) BSUB0006 Z99109 g2633448 Bacillus subtilis 1423 -11530512 3500684469 yitt (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf - ipi orf1) (le:45888) (re:46730) (di:direct) BSY09476 Y09476 g2145413 Bacillus subtilis 1423 -11530512 7000692555 yitt conserved hypothetical protein yitt (db:pir) E69841 E69841 Bacillus subtilis 1423 -11530512

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784438	3631	25787	303	100

Description

GTC ORF with score 170 to: (sr:homo sapiens (clone library: p1) adult dna) (db:genpept-pri1) (ec:1.3.99.13) (de:homo sapiens very long chain acyl-coa dehydrogenase gene, exons1-20, complete cds.) (le:89:226:566:706:868) (re:150:301:631:778:932) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784439	3632	25788	411	136

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784452	3633	25789	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784465	3634	25790	495	164

Description

6500726655 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitU yitU Bacillus subtilis 1423 -11530513 7000692556 yitu conserved hypothetical protein yitu (db:pir2.dat) F69841 F69841 Bacillus subtilis 1423 -11530513 218948 putative::orf (fn:unknown) (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:4492) (re:5304) (di:complement) BS168NPRB Z79580 g1620926 Bacillus subtilis 1423 -11530513 304068 yitu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:190463) (re:191275) (di:complement) BSUB0006 Z99109 g2633450 Bacillus subtilis 1423 -11530513 3500684470 yitu (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:47689) (re:48501) (di:complement) BSY09476 Y09476 g2145415 Bacillus subtilis 1423 -11530513

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784466	3635	25791	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784477	3636	25792	873	291

Description

6500726656 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitV yitV Bacillus subtilis 1423 -11530514 7000692557 yitv conserved hypothetical protein yitv (db:pir2.dat) G69841 G69841 Bacillus subtilis 1423 -11530514 218949 putative::orf (fn:unknown) (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:5425) (re:6192) (di:direct) BS168NPRB Z79580 g1620927 Bacillus subtilis 1423 -11530514 304069 yitv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:191396) (re:192163) (di:direct) BSUB0006 Z99109 g2633451 Bacillus subtilis 1423 -11530514 3500684471 yitv (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:48622) (re:49389) (di:direct) BSY09476 Y09476 g2145416 Bacillus subtilis 1423 -11530514

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784480	3637	25793	474	157

Description

6500726657 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitW yitW Bacillus subtilis 1423 -11530515 7000692558 yitw conserved hypothetical protein yitw (cl:conserved hypothetical protein mj1129) (db:pir2.dat) H69841 H69841 Bacillus subtilis 1423 -11530515 218950 putative::orf (fn:unknown) (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:6256) (re:6564) (di:direct) BS168NPRB Z79580 g1620928 Bacillus subtilis 1423 -11530515 304070 yitw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to hypothetical proteins) (le:192227) (re:192535) (di:direct) BSUB0006 Z99109 g2633452 Bacillus subtilis 1423 -11530515 3500684472 yitw (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:49453) (re:49761) (di:direct) BSY09476 Y09476 g2145417 Bacillus subtilis 1423 -11530515

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784489	3638	25794	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784494	3639	25795	498	165

Description

GTC ORF with score 284 to: (db:genpept-pln2) (de:emericella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj),(stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784495	3640	25796	789	263

Description

6500726658 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitX yitX Bacillus subtilis 1423 -11530516 7000693374 yitx hypothetical protein yitx (db:pir2.dat) A69842 A69842 Bacillus subtilis 1423 -11530516 218951 putative::orf (fn:unknown) (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:6619) (re:6831) (di:direct) BS168NPRB Z79580 g1620929 Bacillus subtilis 1423 -11530516 304071 yitx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:192590) (re:192802) (di:direct) BSUB0006 Z99109 g2633453 Bacillus subtilis 1423 -11530516 3500684473 yitx (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:49816) (re:50028) (di:direct) BSY09476 Y09476 g2145418 Bacillus subtilis 1423 -11530516

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784508	3641	25797	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784514	3642	25798	195	64

Description

6500726659 hypothetical protein:similar to l-gulonolactone oxydase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitY yitY Bacillus subtilis 1423 -11530517 7000694148 yity l-gulonolactone oxydase homolog yity (db:pir2.dat) B69842 B69842 Bacillus subtilis 1423 -11530517 218952 putative::orf (fn:unknown) (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:6889) (re:8289) (di:direct) BS168NPRB Z79580 g1620930 Bacillus subtilis 1423 -11530517 304072 yity (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to l-gulonolactone oxydase) (le:192860) (re:194260) (di:direct) BSUB0006 Z99109 g2633454 Bacillus subtilis 1423 -11530517 3500684474 yity (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:50086) (re:51486) (di:direct) BSY09476 Y09476 g2145419 Bacillus subtilis 1423 -11530517

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784515	3643	25799	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784909	3644	25800	558	185

Description

6500726660 hypothetical protein:similar to multidrug resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yitZ yitZ Bacillus subtilis 1423 -11530518 7000694246 yitz multidrug resistance protein homolog yitz (db:pir2.dat) C69842 C69842 Bacillus subtilis 1423 -11530518 218953 putaive::orf (fn:unknown) (db:genpept-bct1) (de:b.subtilis nprb gene.) (le:8334) (re:8828) (di:direct) BS168NPRB Z79580 g1620931 Bacillus subtilis 1423 -11530518 304073 yitz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to multidrug resistance protein) (le:194305) (re:194799) (di:direct) BSUB0006 Z99109 g2633455 Bacillus subtilis 1423 -11530518 3500684475 yitz (db:genpept-bct1) (de:b.subtilis 54kb genomic dna fragment.) (nt:putative orf) (le:51531) (re:52025) (di:direct) BSY09476 Y09476 g2145420 Bacillus subtilis 1423 -11530518

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784912	3645	25801	348	115

Description

6500726661 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjzC yjzC Bacillus subtilis 1423 -11530519 7000693416 yjzc hypothetical protein yjzc (db:pir2.dat) F69854 F69854 Bacillus subtilis 1423 -11530519 6000690617 yjzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:204472) (re:204651) (di:direct) BSUB0006 Z99109 g2633463 Bacillus subtilis 1423 -11530519 7500964369 yjzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:9582) (re:9761) (di:direct) BSUB0007 Z99110 g2633480 Bacillus subtilis 1423 -11530519

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784913	3646	25802	1083	361

Description

6500726662 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjzD yjzD Bacillus subtilis 1423 -11530520 7000693417 yjzd hypothetical protein yjzd (db:pir2.dat) G69854 G69854 Bacillus subtilis 1423 -11530520 5500704141 yjzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:204697) (re:204882) (di:complement) BSUB0006 Z99109 g2633464 Bacillus subtilis 1423 -11530520 6000690619 yjzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:9807) (re:9992) (di:complement) BSUB0007 Z99110 g2633481 Bacillus subtilis 1423 -11530520 7500964370 (sr:bacillus subtilis (strain:cu741) dna) (db:genpept-bct1) (de:bacillus subtilis argf and med genes, partial and complete cds.) (nt:unnamed protein product) (le:1027) (re:1212) (di:complement) D86376 D86376 g2564027 Bacillus subtilis 1423 -11530520

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784915	3647	25803	408	135

Description

6500726663 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjaU yjaU Bacillus subtilis 1423 -11530521 7000693375 yjau hypothetical protein yjau (db:pir2.dat) D69842 D69842 Bacillus subtilis 1423 -11530521 5500704142 yjau (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:205131) (re:205865) (di:direct) BSUB0006 Z99109 g2633465 Bacillus subtilis 1423 -11530521 6000690621 yjau (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:10241) (re:10975) (di:direct) BSUB0007 Z99110 g2633482 Bacillus subtilis 1423 -11530521 7500964329 (sr:bacillus subtilis (strain:cu741) dna) (db:genpept-bct1) (de:bacillus subtilis argf and med genes, partial and complete cds.) (nt:unnamed protein product) (le:1461) (re:2195) (di:direct) D86376 D86376 g2564028 Bacillus subtilis 1423 -11530521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784922	3648	25804	639	213

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784930	3649	25805	219	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784931	3650	25806	1239	412

Description

GTC ORF with score 353 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c14f5.) (nt:spbc14f5.07, unknown; integral membrane protein,) (le:17309:17437:17541:17665) (re:17382:17475:17614:21206) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784943	3651	25807	513	171

Description

6500726664 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjaV yjaV Bacillus subtilis 1423 -11530522 7000693376 yjav hypothetical protein yjav (db:pir2.dat) E69842 E69842 Bacillus subtilis 1423 -11530522 6000690623 yjav (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:205947) (re:206354) (di:direct) BSUB0006 Z99109 g2633466 Bacillus subtilis 1423 -11530522 7500964330 yjav (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:11057) (re:11464) (di:direct) BSUB0007 Z99110 g2633483 Bacillus subtilis 1423 -11530522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784959	3652	25808	738	246

Description

6500726665 yjaw:med hypothetical protein:positive regulator of comk (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) med med Bacillus subtilis 1423 -11530523 7000694438 med positive regulator of comk med (db:pir2.dat) D69656 D69656 Bacillus subtilis 1423 -11530523 6000690625 med (fn:positive regulator of comk) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:alternate gene name: yjaw) (le:206614) (re:207549) (di:direct) BSUB0006 Z99109 g2633467 Bacillus subtilis 1423 -11530523 7500965093 med (fn:positive regulator of comk) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: yjaw) (le:11724) (re:12659) (di:direct) BSUB0007 Z99110 g2633484 Bacillus subtilis 1423 -11530523

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784960	3653	25809	612	204

Description

6500726666 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjzA yjzA Bacillus subtilis 1423 -11530524 7000693414 yjza hypothetical protein yjza (db:pir2.dat) D69854 D69854 Bacillus subtilis 1423 -11530524 6000690627 yjza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:207564) (re:207755) (di:direct) BSUB0006 Z99109 g2633468 Bacillus subtilis 1423 -11530524 7500964367 yjza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:12674) (re:12865) (di:direct) BSUB0007 Z99110 g2633485 Bacillus subtilis 1423 -11530524

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784967	3654	25810	816	271

Description

6500726667 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjzB yjzB Bacillus subtilis 1423 -11530525 7000693415 yjzb hypothetical protein yjzb (db:pir2.dat) E69854 E69854 Bacillus subtilis 1423 -11530525 5500704146 yjzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (le:207785) (re:208024) (di:complement) BSUB0006 Z99109 g2633469 Bacillus subtilis 1423 -11530525 6000690629 yjzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:12895) (re:13134) (di:complement) BSUB0007 Z99110 g2633486 Bacillus subtilis 1423 -11530525 7500964368 (sr:bacillus subtilis (strain:cu741) dna) (db:genpept-bct1) (de:bacillus subtilis argf and med genes, partial and complete cds.) (nt:unnamed protein product) (le:4114) (re:4353) (di:complement) D86376 D86376 g2564032 Bacillus subtilis 1423 -11530525

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784975	3655	25811	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784978	3656	25812	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501784988	3657	25813	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785008	3658	25814	480	159

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785011	3659	25815	303	100

Description

GTC ORF with score 210 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785013	3660	25816	237	78

Description

6500726668 hypothetical protein:similar to cell wall-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yhdD yhdD Bacillus subtilis 1423 -11530526 7000692337 yhdd cell wall-binding protein homolog yhdd (db:pir2.dat) B69825 B69825 Bacillus subtilis 1423 -11530526 4000714560 yhdd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.) (nt:similar to cell wall-binding protein) (le:11748) (re:13214) (di:complement) BSUB0006 Z99109 g2633272 Bacillus subtilis 1423 -11530526 7500963504 yhdd hypothetical protein (db:genpept-bct1) (de:bacillus subtilis chromosomal dna, region 75 degrees: glppfkdoperon and downstream.) (nt:similarity to the phosphatase-associated) (le:11396) (re:12862) (di:complement) BSY14079 Y14079 g2226145 Bacillus subtilis 1423 -11530526

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785014	3661	25817	486	161

Description

6500726669 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjaZ yjaZ Bacillus subtilis 1423 -11530527 7000693377 yjaz hypothetical protein yjaz (db:pir2.dat) H69842 H69842 Bacillus subtilis 1423 -11530527 7500964331 yjaz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:15577) (re:16362) (di:direct) BSUB0007 Z99110 g2633489 Bacillus subtilis 1423 -11530527

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785017	3662	25818	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785021	3663	25819	690	229

Description

6500726670 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbA yjbA Bacillus subtilis 1423 -11530528 7000693378 yjba hypothetical protein yjba (db:pir2.dat) A69843 A69843 Bacillus subtilis 1423 -11530528 7500964332 yjba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:22408) (re:23160) (di:direct) BSUB0007 Z99110 g2633495 Bacillus subtilis 1423 -11530528

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785027	3664	25820	459	152

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785028	3665	25821	645	214

Description

GTC ORF with score 158 to: (db:genpept-bct1) (de:pseudomonas aeruginosa pyoverdine chromophore biosynthesis genecluster including pvca (pvca), pvcb (pvcb), pvcc (pvcc), and pvcd(pvcd) genes, complete cds, and transcriptional activator ptxr(ptxr) gene, ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785043	3666	25822	735	244

Description

6500726671 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbB yjbB Bacillus subtilis 1423 -11530529 7000692559 yjbb conserved hypothetical protein yjbb (db:pir2.dat) B69843 B69843 Bacillus subtilis 1423 -11530529 7500963684 yjbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:30648) (re:31856) (di:direct) BSUB0007 Z99110 g2633502 Bacillus subtilis 1423 -11530529

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785056	3667	25823	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785067	3668	25824	219	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785080	3669	25825	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785081	3670	25826	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785091	3671	25827	525	175

Description

6500726672 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbC yjbC Bacillus subtilis 1423 -11530530 7000693379 yjbc hypothetical protein yjbc (db:pir2.dat) C69843 C69843 Bacillus subtilis 1423 -11530530 7500964333 yjbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:32020) (re:32598) (di:direct) BSUB0007 Z99110 g2633503 Bacillus subtilis 1423 -11530530

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785094	3672	25828	540	179

Description

6500726673 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbD yjbD Bacillus subtilis 1423 -11530531 7000692560 yjbd conserved hypothetical protein yjbd (cl:hypothetical protein yjbd) (db:pir2.dat) D69843 D69843 Bacillus subtilis 1423 -11530531 7500955936 yjbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:32779) (re:33174) (di:direct) BSUB0007 Z99110 g2633504 Bacillus subtilis 1423 -11530531

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785105	3673	25829	999	332

Description

6500726674 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbE yjbE Bacillus subtilis 1423 -11530532 7000692561 yjbe conserved hypothetical protein yjbe (db:pir2.dat) E69843 E69843 Bacillus subtilis 1423 -11530532 7500963685 yjbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:33217) (re:33873) (di:complement) BSUB0007 Z99110 g2633505 Bacillus subtilis 1423 -11530532

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785113	3674	25830	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785128	3675	25831	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785168	3676	25832	261	86

Description

6500726675 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbF yjbF Bacillus subtilis 1423 -11530533 7000693380 yjbf hypothetical protein yjbf (db:pir2.dat) F69843 F69843 Bacillus subtilis 1423 -11530533 7500964334 yjbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:34997) (re:36118) (di:direct) BSUB0007 Z99110 g2633507 Bacillus subtilis 1423 -11530533

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785170	3677	25833	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785171	3678	25834	300	99

Description

6500726676 hypothetical protein:similar to oligoendopeptidase (gtcfc:14.1) (ec:3.4.24.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbG yjbG Bacillus subtilis 1423 -11530534 7000694334 yjbg oligoendopeptidase homolog yjbg (cl:oligoendopeptidase f) (db:pir2.dat) G69843 G69843 Bacillus subtilis 1423 -11530534 7500955938 yjbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to oligoendopeptidase) (le:36348) (re:38177) (di:direct) BSUB0007 Z99110 g2633508 Bacillus subtilis 1423 -11530534

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785185	3679	25835	465	154

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785186	3680	25836	408	136

Description

6500726677 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbH yjbH Bacillus subtilis 1423 -11530535 7000693381 yjbh hypothetical protein yjbh (db:pir2.dat) H69843 H69843 Bacillus subtilis 1423 -11530535 7500964335 yjbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:38695) (re:39522) (di:complement) BSUB0007 Z99110 g2633509 Bacillus subtilis 1423 -11530535

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785190	3681	25837	252	83

Description

6500726678 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbI yjbI Bacillus subtilis 1423 -11530536 7000693382 yjbi hypothetical protein yjbi (db:pir2.dat) A69844 A69844 Bacillus subtilis 1423 -11530536 7500964336 yjbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:39591) (re:39989) (di:complement) BSUB0007 Z99110 g2633510 Bacillus subtilis 1423 -11530536

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785192	3682	25838	372	123

Description

6500726679 hypothetical protein:similar to lytic transglycosylase (gtcfc:14.1) (ec:3.2.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbJ yjbJ Bacillus subtilis 1423 -11530537 7000694176 yjbj lytic transglycosylase homolog yjbj (db:pir2.dat) B69844 B69844 Bacillus subtilis 1423 -11530537 7500964906 yjbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to lytic transglycosylase) (le:40244) (re:40789) (di:complement) BSUB0007 Z99110 g2633511 Bacillus subtilis 1423 -11530537

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785193	3683	25839	186	61

Description

6500726680 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbK yjbK Bacillus subtilis 1423 -11530538 7000693383 yjbk hypothetical protein yjbk (db:pir2.dat) C69844 C69844 Bacillus subtilis 1423 -11530538 7500964337 yjbk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:40993) (re:41565) (di:complement) BSUB0007 Z99110 g2633512 Bacillus subtilis 1423 -11530538

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785203	3684	25840	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785210	3685	25841	717	238

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785211	3686	25842	1191	397

Description

6500726681 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbL yjbL Bacillus subtilis 1423 -11530539 7000693384 yjbl hypothetical protein yjbl (db:pir2.dat) D69844 D69844 Bacillus subtilis 1423 -11530539 7500964338 yjbl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:41690) (re:42058) (di:direct) BSUB0007 Z99110 g2633513 Bacillus subtilis 1423 -11530539

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785213	3687	25843	768	255

Description

6500726682 hypothetical protein:similar to gtp pyrophosphokinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbM yjbM Bacillus subtilis 1423 -11530540 7000693075 yjbm gtp pyrophosphokinase homolog yjbm (cl:gtp pyrophosphokinase related protein) (db:pir2.dat) E69844 E69844 Bacillus subtilis 1423 -11530540 7500954206 yjbm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to gtp pyrophosphokinase) (le:42087) (re:42722) (di:direct) BSUB0007 Z99110 g2633514 Bacillus subtilis 1423 -11530540

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785214	3688	25844	702	234

Description

6500726683 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbN yjbN Bacillus subtilis 1423 -11530541 7000692562 yjbn conserved hypothetical protein yjbn (cl:conserved hypothetical protein hi0072) (db:pir2.dat) F69844 F69844 Bacillus subtilis 1423 -11530541 7500963686 yjbn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:42741) (re:43541) (di:direct) BSUB0007 Z99110 g2633515 Bacillus subtilis 1423 -11530541

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785230	3689	25845	897	298

Description

6500726684 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbO yjbO Bacillus subtilis 1423 -11530542 7502851675 yjbo (de:hypothetical 31.5 kd protein in meca-tena intergenic region) (db:swissprot) YJBO_BACSU O31613 BACILLUS SUBTILIS 1423 -11530542 7000692563 yjbo conserved hypothetical protein yjbo (cl:conserved hypothetical protein hi0176) (db:pir2.dat) G69844 G69844 Bacillus subtilis 1423 -11530542 7500963687 yjbo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:43604) (re:44455) (di:direct) BSUB0007 Z99110 g2633516 Bacillus subtilis 1423 -11530542

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785232	3690	25846	687	229

Description

6500726685 hypothetical protein:similar to na+/h+ antiporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbQ yjbQ Bacillus subtilis 1423 -11530543 7000694293 yjbq na+/h+ antiporter homolog yjbq (db:pir2.dat) A69845 A69845 Bacillus subtilis 1423 -11530543 7500965002 yjbq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to na+/h+ antiporter) (le:45437) (re:47281) (di:direct) BSUB0007 Z99110 g2633518 Bacillus subtilis 1423 -11530543

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785579	3691	25847	219	72

Description

GTC ORF with score 93 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0162.) (nt:simslar to saccharomyces cerevisiae hypothetical) (le:<1) (re:647) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785583	3692	25848	927	308

Description

6500726686 hypothetical protein:similar to sarcosine oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbR yjbR Bacillus subtilis 1423 -11530544 7502851676 yjbr (ec:1.5.3.-) (de:glycine oxidase,) (db:swissprot) GLOX_BACSU O31616 BACILLUS SUBTILIS 1423 -11530544 7000694572 yjbr sarcosine oxidase homolog yjbr (db:pir2.dat) B69845 B69845 Bacillus subtilis 1423 -11530544 7500965172 yjbr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to sarcosine oxidase) (le:48816) (re:49925) (di:direct) BSUB0007 Z99110 g2633521 Bacillus subtilis 1423 -11530544

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785590	3693	25849	540	179

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785615	3694	25850	216	71

Description

6500726687 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbS yjbS Bacillus subtilis 1423 -11530545 7000693385 yjbs hypothetical protein yjbs (db:pir2.dat) C69845 C69845 Bacillus subtilis 1423 -11530545 7500964339 yjbs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:49925) (re:50125) (di:direct) BSUB0007 Z99110 g2633522 Bacillus subtilis 1423 -11530545

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785617	3695	25851	492	163

Description

GTC ORF with score 109 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0224 gene, complete cds.) (nt:similar to putative atp-dependent rna helicase) (le:137) (re:3820) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785624	3696	25852	549	183

Description

6500726688 hypothetical protein:similar to thiamin biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbT yjbT Bacillus subtilis 1423 -11530546 7000694672 yjbt thiamin biosynthesis homolog yjbt (cl:thiamine biosynthesis protein thig) (db:pir2.dat) D69845 D69845 Bacillus subtilis 1423 -11530546 7500965256 yjbt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to thiamin biosynthesis) (le:50122) (re:50892) (di:direct) BSUB0007 Z99110 g2633523 Bacillus subtilis 1423 -11530546

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785635	3697	25853	252	83

Description

6500726689 hypothetical protein:similar to thiamin biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbU yjbU Bacillus subtilis 1423 -11530547 7000694673 yjbu thiamin biosynthesis homolog yjbu (db:pir2.dat) E69845 E69845 Bacillus subtilis 1423 -11530547 7500965257 yjbu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to thiamin biosynthesis) (le:50889) (re:51899) (di:direct) BSUB0007 Z99110 g2633524 Bacillus subtilis 1423 -11530547

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785638	3698	25854	402	133

Description

6500726690 hypothetical protein:similar to phosphomethylpyrimidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbV yjbV Bacillus subtilis 1423 -11530548 7000694417 yjbv phosphomethylpyrimidine kinase homolog yjbv (cl:phosphomethylpyrimidine phosphate kinase) (db:pir2.dat) F69845 F69845 Bacillus subtilis 1423 -11530548 7500965074 yjbv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to phosphomethylpyrimidine kinase) (le:51918) (re:52733) (di:direct) BSUB0007 Z99110 g2633525 Bacillus subtilis 1423 -11530548

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785639	3699	25855	768	255

Description

6500726691 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjbX yjbX Bacillus subtilis 1423 -11530549 7000693386 yjbx hypothetical protein yjbx (db:pir2.dat) H69845 H69845 Bacillus subtilis 1423 -11530549 7500964340 yjbx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:53746) (re:54429) (di:direct) BSUB0007 Z99110 g2633527 Bacillus subtilis 1423 -11530549

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785651	3700	25856	621	207

Description

6500726692 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcA yjcA Bacillus subtilis 1423 -11530550 7000692564 yjca conserved hypothetical protein yjca (cl:hypothetical protein yngl) (db:pir2.dat) A69846 A69846 Bacillus subtilis 1423 -11530550 7500955832 yjca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:57258) (re:57614) (di:direct) BSUB0007 Z99110 g2633533 Bacillus subtilis 1423 -11530550

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785671	3701	25857	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785675	3702	25858	258	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785695	3703	25859	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785701	3704	25860	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785717	3705	25861	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785719	3706	25862	393	130

Description

6500726693 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcB yjcB Bacillus subtilis 1423 -11530551 7000693387 yjcb hypothetical protein yjcb (db:pir2.dat) B69846 B69846 Bacillus subtilis 1423 -11530551 7500964341 yjcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:57939) (re:58154) (di:direct) BSUB0007 Z99110 g2633534 Bacillus subtilis 1423 -11530551

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785721	3707	25863	333	110

Description

6500726694 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcC yjcC Bacillus subtilis 1423 -11530552 7000693388 yjcc hypothetical protein yjcc (db:pir2.dat) C69846 C69846 Bacillus subtilis 1423 -11530552 7500964342 yjcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:58418) (re:58720) (di:direct) BSUB0007 Z99110 g2633535 Bacillus subtilis 1423 -11530552

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785723	3708	25864	435	144

Description

GTC ORF with score 178 to: (or:Glomerella cingulata) (db:genpept-pln1) (de:colletotrichum gloeosporioides nitrogen starvation-inducedglutamine rich protein mrna, complete cds.) (nt:glutamine rich protein similar to glutenins;) (le:74) (re:721) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785739	3709	25865	606	201

Description

6500726695 hypothetical protein:similar to atp-dependent dna helicase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcD yjcD Bacillus subtilis 1423 -11530553 7000692249 yjcd atp-dependent dna helicase homolog yjcd (db:pir2.dat) D69846 D69846 Bacillus subtilis 1423 -11530553 7500963441 yjcd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to atp-dependent dna helicase) (le:58794) (re:61073) (di:complement) BSUB0007 Z99110 g2633536 Bacillus subtilis 1423 -11530553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785740	3710	25866	195	64

Description

Hypothetical protein

jc542 U.S. PTO 09/417507 10/14/99

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785756	3711	25867	1428	476

Description

6500726696 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcE yjcE Bacillus subtilis 1423 -11530554 7000693389 yjce hypothetical protein yjce (db:pir2.dat) E69846 E69846 Bacillus subtilis 1423 -11530554 7500964343 yjce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:61154) (re:61456) (di:complement) BSUB0007 Z99110 g2633537 Bacillus subtilis 1423 -11530554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785763	3712	25868	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785764	3713	25869	348	115

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785767	3714	25870	390	129

Description

6500726697 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcF yjcF Bacillus subtilis 1423 -11530555 7000692565 yjcf conserved hypothetical protein yjcf (cl:hypothetical protein yjcf) (db:pir2.dat) F69846 F69846 Bacillus subtilis 1423 -11530555 7500955916 yjcf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:61517) (re:61939) (di:complement) BSUB0007 Z99110 g2633538 Bacillus subtilis 1423 -11530555

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785788	3715	25871	1128	375

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785791	3716	25872	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785796	3717	25873	516	171

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785802	3718	25874	516	171

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785815	3719	25875	1383	460

Description

6500726698 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcG yjcG Bacillus subtilis 1423 -11530556 7000693390 yjcg hypothetical protein yjcg (db:pir2.dat) G69846 G69846 Bacillus subtilis 1423 -11530556 7500964344 yjcg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:61943) (re:62458) (di:complement) BSUB0007 Z99110 g2633539 Bacillus subtilis 1423 -11530556

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785817	3720	25876	345	114

Description

6500726699 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcH yjcH Bacillus subtilis 1423 -11530557 7000693391 yjch hypothetical protein yjch (db:pir2.dat) H69846 H69846 Bacillus subtilis 1423 -11530557 7500964345 yjch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:62495) (re:63217) (di:complement) BSUB0007 Z99110 g2633540 Bacillus subtilis 1423 -11530557

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785818	3721	25877	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785830	3722	25878	969	323

Description

6500726700 hypothetical protein:similar to cystathionine beta-lyase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcJ yjcJ Bacillus subtilis 1423 -11530558 7000692884 yjcj cystathionine beta-lyase homolog yjcj (cl:o-succinylhomoserine (thiol)-lyase) (db:pir2.dat) B69847 B69847 Bacillus subtilis 1423 -11530558 7500963914 yjcj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to cystathionine beta-lyase) (le:64687) (re:65859) (di:direct) BSUB0007 Z99110 g2633542 Bacillus subtilis 1423 -11530558

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785851	3723	25879	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785867	3724	25880	447	148

Description

6500726701 hypothetical protein:similar to ribosomal-protein-alanine n-acetyltransferase (gtcfc:14.1) (ec:2.3.1.128) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcK yjcK Bacillus subtilis 1423 -11530559 7000694545 yjck ribosomal-protein-alanine n-acetyltransfer homolog yjck (cl:hypothetical protein yoaa) (db:pir2.dat) C69847 C69847 Bacillus subtilis 1423 -11530559 7500955879 yjck (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to ribosomal-protein-alanine) (le:65892) (re:66437) (di:complement) BSUB0007 Z99110 g2633543 Bacillus subtilis 1423 -11530559

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785871	3725	25881	603	200

Description

6500726702 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcL yjcL Bacillus subtilis 1423 -11530560 7000693392 yjcl hypothetical protein yjcl (db:pir2.dat) D69847 D69847 Bacillus subtilis 1423 -11530560 7500964346 yjcl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:66507) (re:67697) (di:complement) BSUB0007 Z99110 g2633544 Bacillus subtilis 1423 -11530560

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501785885	3726	25882	1026	341

Description

6500726703 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcM yjcM Bacillus subtilis 1423 -11530561 7000693393 yjcm hypothetical protein yjcm (db:pir2.dat) E69847 E69847 Bacillus subtilis 1423 -11530561 7500964347 yjcm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:68783) (re:70012) (di:complement) BSUB0007 Z99110 g2633545 Bacillus subtilis 1423 -11530561

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786308	3727	25883	957	319

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786326	3728	25884	213	70

Description

6500726704 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcN yjcN Bacillus subtilis 1423 -11530562 7000693394 yjcn hypothetical protein yjcn (db:pir2.dat) F69847 F69847 Bacillus subtilis 1423 -11530562 7500964348 yjcn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:70138) (re:70458) (di:direct) BSUB0007 Z99110 g2633546 Bacillus subtilis 1423 -11530562

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786328	3729	25885	252	83

Description

GTC ORF with score 224 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c31h12.) (nt:spcc31h12.07, len:759, similarity:homo sapiens,) (le:14184:14264:14495:14592) (re:14214:14435:14526:16636) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786330	3730	25886	378	126

Description

6500726705 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcO yjcO Bacillus subtilis 1423 -11530563 7000692566 yjco conserved hypothetical protein yjco (cl:hypothetical protein yjco) (db:pir2.dat) G69847 G69847 Bacillus subtilis 1423 -11530563 7500955940 yjco (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:70968) (re:71429) (di:direct) BSUB0007 Z99110 g2633547 Bacillus subtilis 1423 -11530563

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786342	3731	25887	729	242

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786344	3732	25888	315	104

Description

6500726706 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcP yjcP Bacillus subtilis 1423 -11530564 7000693395 yjcp hypothetical protein yjcp (db:pir2.dat) H69847 H69847 Bacillus subtilis 1423 -11530564 7500964349 yjcp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:71695) (re:72198) (di:direct) BSUB0007 Z99110 g2633548 Bacillus subtilis 1423 -11530564

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786346	3733	25889	1074	358

Description

6500726707 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcQ yjcQ Bacillus subtilis 1423 -11530565 7000693396 yjcq hypothetical protein yjcq (db:pir2.dat) A69848 A69848 Bacillus subtilis 1423 -11530565 7500964350 yjcq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:72210) (re:72494) (di:direct) BSUB0007 Z99110 g2633549 Bacillus subtilis 1423 -11530565

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786366	3734	25890	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786371	3735	25891	561	186

Description

GTC ORF with score 533 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c576.) (nt:spcc576.14, len:283, similarity:saccharomyces) (le:22418:22963:23236:23416) (re:22677:23192:23367:23645) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786378	3736	25892	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786395	3737	25893	444	147

Description

6500726708 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcR yjcR Bacillus subtilis 1423 -11530566 7000692567 yjcr conserved hypothetical protein yjcr (db:pir2.dat) B69848 B69848 Bacillus subtilis 1423 -11530566 7500963688 yjcr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:72655) (re:73182) (di:direct) BSUB0007 Z99110 g2633550 Bacillus subtilis 1423 -11530566

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786397	3738	25894	489	162

Description

6500726709 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjcS yjcS Bacillus subtilis 1423 -11530567 7000693397 yjcs hypothetical protein yjcs (db:pir2.dat) C69848 C69848 Bacillus subtilis 1423 -11530567 7500964351 yjcs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:73356) (re:73673) (di:direct) BSUB0007 Z99110 g2633551 Bacillus subtilis 1423 -11530567

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786402	3739	25895	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786421	3740	25896	501	167

Description

6500726710 yida:yjda hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdA yjdA Bacillus subtilis 1423 -11530568 7000692052 yjda 3-oxoacyl-acyl-carrier protein reductase homolog yjda (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D69848 D69848 Bacillus subtilis 1423 -11530568 7500963297 yjda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: yida; similar to 3-oxoacyl-) (le:73910) (re:74665) (di:direct) BSUB0007 Z99110 g2633552 Bacillus subtilis 1423 -11530568

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786431	3741	25897	456	152

Description

6500726711 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdB yjdB Bacillus subtilis 1423 -11530569 7000693398 yjdb hypothetical protein yjdb (db:pir2.dat) E69848 E69848 Bacillus subtilis 1423 -11530569 7500964352 yjdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:74814) (re:75161) (di:complement) BSUB0007 Z99110 g2633553 Bacillus subtilis 1423 -11530569

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786432	3742	25898	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786446	3743	25899	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786469	3744	25900	270	89

Description

6500726712 hypothetical protein:similar to transcriptional antiterminator:bglg family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdC yjdC Bacillus subtilis 1423 -11530570 7000694707 yjdc transcription antiterminator bglg family homolog yjdc (cl:phosphotransferase system mannitol-specific enzyme ii factor iii homology) (db:pir2.dat) F69848 F69848 Bacillus subtilis 1423 -11530570 7500965280 yjdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to transcriptional antiterminator (bglg) (le:75712) (re:77658) (di:direct) BSUB0007 Z99110 g2633554 Bacillus subtilis 1423 -11530570

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786472	3745	25901	1011	336

Description

6500726713 hypothetical protein:similar to fructose phosphotransferase system enzyme ii (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdD yjdD Bacillus subtilis 1423 -11530571 7000693011 yjdd fructose phosphotransferase system enzyme homolog yjdd (db:pir2.dat) G69848 G69848 Bacillus subtilis 1423 -11530571 7500963999 yjdd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to fructose phosphotransferase system) (le:77806) (re:79575) (di:direct) BSUB0007 Z99110 g2633555 Bacillus subtilis 1423 -11530571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786483	3746	25902	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786485	3747	25903	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786495	3748	25904	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786496	3749	25905	555	184

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786511	3750	25906	777	259

Description

6500726714 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdF yjdF Bacillus subtilis 1423 -11530572 7000693399 yjdf hypothetical protein yjdf (db:pir2.dat) A69849 A69849 Bacillus subtilis 1423 -11530572 7500964353 yjdf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:80891) (re:81373) (di:direct) BSUB0007 Z99110 g2633557 Bacillus subtilis 1423 -11530572

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786515	3751	25907	1050	349

Description

6500726715 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdG yjdG Bacillus subtilis 1423 -11530573 7000692568 yjdg conserved hypothetical protein yjdg (db:pir2.dat) B69849 B69849 Bacillus subtilis 1423 -11530573 7500963689 yjdg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:81419) (re:81925) (di:complement) BSUB0007 Z99110 g2633558 Bacillus subtilis 1423 -11530573

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786518	3752	25908	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786541	3753	25909	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786544	3754	25910	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786550	3755	25911	264	87

Description

GTC ORF with score 90 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de:caenorhabditis elegans cosmid c56a3, complete sequence.) (nt:weak similarity to human calcium-dependent proetase) (le:35772:36005:36688) (re:35960:36636:36777) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786553	3756	25912	216	71

Description

6500726716 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdH yjdH Bacillus subtilis 1423 -11530574 7000693400 yjdh hypothetical protein yjdh (db:pir2.dat) C69849 C69849 Bacillus subtilis 1423 -11530574 7500964354 yjdh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:82157) (re:82561) (di:complement) BSUB0007 Z99110 g2633559 Bacillus subtilis 1423 -11530574

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786569	3757	25913	276	91

Description

GTC ORF with score 134 to: (sr:aspergillus aculeatus (strain ksm 510) cdna to mrna) (db:genpept-pln1) (de:aspergillus aculeatus mannanase (man1) mrna, complete cds.) (nt:n-linked glycosylation sites at bp 105, bp 255, bp) (le:24) (re:1157) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786573	3758	25914	528	175

Description

GTC ORF with score 574 to: (sr:aspergillus aculeatus (strain ksm 510) cdna to mrna) (db:genpept-pln1) (de:aspergillus aculeatus mannanase (man1) mrna, complete cds.) (nt:n-linked glycosylation sites at bp 105, bp 255, bp) (le:24) (re:1157) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786574	3759	25915	303	100

Description

GTC ORF with score 301 to: (sr:aspergillus aculeatus (strain ksm 510) cdna to mrna) (db:genpept-pln1) (de:aspergillus aculeatus mannanase (man1) mrna, complete cds.) (nt:n-linked glycosylation sites at bp 105, bp 255, bp) (le:24) (re:1157) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786576	3760	25916	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786586	3761	25917	1158	386

Description

6500726717 hypothetical protein:similar to transcription regulation (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdI yjdI Bacillus subtilis 1423 -11530575 7000694697 yjdi transcription regulation homolog yjdi (cl:conserved hypothetical protein hi1434) (db:pir2.dat) D69849 D69849 Bacillus subtilis 1423 -11530575 7500965276 yjdi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to transcription regulation) (le:82766) (re:83245) (di:direct) BSUB0007 Z99110 g2633560 Bacillus subtilis 1423 -11530575

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786595	3762	25918	345	114

Description

GTC ORF with score 140 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f12c20 genomic sequence,complete sequence.) (nt:unknown protein) (le:45171:46239:46705) (re:45637:46611:47409) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786609	3763	25919	900	300

Description

6500726718 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdJ yjdJ Bacillus subtilis 1423 -11530576 7000693401 yjdj hypothetical protein yjdj (db:pir2.dat) E69849 E69849 Bacillus subtilis 1423 -11530576 7500964355 yjdj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:83645) (re:83974) (di:complement) BSUB0007 Z99110 g2633561 Bacillus subtilis 1423 -11530576

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786613	3764	25920	696	231

Description

6500726719 hypothetical protein:similar to cytochrome c oxidase assembly factor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjdK yjdK Bacillus subtilis 1423 -11530577 7000692891 yjdk probable heme a farnesyltransferase::cytochrome-c oxidase assembly factor homolog yjdk (cl:heme o synthase) (ec:2.5.1.-) (db:pir2.dat) F69849 F69849 Bacillus subtilis 1423 -11530577 7500963920 yjdk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to cytochrome c oxidase assembly factor) (le:84594) (re:85583) (di:complement) BSUB0007 Z99110 g2633562 Bacillus subtilis 1423 -11530577

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786623	3765	25921	657	218

Description

6500726720 hypothetical protein:similar to endo-1:4-beta-xylanase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjeA yjeA Bacillus subtilis 1423 -11530578 7000692962 yjea endo-1:4-beta-xylanase homolog yjea (cl:nodb homology) (db:pir2.dat) G69849 G69849 Bacillus subtilis 1423 -11530578 5500701544 yjea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to endo-1,4-beta-xylanase) (le:86208) (re:87611) (di:direct) BSUB0007 Z99110 g2633564 Bacillus subtilis 1423 -11530578 7500963968 yjea nodb-like protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to rhizobium leguminosarum nodb protein) (le:368) (re:1771) (di:direct) AF015825 AF015825 g2612882 Bacillus subtilis 1423 -11530578

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786632	3766	25922	1656	552

Description

6500726721 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjfA yjfA Bacillus subtilis 1423 -11530579 7000693402 yjfa hypothetical protein yjfa (db:pir2.dat) H69849 H69849 Bacillus subtilis 1423 -11530579 5500701545 yjfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:87651) (re:88124) (di:complement) BSUB0007 Z99110 g2633565 Bacillus subtilis 1423 -11530579 7500964356 yjfa unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:1811) (re:2284) (di:complement) AF015825 AF015825 g2612883 Bacillus subtilis 1423 -11530579

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786650	3767	25923	258	85

Description

GTC ORF with score 169 to: (sr:tomato) (db:genpept-pln2) (de:lycopersicon esculentum farnesyl protein transferase subunit a(lefta) mrna, complete cds.) (nt:similar to saccharomyces cerevisiae ram2p) (le:73) (re:1113) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501786651	3768	25924	501	166

Description

6500726722 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjfB yjfB Bacillus subtilis 1423 -11530580 7000693403 yjfb hypothetical protein yjfb (db:pir2.dat) A69850 A69850 Bacillus subtilis 1423 -11530580 5500701546 yjfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:88249) (re:88416) (di:complement) BSUB0007 Z99110 g2633566 Bacillus subtilis 1423 -11530580 7500964357 yjfb unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:2409) (re:2576) (di:complement) AF015825 AF015825 g2612884 Bacillus subtilis 1423 -11530580

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787090	3769	25925	453	150

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787091	3770	25926	387	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787093	3771	25927	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787106	3772	25928	1080	359

Description

GTC ORF with score 216 to: (sr:baker's yeast) (db:genpept-pln2) (de:skt5 (skt5)=protoplast regeneration and killer toxin resistancegene (saccharomyces cerevisiae, genomic mutant, 2177 nt).) (nt:protoplast regeneration and killer toxin resistance) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787113	3773	25929	1395	464

Description

6500726723 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjfC yjfC Bacillus subtilis 1423 -11530581 7000693404 yjfc hypothetical protein yjfc (db:pir2.dat) B69850 B69850 Bacillus subtilis 1423 -11530581 5500701547 yjfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:88543) (re:89472) (di:direct) BSUB0007 Z99110 g2633567 Bacillus subtilis 1423 -11530581 7500964358 yjfc unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:2703) (re:3632) (di:direct) AF015825 AF015825 g2612885 Bacillus subtilis 1423 -11530581

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787123	3774	25930	1212	404

Description

6500726724 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjgA yjgA Bacillus subtilis 1423 -11530582 7000693405 yjga hypothetical protein yjga (db:pir2.dat) C69850 C69850 Bacillus subtilis 1423 -11530582 5500701548 yjga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:89450) (re:89848) (di:complement) BSUB0007 Z99110 g2633568 Bacillus subtilis 1423 -11530582 7500964359 yjga unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:3610) (re:4008) (di:complement) AF015825 AF015825 g2612886 Bacillus subtilis 1423 -11530582

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787137	3775	25931	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787164	3776	25932	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787168	3777	25933	1029	342

Description

6500726725 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjgB yjgB Bacillus subtilis 1423 -11530583 7000693406 yjgb hypothetical protein yjgb (db:pir2.dat) D69850 D69850 Bacillus subtilis 1423 -11530583 5500701549 yjgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:89949) (re:90524) (di:complement) BSUB0007 Z99110 g2633569 Bacillus subtilis 1423 -11530583 7500964360 yjgb putative lipoprotein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:4109) (re:4684) (di:complement) AF015825 AF015825 g2612887 Bacillus subtilis 1423 -11530583

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787180	3778	25934	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787182	3779	25935	366	121

Description

6500726726 hypothetical protein:similar to formate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjgC yjgC Bacillus subtilis 1423 -11530584 7000693000 yjgc formate dehydrogenase homolog yjgc (db:pir2.dat) E69850 E69850 Bacillus subtilis 1423 -11530584 5500701550 yjgc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to formate dehydrogenase) (le:90670) (re:93627) (di:direct) BSUB0007 Z99110 g2633570 Bacillus subtilis 1423 -11530584 7500963991 yjgc formate dehydrogenase alpha subunit homolog (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to formate dehydrogenase alpha subunit of) (le:4830) (re:7787) (di:direct) AF015825 AF015825 g2612888 Bacillus subtilis 1423 -11530584

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787201	3780	25936	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787202	3781	25937	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787207	3782	25938	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787218	3783	25939	366	121

Description

6500726727 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjgD yjgD Bacillus subtilis 1423 -11530585 7000692569 yjgd conserved hypothetical protein yjgd (db:pir2.dat) F69850 F69850 Bacillus subtilis 1423 -11530585 5500701551 yjgd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:93620) (re:94180) (di:direct) BSUB0007 Z99110 g2633571 Bacillus subtilis 1423 -11530585 7500963690 yjgd unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:7780) (re:8340) (di:direct) AF015825 AF015825 g2612889 Bacillus subtilis 1423 -11530585

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787222	3784	25940	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787227	3785	25941	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787230	3786	25942	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787241	3787	25943	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787243	3788	25944	756	251

Description

6500726728 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjhA yjhA Bacillus subtilis 1423 -11530586 7000693407 yjha hypothetical protein yjha (db:pir2.dat) G69850 G69850 Bacillus subtilis 1423 -11530586 5500701552 yjha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:94377) (re:95018) (di:direct) BSUB0007 Z99110 g2633572 Bacillus subtilis 1423 -11530586 7500964361 yjha putative lipoprotein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:8537) (re:9178) (di:direct) AF015825 AF015825 g2612890 Bacillus subtilis 1423 -11530586

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787255	3789	25945	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787256	3790	25946	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787257	3791	25947	273	91

Description

6500726729 hypothetical protein:similar to mutator mutt protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjhB yjhB Bacillus subtilis 1423 -11530587 7000694269 yjhb mutator mutt protein homolog yjhb (db:pir2.dat) H69850 H69850 Bacillus subtilis 1423 -11530587 5500701553 yjhb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to mutator mutt protein) (le:95211) (re:95723) (di:direct) BSUB0007 Z99110 g2633573 Bacillus subtilis 1423 -11530587 7500964986 yjhb mutt homolog (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to mutator mutt protein of methanococcus) (le:9371) (re:9883) (di:direct) AF015825 AF015825 g2612891 Bacillus subtilis 1423 -11530587

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787272	3792	25948	378	125

Description

6500726730 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjiA yjiA Bacillus subtilis 1423 -11530588 7000693408 yjia hypothetical protein yjia (db:pir2.dat) A69851 A69851 Bacillus subtilis 1423 -11530588 5500701554 yjia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:95754) (re:96032) (di:complement) BSUB0007 Z99110 g2633574 Bacillus subtilis 1423 -11530588 7500964362 yjia unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:9914) (re:10192) (di:complement) AF015825 AF015825 g2612892 Bacillus subtilis 1423 -11530588

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787273	3793	25949	258	85

Description

6500726731 hypothetical protein:similar to monooxygenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjiB yjiB Bacillus subtilis 1423 -11530589 7000694236 yjib monooxygenase homolog yjib (cl:cytochrome p450) (db:pir2.dat) B69851 B69851 Bacillus subtilis 1423 -11530589 5500701555 yjib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to monooxygenase) (le:96423) (re:97613) (di:direct) BSUB0007 Z99110 g2633575 Bacillus subtilis 1423 -11530589 7500964963 yjib p450 heme-thiolate protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:member of the p450 heme-thiolate (cytochrome p450)) (le:10583) (re:11773) (di:direct) AF015825 AF015825 g2612893 Bacillus subtilis 1423 -11530589

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787285	3794	25950	489	162

Description

6500726732 hypothetical protein:similar to macrolide glycosyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjiC yjiC Bacillus subtilis 1423 -11530590 7000694178 yjic macrolide glycosyltransferase homolog yjic (cl:glycosyltransferase) (db:pir2.dat) C69851 C69851 Bacillus subtilis 1423 -11530590 5500701556 yjic (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to macrolide glycosyltransferase) (le:97636) (re:98814) (di:direct) BSUB0007 Z99110 g2633576 Bacillus subtilis 1423 -11530590 7500954260 yjic hypothetical glycosyl transferase (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:11796) (re:12974) (di:direct) AF015825 AF015825 g2612894 Bacillus subtilis 1423 -11530590

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787291	3795	25951	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787314	3796	25952	918	306

Description

6500726733 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjjA yjjA Bacillus subtilis 1423 -11530591 7000692570 yjja conserved hypothetical protein yjja (db:pir2.dat) D69851 D69851 Bacillus subtilis 1423 -11530591 5500701557 yjja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:99217) (re:100029) (di:direct) BSUB0007 Z99110 g2633577 Bacillus subtilis 1423 -11530591 7500963691 yjja unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:weakly similar to uroporphyrinogeniii cosynthase of) (le:13377) (re:14189) (di:direct) AF015825 AF015825 g2612895 Bacillus subtilis 1423 -11530591

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787315	3797	25953	360	119

Description

6500726734 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjkA yjkA Bacillus subtilis 1423 -11530592 7000692571 yjka conserved hypothetical protein yjka (cl:conserved hypothetical protein mj0938) (db:pir2.dat) E69851 E69851 Bacillus subtilis 1423 -11530592 5500701558 yjka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:100075) (re:100827) (di:complement) BSUB0007 Z99110 g2633578 Bacillus subtilis 1423 -11530592 7500963692 yjka unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to methanococcus jannaschii mj0938) (le:14235) (re:14987) (di:complement) AF015825 AF015825 g2612896 Bacillus subtilis 1423 -11530592

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787337	3798	25954	372	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787340	3799	25955	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787350	3800	25956	261	86

Description

6500726735 hypothetical protein:similar to amino acid abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjkB yjkB Bacillus subtilis 1423 -11530593 7000692186 yjkb amino acid abc transporter atp-binding pr homolog yjkb (cl:atp-binding cassette homology) (db:pir2.dat) F69851 F69851 Bacillus subtilis 1423 -11530593 5500701559 yjkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to amino acid abc transporter (atp-binding) (le:100827) (re:101579) (di:complement) BSUB0007 Z99110 g2633579 Bacillus subtilis 1423 -11530593 7500963397 yjkb hypothetical abc transporter (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:14987) (re:15739) (di:complement) AF015825 AF015825 g2612897 Bacillus subtilis 1423 -11530593

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787351	3801	25957	600	200

Description

6500726736 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjlA yjlA Bacillus subtilis 1423 -11530594 7000692572 yjla conserved hypothetical protein yjla (db:pir2.dat) G69851 G69851 Bacillus subtilis 1423 -11530594 5500701560 yjla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:101699) (re:102673) (di:complement) BSUB0007 Z99110 g2633580 Bacillus subtilis 1423 -11530594 7500963693 yjla yisp-like protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to yisp protein of bacillus sp. strain 221) (le:15859) (re:16833) (di:complement) AF015825 AF015825 g2612898 Bacillus subtilis 1423 -11530594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787364	3802	25958	318	105

Description

6500726737 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjlB yjlB Bacillus subtilis 1423 -11530595 7000693409 yjlb hypothetical protein yjlb (db:pir2.dat) H69851 H69851 Bacillus subtilis 1423 -11530595 5500701561 yjlb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:102805) (re:103302) (di:direct) BSUB0007 Z99110 g2633581 Bacillus subtilis 1423 -11530595 7500964363 yjlb unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:16965) (re:17462) (di:direct) AF015825 AF015825 g2612899 Bacillus subtilis 1423 -11530595

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787366	3803	25959	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787378	3804	25960	627	208

Description

6500726738 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjlC yjlC Bacillus subtilis 1423 -11530596 7000693410 yjlc hypothetical protein yjlc (db:pir2.dat) A69852 A69852 Bacillus subtilis 1423 -11530596 5500701562 yjlc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:103691) (re:104113) (di:direct) BSUB0007 Z99110 g2633582 Bacillus subtilis 1423 -11530596 7500964364 yjlc unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:17851) (re:18273) (di:direct) AF015825 AF015825 g2612900 Bacillus subtilis 1423 -11530596

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787379	3805	25961	633	211

Description

GTC ORF with score 134 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787382	3806	25962	303	100

Description

6500726739 hypothetical protein:similar to nadh dehydrogenase (gtcfc:14.1) (ec:1.6.99.3) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjlD yjlD Bacillus subtilis 1423 -11530597 7000694304 yjld nadh dehydrogenase homolog yjld (cl:nadh dehydrogenase) (db:pir2.dat) B69852 B69852 Bacillus subtilis 1423 -11530597 5500701563 yjld (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to nadh dehydrogenase) (le:104153) (re:105331) (di:direct) BSUB0007 Z99110 g2633583 Bacillus subtilis 1423 -11530597 7500953889 yjld nadh dehydrogenase-like protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:18313) (re:19491) (di:direct) AF015825 AF015825 g2612901 Bacillus subtilis 1423 -11530597

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787384	3807	25963	642	213

Description

6500726740 hypothetical protein:similar to na+:galactoside symporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmB yjmB Bacillus subtilis 1423 -11530598 7502851677 yjmb (de:hypothetical symporter in cott-rapa intergenic region) (db:swissprot) YJMB_BACSU O34961 BACILLUS SUBTILIS 1423 -11530598 7000694297 yjmb na+:galactoside symporter homolog yjmb (cl:melibiose carrier protein) (db:pir2.dat) D69852 D69852 Bacillus subtilis 1423 -11530598 5500701565 yjmb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to na+:galactoside symporter) (le:107018) (re:108397) (di:direct) BSUB0007 Z99110 g2633585 Bacillus subtilis 1423 -11530598 7500965006 yjmb sodium:galactoside symporter protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to bacterial sugar permeases; member of the) (le:21178) (re:22557) (di:direct) AF015825 AF015825 g2612903 Bacillus subtilis 1423 -11530598

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787390	3808	25964	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787394	3809	25965	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787398	3810	25966	306	101

Description

GTC ORF with score 191 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787399	3811	25967	693	230

Description

6500726741 hypothetical protein:similar to sorbitol dehydrogenase (gtcfc:14.1) (ec:1.1.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmD yjmD Bacillus subtilis 1423 -11530599 7000694598 yjmd l-iditol 2-dehydrogenase:homolog yjmd:sorbitol dehydrogenase homolog (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.14) (db:pir1.dat) F69852 F69852 Bacillus subtilis 1423 -11530599 5500701567 yjmd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to sorbitol dehydrogenase) (le:109521) (re:110540) (di:direct) BSUB0007 Z99110 g2633587 Bacillus subtilis 1423 -11530599 7500953162 yjmd zinc-containing alcohol dehydrogenase (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to starvation sensing protein rspb of) (le:23681) (re:24700) (di:direct) AF015825 AF015825 g2612905 Bacillus subtilis 1423 -11530599

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787401	3812	25968	918	305

Description

6500726742 hypothetical protein:similar to 2-deoxy-d-gluconate 3-dehydrogenase (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmF yjmF Bacillus subtilis 1423 -11530600 7000692037 yjmf 2-deoxy-d-gluconate 3-dehydrogenase homolog yjmf (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) H69852 H69852 Bacillus subtilis 1423 -11530600 5500701569 yjmf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to 2-deoxy-d-gluconate 3-dehydrogenase) (le:111641) (re:112477) (di:direct) BSUB0007 Z99110 g2633589 Bacillus subtilis 1423 -11530600 7500963289 yjmf short-chain alcohol dehydrogenase (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to several oxidoreductases; member of the) (le:25801) (re:26637) (di:direct) AF015825 AF015825 g2612907 Bacillus subtilis 1423 -11530600

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787405	3813	25969	579	193

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787413	3814	25970	666	221

Description

6500726743 hypothetical protein:similar to hexuronate transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmG yjmG Bacillus subtilis 1423 -11530601 7000693091 yjmg hexuronate transporter homolog yjmg (cl:hexuronate transporter) (db:pir2.dat) A69853 A69853 Bacillus subtilis 1423 -11530601 5500701570 yjmg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hexuronate transporter) (le:112525) (re:113793) (di:direct) BSUB0007 Z99110 g2633590 Bacillus subtilis 1423 -11530601 7500955184 yjmg hexuronate transporter-like protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to hexuronate transporter of escherichia) (le:26685) (re:27953) (di:direct) AF015825 AF015825 g2612908 Bacillus subtilis 1423 -11530601

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787415	3815	25971	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787427	3816	25972	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787432	3817	25973	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787437	3818	25974	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787439	3819	25975	624	207

Description

6500726744 hypothetical protein:similar to transcriptional regulator:laci family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjmH yjmH Bacillus subtilis 1423 -11530602 7000694746 yjmh transcription regulator laci family homolog yjmh (cl:lac repressor) (db:pir2.dat) B69853 B69853 Bacillus subtilis 1423 -11530602 5500701571 yjmh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to transcriptional regulator (laci family)) (le:113881) (re:114882) (di:direct) BSUB0007 Z99110 g2633591 Bacillus subtilis 1423 -11530602 7500965318 yjmh laci repressor-like protein (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to several bacterial repressors of sugars) (le:28041) (re:29042) (di:direct) AF015825 AF015825 g2612909 Bacillus subtilis 1423 -11530602

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787441	3820	25976	633	210

Description

6500726745 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjnA yjnA Bacillus subtilis 1423 -11530603 7000692573 yjna conserved hypothetical protein yjna (db:pir2.dat) E69853 E69853 Bacillus subtilis 1423 -11530603 5500701574 yjna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:117930) (re:118694) (di:complement) BSUB0007 Z99110 g2633594 Bacillus subtilis 1423 -11530603 7500963694 yjna unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:32090) (re:32854) (di:complement) AF015825 AF015825 g2612912 Bacillus subtilis 1423 -11530603

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787457	3821	25977	705	234

Description

6500726746 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjoA yjoA Bacillus subtilis 1423 -11530604 7000693411 yjoa hypothetical protein yjoa (db:pir2.dat) F69853 F69853 Bacillus subtilis 1423 -11530604 5500701575 yjoa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:118919) (re:119383) (di:complement) BSUB0007 Z99110 g2633595 Bacillus subtilis 1423 -11530604 7500964365 yjoa unknown (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (le:33079) (re:33543) (di:complement) AF015825 AF015825 g2612913 Bacillus subtilis 1423 -11530604

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787462	3822	25978	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787465	3823	25979	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787472	3824	25980	1248	415

Description

6500726747 hypothetical protein:similar to cell-division protein ftsh homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjoB yjoB Bacillus subtilis 1423 -11530605 7000692346 yjob cell-division protein ftsh homolog homolog yjob (cl:ftsh/sec18/cdc48-type atp-binding domain homology) (db:pir2.dat) G69853 G69853 Bacillus subtilis 1423 -11530605 5500701576 yjob (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to cell-division protein ftsh homolog) (le:119532) (re:120803) (di:direct) BSUB0007 Z99110 g2633596 Bacillus subtilis 1423 -11530605 7500963511 yjob cell division cycle cdc48 homolog (db:genpept-bct2) (de:bacillus subtilis 168 cott-rapa region sequence.) (nt:similar to cell division cycle protein cdc48 of) (le:33692) (re:34963) (di:direct) AF015825 AF015825 g2612914 Bacillus subtilis 1423 -11530605

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787474	3825	25981	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787480	3826	25982	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787486	3827	25983	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787919	3828	25984	426	141

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787923	3829	25985	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787939	3830	25986	495	164

Description

6500726748 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjpA yjpA Bacillus subtilis 1423 -11530606 7000693412 yjpa hypothetical protein yjpa (db:pir2.dat) H69853 H69853 Bacillus subtilis 1423 -11530606 6000689465 yjpa unknown (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (le:1... AF034138 AF034138 g2645865 Bacillus subtilis 1423 -11530606 7500964366 yjpa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:122239) (re:122481) (di:complement) BSUB0007 Z99110 g2633599 Bacillus subtilis 1423 -11530606

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787943	3831	25987	1074	358

Description

GTC ORF with score 140 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid c04a11, complete sequence.) (nt:predicted using genefinder; similarity to protein) (le:20207:20332:20820:21149) (re:20281:20577:21091:21782) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787964	3832	25988	408	136

Description

6500726749 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjqA yjqA Bacillus subtilis 1423 -11530607 7000693413 yjqa hypothetical protein yjqa (cl:hypothetical protein yozo) (db:pir2.dat) A69854 A69854 Bacillus subtilis 1423 -11530607 6000689469 yjqa unknown (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (le:3... AF034138 AF034138 g2645867 Bacillus subtilis 1423 -11530607 7500955881 yjqa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:123608) (re:123985) (di:complement) BSUB0007 Z99110 g2633601 Bacillus subtilis 1423 -11530607

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787965	3833	25989	447	148

Description

GTC ORF with score 146 to: (sr:homo sapiens (library: lambda zap library from nidr/nih) bone cdn) (db:genpept-pri1) (de:homo sapiens adenosine triphosphatase mrna, complete cds.) (nt:plasma membrane calciun pump ho-2) (le:134) (re:3022) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787966	3834	25990	612	203

Description

6500726750 hypothetical protein:similar to phage-related replication protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjqB yjqB Bacillus subtilis 1423 -11530608 7000694388 yjqb phage-related replication protein homolog yjqb (cl:phage-related replication protein) (db:pir2.dat) B69854 B69854 Bacillus subtilis 1423 -11530608 6000689471 yjqb (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (nt:s... AF034138 AF034138 g2645868 Bacillus subtilis 1423 -11530608 7500955719 yjqb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to phage-related replication protein) (le:124091) (re:124693) (di:direct) BSUB0007 Z99110 g2633602 Bacillus subtilis 1423 -11530608

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787972	3835	25991	276	91

Description

6500726751 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yjqC yjqC Bacillus subtilis 1423 -11530609 7000692574 yjqc conserved hypothetical protein yjqc (db:pir2.dat) C69854 C69854 Bacillus subtilis 1423 -11530609 6000689473 yjqc (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (nt:s... AF034138 AF034138 g2645869 Bacillus subtilis 1423 -11530609 7500963695 yjqc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:124770) (re:125606) (di:direct) BSUB0007 Z99110 g2633603 Bacillus subtilis 1423 -11530609

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787975	3836	25992	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787981	3837	25993	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787993	3838	25994	693	230

Description

6500726752 ykxa:xkda hypothetical protein:pbsx prophage (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdA xkdA Bacillus subtilis 1423 -11530610 7000694350 xkda pbsx prophage orf xkda (db:pir2.dat) A69731 A69731 Bacillus subtilis 1423 -11530610 6000689475 xkda (db:genpept-bct1) (de:bacillus subtilis yjob gene, partial cds; aspartate phosphatase ofthe phosphorelay (rapa), pre-inhibitor protein of rapa (phra),yjpa, n-acetylmuramoyl-l-alanine amidase (xlyb), yjqa, yjqb, yjqc,and xkda genes, complete cds.) (nt:h... AF034138 AF034138 g2645870 Bacillus subtilis 1423 -11530610 7500965040 xkda (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykxa; pbsx prophage) (le:125650) (re:126102) (di:complement) BSUB0007 Z99110 g2633604 Bacillus subtilis 1423 -11530610

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501787999	3839	25995	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788002	3840	25996	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788008	3841	25997	1983	660

Description

6500726753 ykxb:xkdb hypothetical protein:phage-like element pbsx protein xkdb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdB xkdB Bacillus subtilis 1423 -11530611 108110 xkdb (de:phage-like element pbsx protein xkdb) (db:swissprot) XKDB_BACSU P39781 BACILLUS SUBTILIS 1423 -11530611 219479 xkdb (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqal of the skin element) (le:1145) (re:1978) (di:direct) BSPBSXSE Z70177 g1225937 Bacillus subtilis 1423 -11530611 7500894445 xkdb (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykxb; pbsx prophage) (le:127094) (re:127927) (di:direct) BSUB0007 Z99110 g2633606 Bacillus subtilis 1423 -11530611 7000687025 xkdb pbsx prophage orf xkdb (db:pir) B69731 B69731 Bacillus subtilis 1423 -11530611 5000689113 (de:(xkdb) (pn:phage-like element pbsx protein xkdb) (gtcfc:13.07) (ec:) (xkdb_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) xkdB xkdB Bacillus subtilis 1423 10049842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788019	3842	25998	369	123

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788031	3843	25999	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788035	3844	26000	1530	510

Description

6500726754 ykxc:xkdc hypothetical protein:phage-like element pbsx protein xkdc (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdC xkdC Bacillus subtilis 1423 -11530612 108111 xkdc (de:phage-like element pbsx protein xkdc) (db:swissprot) XKDC_BACSU P39782 BACILLUS SUBTILIS 1423 -11530612 219480 xkdc (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqam of the skin element) (le:1878) (re:2678) (di:direct) BSPBSXSE Z70177 g1225938 Bacillus subtilis 1423 -11530612 7500894446 xkdc (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykxc; pbsx prophage) (le:127827) (re:128627) (di:direct) BSUB0007 Z99110 g2633607 Bacillus subtilis 1423 -11530612 7000687026 xkdc pbsx prophage orf xkdc (db:pir) C69731 C69731 Bacillus subtilis 1423 -11530612 5000689114 (de:(xkdc) (pn:phage-like element pbsx protein xkdc) (gtcfc:13.07) (ec:) (xkdc_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) xkdC xkdC Bacillus subtilis 1423 10049843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788050	3845	26001	474	157

Description

6500726755 ykxd:xkdd hypothetical protein:phage-like element pbsx protein xkdd (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdD xkdD Bacillus subtilis 1423 -11530613 108112 xkdd (de:phage-like element pbsx protein xkdd) (db:swissprot) XKDD_BACSU P39783 BACILLUS SUBTILIS 1423 -11530613 7000687027 xkdd pbsx prophage orf xkdd (db:pir2.dat) D69731 D69731 Bacillus subtilis 1423 -11530613 219481 xkdd (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (le:2930) (re:3280) (di:direct) BSPBSXSE Z70177 g1225939 Bacillus subtilis 1423 -11530613 7500894447 xkdd (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykxd; pbsx prophage) (le:128879) (re:129229) (di:direct) BSUB0007 Z99110 g2633608 Bacillus subtilis 1423 -11530613 5000689115 (de:(xkdd) (pn:phage-like element pbsx protein xkdd) (gtcfc:13.07) (ec:) (xkdd_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) xkdD xkdD Bacillus subtilis 1423 10049844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788052	3846	26002	447	148

Description

5000689116 hypothetical protein:phage-like element pbsx protein xkde (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdE xkdE Bacillus subtilis 1423 -11530614 108113 xkde (de:phage-like element pbsx protein xkde) (db:swissprot) XKDE_BACSU P54325 BACILLUS SUBTILIS 1423 -11530614 7000687028 xkde pbsx prophage orf xkde (db:pir2.dat) E69731 E69731 Bacillus subtilis 1423 -11530614 219486 xkde (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqba of the skin element) (le:6323) (re:7810) (di:direct) BSPBSXSE Z70177 g1225944 Bacillus subtilis 1423 -11530614 7500894448 xkde (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:132272) (re:133759) (di:direct) BSUB0007 Z99110 g2633613 Bacillus subtilis 1423 -11530614 6500726756 hypothetical protein:phage-like element pbsx protein xkde (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdE xkdE Bacillus subtilis 1423 -11530614

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788053	3847	26003	288	96

Description

5000689117 hypothetical protein:phage-like element pbsx protein xkdf (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdF xkdF Bacillus subtilis 1423 -11530615 108114 xkdf (de:phage-like element pbsx protein xkdf) (db:swissprot) XKDF_BACSU P54326 BACILLUS SUBTILIS 1423 -11530615 7000687029 xkdf pbsx prophage orf xkdf (db:pir2.dat) F69731 F69731 Bacillus subtilis 1423 -11530615 219487 xkdf (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbd of the skin element) (le:7830) (re:8657) (di:direct) BSPBSXSE Z70177 g1225945 Bacillus subtilis 1423 -11530615 7500894449 xkdf (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:133779) (re:134606) (di:direct) BSUB0007 Z99110 g2633614 Bacillus subtilis 1423 -11530615 6500726757 hypothetical protein:phage-like element pbsx protein xkdf (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdF xkdF Bacillus subtilis 1423 -11530615

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788057	3848	26004	663	220

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788058	3849	26005	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788061	3850	26006	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788069	3851	26007	447	148

Description

5000689118 hypothetical protein:phage-like element pbsx protein xkdg (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdG xkdG Bacillus subtilis 1423 -11530616 108115 xkdg (de:phage-like element pbsx protein xkdg) (db:swissprot) XKDG_BACSU P54327 BACILLUS SUBTILIS 1423 -11530616 7000687030 xkdg pbsx prophage orf xkdg (db:pir2.dat) G69731 G69731 Bacillus subtilis 1423 -11530616 219488 xkdg (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbe of the skin element) (le:8683) (re:9618) (di:direct) BSPBSXSE Z70177 g1225946 Bacillus subtilis 1423 -11530616 7500894450 xkdg (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:134632) (re:135567) (di:direct) BSUB0007 Z99110 g2633615 Bacillus subtilis 1423 -11530616 6500726758 hypothetical protein:phage-like element pbsx protein xkdg (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdG xkdG Bacillus subtilis 1423 -11530616

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788075	3852	26008	276	91

Description

5000689119 hypothetical protein:phage-like element pbsx protein xkdh (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdH xkdH Bacillus subtilis 1423 -11530617 108116 xkdh (de:phage-like element pbsx protein xkdh) (db:swissprot) XKDH_BACSU P54328 BACILLUS SUBTILIS 1423 -11530617 7000687031 xkdh pbsx prophage orf xkdh (db:pir2.dat) H69731 H69731 Bacillus subtilis 1423 -11530617 219489 xkdh (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbh of the skin element) (le:10022) (re:10378) (di:direct) BSPBSXSE Z70177 g1225947 Bacillus subtilis 1423 -11530617 7500894451 xkdh (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:135971) (re:136327) (di:direct) BSUB0007 Z99110 g2633616 Bacillus subtilis 1423 -11530617 6500726759 hypothetical protein:phage-like element pbsx protein xkdh (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdH xkdH Bacillus subtilis 1423 -11530617

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788082	3853	26009	915	304

Description

5000689120 hypothetical protein:phage-like element pbsx protein xkdi (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdI xkdI Bacillus subtilis 1423 -11530618 108117 xkdi (de:phage-like element pbsx protein xkdi) (db:swissprot) XKDI_BACSU P54329 BACILLUS SUBTILIS 1423 -11530618 7000687032 xkdi pbsx prophage orf xkdi (db:pir2.dat) A69732 A69732 Bacillus subtilis 1423 -11530618 219490 xkdi (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbi of the skin element) (le:10375) (re:10860) (di:direct) BSPBSXSE Z70177 g1225948 Bacillus subtilis 1423 -11530618 7500894452 xkdi (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:136324) (re:136809) (di:direct) BSUB0007 Z99110 g2633617 Bacillus subtilis 1423 -11530618 6500726760 hypothetical protein:phage-like element pbsx protein xkdi (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdI xkdI Bacillus subtilis 1423 -11530618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788083	3854	26010	690	229

Description

5000689121 hypothetical protein:phage-like element pbsx protein xkdj (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdJ xkdJ Bacillus subtilis 1423 -11530619 108118 xkdj (de:phage-like element pbsx protein xkdj) (db:swissprot) XKDJ_BACSU P54330 BACILLUS SUBTILIS 1423 -11530619 7000687033 xkdj pbsx prophage orf xkdj (db:pir2.dat) B69732 B69732 Bacillus subtilis 1423 -11530619 219491 xkdj (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbj of the skin element) (le:10873) (re:11313) (di:direct) BSPBSXSE Z70177 g1225949 Bacillus subtilis 1423 -11530619 7500894453 xkdj (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:136822) (re:137262) (di:direct) BSUB0007 Z99110 g2633618 Bacillus subtilis 1423 -11530619 6500726761 hypothetical protein:phage-like element pbsx protein xkdj (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdJ xkdJ Bacillus subtilis 1423 -11530619

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788085	3855	26011	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788093	3856	26012	1194	397

Description

5000689122 hypothetical protein:phage-like element pbsx protein xkdk (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdK xkdK Bacillus subtilis 1423 -11530620 108119 xkdk (de:phage-like element pbsx protein xkdk) (db:swissprot) XKDK_BACSU P54331 BACILLUS SUBTILIS 1423 -11530620 7000687034 xkdk pbsx prophage orf xkdk (db:pir2.dat) C69732 C69732 Bacillus subtilis 1423 -11530620 219492 xkdk (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (le:11532) (re:12926) (di:direct) BSPBSXSE Z70177 g1225950 Bacillus subtilis 1423 -11530620 7500894454 xkdk (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:137481) (re:138875) (di:direct) BSUB0007 Z99110 g2633619 Bacillus subtilis 1423 -11530620 6500726762 hypothetical protein:phage-like element pbsx protein xkdk (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdK xkdK Bacillus subtilis 1423 -11530620

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788094	3857	26013	282	93

Description

5000689123 hypothetical protein:phage-like element pbsx protein xkdm (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdM xkdM Bacillus subtilis 1423 -11530621 108120 xkdm (de:phage-like element pbsx protein xkdm) (db:swissprot) XKDM_BACSU P54332 BACILLUS SUBTILIS 1423 -11530621 7000687035 xkdm pbsx prophage orf xkdm (db:pir2.dat) D69732 D69732 Bacillus subtilis 1423 -11530621 219493 xkdm (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbm of the skin element) (le:12933) (re:13376) (di:direct) BSPBSXSE Z70177 g1225951 Bacillus subtilis 1423 -11530621 7500894455 xkdm (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:138882) (re:139325) (di:direct) BSUB0007 Z99110 g2633620 Bacillus subtilis 1423 -11530621 6500726763 hypothetical protein:phage-like element pbsx protein xkdm (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdM xkdM Bacillus subtilis 1423 -11530621

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788097	3858	26014	1266	422

Description

5000689124 hypothetical protein:phage-like element pbsx protein xkdn (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdN xkdN Bacillus subtilis 1423 -11530622 108121 xkdn (de:phage-like element pbsx protein xkdn) (db:swissprot) XKDN_BACSU P54333 BACILLUS SUBTILIS 1423 -11530622 7000687036 xkdn pbsx prophage orf xkdn (db:pir2.dat) E69732 E69732 Bacillus subtilis 1423 -11530622 219494 xkdn (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbn of the skin element) (le:13468) (re:14094) (di:direct) BSPBSXSE Z70177 g1225952 Bacillus subtilis 1423 -11530622 7500894456 xkdn (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:139417) (re:140043) (di:direct) BSUB0007 Z99110 g2633621 Bacillus subtilis 1423 -11530622 6500726764 hypothetical protein:phage-like element pbsx protein xkdn (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdN xkdN Bacillus subtilis 1423 -11530622

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788101	3859	26015	828	275

Description

5000689125 hypothetical protein:phage-like element pbsx protein xkdo (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdO xkdO Bacillus subtilis 1423 -11530623 108122 xkdo (de:phage-like element pbsx protein xkdo) (db:swissprot) XKDO_BACSU P54334 BACILLUS SUBTILIS 1423 -11530623 7000687037 xkdo pbsx prophage orf xkdo (db:pir2.dat) F69732 F69732 Bacillus subtilis 1423 -11530623 219495 xkdo (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbo of the skin element) (le:14099) (re:18097) (di:direct) BSPBSXSE Z70177 g1225953 Bacillus subtilis 1423 -11530623 7500894457 xkdo (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:140048) (re:144046) (di:direct) BSUB0007 Z99110 g2633622 Bacillus subtilis 1423 -11530623 6500726765 hypothetical protein:phage-like element pbsx protein xkdo (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdO xkdO Bacillus subtilis 1423 -11530623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788106	3860	26016	870	289

Description

5000689126 hypothetical protein:phage-like element pbsx protein xkdp (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdP xkdP Bacillus subtilis 1423 -11530624 108123 xkdp (de:phage-like element pbsx protein xkdp) (db:swissprot) XKDP_BACSU P54335 BACILLUS SUBTILIS 1423 -11530624 7000687038 xkdp pbsx prophage orf xkdp (db:pir2.dat) G69732 G69732 Bacillus subtilis 1423 -11530624 219496 xkdp (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbp of the skin element) (le:18042) (re:18749) (di:direct) BSPBSXSE Z70177 g1225954 Bacillus subtilis 1423 -11530624 7500894458 xkdp (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:143991) (re:144698) (di:direct) BSUB0007 Z99110 g2633623 Bacillus subtilis 1423 -11530624 6500726766 hypothetical protein:phage-like element pbsx protein xkdp (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdP xkdP Bacillus subtilis 1423 -11530624

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788113	3861	26017	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788119	3862	26018	576	191

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788131	3863	26019	369	122

Description

5000689127 hypothetical protein:phage-like element pbsx protein xkdq (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdQ xkdQ Bacillus subtilis 1423 -11530625 108124 xkdq (de:phage-like element pbsx protein xkdq) (db:swissprot) XKDQ_BACSU P54336 BACILLUS SUBTILIS 1423 -11530625 7000687039 xkdq pbsx prophage orf xkdq (db:pir2.dat) H69732 H69732 Bacillus subtilis 1423 -11530625 219497 xkdq (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbq of the skin element) (le:18765) (re:19742) (di:direct) BSPBSXSE Z70177 g1225966 Bacillus subtilis 1423 -11530625 7500894459 xkdq (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:144714) (re:145691) (di:direct) BSUB0007 Z99110 g2633624 Bacillus subtilis 1423 -11530625 6500726767 hypothetical protein:phage-like element pbsx protein xkdq (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdQ xkdQ Bacillus subtilis 1423 -11530625

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788133	3864	26020	345	114

Description

5000689128 hypothetical protein:phage-like element pbsx protein xkdr (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdR xkdR Bacillus subtilis 1423 -11530626 108125 xkdr (de:phage-like element pbsx protein xkdr) (db:swissprot) XKDR_BACSU P54337 BACILLUS SUBTILIS 1423 -11530626 7000687040 xkdr pbsx prophage orf xkdr (db:pir2.dat) A69733 A69733 Bacillus subtilis 1423 -11530626 219498 xkdr (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbr of the skin element) (le:19742) (re:20008) (di:direct) BSPBSXSE Z70177 g1225955 Bacillus subtilis 1423 -11530626 7500894460 xkdr (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:145691) (re:145957) (di:direct) BSUB0007 Z99110 g2633625 Bacillus subtilis 1423 -11530626 6500726768 hypothetical protein:phage-like element pbsx protein xkdr (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdR xkdR Bacillus subtilis 1423 -11530626

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788136	3865	26021	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788137	3866	26022	336	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788139	3867	26023	891	296

Description

5000689129 hypothetical protein:phage-like element pbsx protein xkds (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdS xkdS Bacillus subtilis 1423 -11530627 108126 xkds (de:phage-like element pbsx protein xkds) (db:swissprot) XKDS_BACSU P54338 BACILLUS SUBTILIS 1423 -11530627 7000687041 xkds pbsx prophage orf xkds (db:pir2.dat) B69733 B69733 Bacillus subtilis 1423 -11530627 219499 xkds (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbs of the skin element) (le:20065) (re:20490) (di:direct) BSPBSXSE Z70177 g1225956 Bacillus subtilis 1423 -11530627 7500894461 xkds (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:146014) (re:146439) (di:direct) BSUB0007 Z99110 g2633626 Bacillus subtilis 1423 -11530627 6500726769 hypothetical protein:phage-like element pbsx protein xkds (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdS xkdS Bacillus subtilis 1423 -11530627

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788145	3868	26024	933	310

Description

5000689130 hypothetical protein:phage-like element pbsx protein xkdt (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdT xkdT Bacillus subtilis 1423 -11530628 108127 xkdt (de:phage-like element pbsx protein xkdt) (db:swissprot) XKDT_BACSU P54339 BACILLUS SUBTILIS 1423 -11530628 7000687042 xkdt pbsx prophage orf xkdt (db:pir2.dat) C69733 C69733 Bacillus subtilis 1423 -11530628 219500 xkdt (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqbt of the skin element) (le:20483) (re:21529) (di:direct) BSPBSXSE Z70177 g1225957 Bacillus subtilis 1423 -11530628 7500894462 xkdt (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:146432) (re:147478) (di:direct) BSUB0007 Z99110 g2633627 Bacillus subtilis 1423 -11530628 6500726770 hypothetical protein:phage-like element pbsx protein xkdt (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdT xkdT Bacillus subtilis 1423 -11530628

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788147	3869	26025	876	291

Description

5000689131 hypothetical protein:phage-like element pbsx protein xkdt (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdU xkdU Bacillus subtilis 1423 -11530629 108128 xkdu (de:phage-like element pbsx protein xkdt) (db:swissprot) XKDU_BACSU P54340 BACILLUS SUBTILIS 1423 -11530629 7000687043 xkdu pbsx prophage orf xkdu (db:pir2.dat) D69733 D69733 Bacillus subtilis 1423 -11530629 219501 xkdu (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqca of the skin element) (le:21513) (re:22091) (di:direct) BSPBSXSE Z70177 g1225958 Bacillus subtilis 1423 -11530629 7500894463 xkdu (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:147462) (re:148040) (di:direct) BSUB0007 Z99110 g2633628 Bacillus subtilis 1423 -11530629 6500726771 hypothetical protein:phage-like element pbsx protein xkdt (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdU xkdU Bacillus subtilis 1423 -11530629

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788150	3870	26026	741	246

Description

5000689132 hypothetical protein:phage-like element pbsx protein xkdv (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdV xkdV Bacillus subtilis 1423 -11530630 108129 xkdv (de:phage-like element pbsx protein xkdv) (db:swissprot) XKDV_BACSU P54341 BACILLUS SUBTILIS 1423 -11530630 7000687044 xkdv pbsx prophage orf xkdv (db:pir2.dat) E69733 E69733 Bacillus subtilis 1423 -11530630 219502 xkdv (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqcc of the skin element) (le:22362) (re:24425) (di:direct) BSPBSXSE Z70177 g1225959 Bacillus subtilis 1423 -11530630 7500894464 xkdv (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:148311) (re:150374) (di:direct) BSUB0007 Z99110 g2633629 Bacillus subtilis 1423 -11530630 6500726772 hypothetical protein:phage-like element pbsx protein xkdv (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdV xkdV Bacillus subtilis 1423 -11530630

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788167	3871	26027	996	331

Description

5000689133 hypothetical protein:phage-like element pbsx protein xkdw (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdW xkdW Bacillus subtilis 1423 -11530631 108130 xkdw (de:phage-like element pbsx protein xkdw) (db:swissprot) XKDW_BACSU P54342 BACILLUS SUBTILIS 1423 -11530631 7000687045 xkdw pbsx prophage orf xkdw (db:pir2.dat) F69733 F69733 Bacillus subtilis 1423 -11530631 219503 xkdw (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqcd of the skin element) (le:24437) (re:24766) (di:direct) BSPBSXSE Z70177 g1225960 Bacillus subtilis 1423 -11530631 7500894465 xkdw (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:150386) (re:150715) (di:direct) BSUB0007 Z99110 g2633630 Bacillus subtilis 1423 -11530631 6500726773 hypothetical protein:phage-like element pbsx protein xkdw (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdW xkdW Bacillus subtilis 1423 -11530631

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788168	3872	26028	693	230

Description

5000689134 hypothetical protein:phage-like element pbsx protein xkdx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdX xkdX Bacillus subtilis 1423 -11530632 108131 xkdx (de:phage-like element pbsx protein xkdx) (db:swissprot) XKDX_BACSU P54343 BACILLUS SUBTILIS 1423 -11530632 7000687046 xkdx pbsx prophage orf xkdx (db:pir2.dat) G69733 G69733 Bacillus subtilis 1423 -11530632 219504 xkdx (db:genpept-bct1) (de:b.subtilis dna (28 kb pbsx/skin element region).) (nt:homologous to yqce of the skin element) (le:24763) (re:24927) (di:direct) BSPBSXSE Z70177 g1225961 Bacillus subtilis 1423 -11530632 7500894466 xkdx (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:pbsx prophage) (le:150712) (re:150876) (di:direct) BSUB0007 Z99110 g2633631 Bacillus subtilis 1423 -11530632 6500726774 hypothetical protein:phage-like element pbsx protein xkdx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) xkdX xkdX Bacillus subtilis 1423 -11530632

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788171	3873	26029	810	269

Description

6500726775 hypothetical protein:similar to low-affinity inorganic phosphate transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykaB ykaB Bacillus subtilis 1423 -11530633 7000694174 ykab low-affinity inorganic phosphate transport homolog ykab (db:pir2.dat) A69855 A69855 Bacillus subtilis 1423 -11530633 6000689722 ykab ykab (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to low affinity phosphate transporter) (le:1614) (re:2600) (di:complement) BSAJ2571 AJ002571 g2632005 Bacillus subtilis 1423 -11530633 7500964904 ykab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to low-affinity inorganic phosphate) (le:154563) (re:155549) (di:complement) BSUB0007 Z99110 g2633638 Bacillus subtilis 1423 -11530633

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788180	3874	26030	687	228

Description

6500726776 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykaA ykaA Bacillus subtilis 1423 -11530634 7000693418 ykaa hypothetical protein ykaa (db:pir2.dat) H69854 H69854 Bacillus subtilis 1423 -11530634 6000689724 ykaa ykaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:2613) (re:3230) (di:complement) BSAJ2571 AJ002571 g2632006 Bacillus subtilis 1423 -11530634 7500964371 ykaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:155562) (re:156179) (di:complement) BSUB0007 Z99110 g2633639 Bacillus subtilis 1423 -11530634

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788197	3875	26031	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788208	3876	26032	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788212	3877	26033	1029	342

Description

6500726777 hypothetical protein:similar to amino acid permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykbA ykbA Bacillus subtilis 1423 -11530635 7000692197 ykba amino acid permease homolog ykba (cl:arginine permease) (db:pir2.dat) B69855 B69855 Bacillus subtilis 1423 -11530635 6000689726 ykba ykba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:3506) (re:4822) (di:complement) BSAJ2571 AJ002571 g2632007 Bacillus subtilis 1423 -11530635 7500963404 ykba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to amino acid permease) (le:156455) (re:157771) (di:complement) BSUB0007 Z99110 g2633640 Bacillus subtilis 1423 -11530635

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788213	3878	26034	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788222	3879	26035	588	195

Description

6500726778 hypothetical protein:similar to abc transporter:binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykcA ykcA Bacillus subtilis 1423 -11530636 7000692113 ykca abc transporter binding protein homolog ykca (cl:probable abc transporter protein ydfo) (db:pir2.dat) C69855 C69855 Bacillus subtilis 1423 -11530636 6000689728 ykca ykca (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:putative dioxygenase) (le:5211) (re:6161) (di:direct) BSAJ2571 AJ002571 g2632008 Bacillus subtilis 1423 -11530636 7500963353 ykca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to abc transporter (binding protein)) (le:158160) (re:159110) (di:direct) BSUB0007 Z99110 g2633641 Bacillus subtilis 1423 -11530636

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788225	3880	26036	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788253	3881	26037	1806	601

Description

GTC ORF with score 218 to: (or:Homo sapiens) (de:or:homo sapiens pn:protein related n-ternimus of tre oncogene gn:rn-tre le:280 re:2762 di:direct sr:homo sapiens male myeloblast cell_line kg-1 cdna to mrna nt:kiaa0019; author-given protein sequence is in)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788263	3882	26038	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788268	3883	26039	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788302	3884	26040	525	174

Description

6500726779 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykcB ykcB Bacillus subtilis 1423 -11530637 7000692575 ykcb conserved hypothetical protein ykcb (db:pir2.dat) D69855 D69855 Bacillus subtilis 1423 -11530637 6000689730 ykcb ykcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:6412) (re:8562) (di:direct) BSAJ2571 AJ002571 g2632009 Bacillus subtilis 1423 -11530637 7500963696 ykcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:159361) (re:161511) (di:direct) BSUB0007 Z99110 g2633642 Bacillus subtilis 1423 -11530637

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788304	3885	26041	483	160

Description

GTC ORF with score 141 to: (fn:helicase, helicase-primase complex) (db:genpept-vrl) (de:human herpesvirus 6 serotype b putative major immediate-earlygenes.) (nt:similar to hhv6a u86, region ie-b) (le:16386) (re:19235) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788305	3886	26042	426	141

Description

6500726780 yzca:ykea hypothetical protein:similar to pyrroline-5-carboxylate reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykeA ykeA Bacillus subtilis 1423 -11530638 7000694480 ykea pyrroline-5-carboxylate reductase homolog ykea:hypothetical protein x dciaa 5 region (cl:pyrroline-5-carboxylate reductase) (db:pir2.dat) F69855 F69855 Bacillus subtilis 1423 -11530638 6000689736 ykea ykea (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:putative pyrroline-5-carboxylate reductase) (le:11581) (re:12399) (di:direct) BSAJ2571 AJ002571 g2632012 Bacillus subtilis 1423 -11530638 7500953853 ykea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: yzca; similar to) (le:164530) (re:165348) (di:direct) BSUB0007 Z99110 g2633645 Bacillus subtilis 1423 -11530638

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788307	3887	26043	969	323

Description

GTC ORF with score 345 to: (sr:human) (db:genpept) (de:homo sapiens s164 gene, partial cds; ps1 and hypothetical proteingenes, complete cds; and s171 gene, partial cds.) (nt:unknown; intron-exon boundaries defined by ests) (le:<1465:5979:14890:17363) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788727	3888	26044	1644	547

Description

6500726781 hypothetical protein:similar to immunity to bacteriotoxins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykfA ykfA Bacillus subtilis 1423 -11530639 7000694102 ykfa immunity to bacteriotoxins homolog ykfa (db:pir2.dat) G69855 G69855 Bacillus subtilis 1423 -11530639 6000689742 ykfa ykfa (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to mccf, an e. coli microcin immunity) (le:18268) (re:18972) (di:direct) BSAJ2571 AJ002571 g2632018 Bacillus subtilis 1423 -11530639 7500964863 ykfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to immunity to bacteriotoxins) (le:171217) (re:171921) (di:direct) BSUB0007 Z99110 g2633651 Bacillus subtilis 1423 -11530639

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788759	3889	26045	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788776	3890	26046	1029	342

Description

6500726782 hypothetical protein:similar to chloromuconate cycloisomerase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykfB ykfB Bacillus subtilis 1423 -11530640 7000692366 ykfb chloromuconate cycloisomerase homolog ykfb (cl:muconate cycloisomerase) (db:pir2.dat) H69855 H69855 Bacillus subtilis 1423 -11530640 6000689744 ykfb ykfb (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:putative muconate cycloisomerase) (le:18969) (re:20069) (di:direct) BSAJ2571 AJ002571 g2632019 Bacillus subtilis 1423 -11530640 7500954466 ykfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to chloromuconate cycloisomerase) (le:171918) (re:173018) (di:direct) BSUB0007 Z99110 g2633652 Bacillus subtilis 1423 -11530640

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788795	3891	26047	405	135

Description

6500726783 hypothetical protein:similar to polysugar degrading enzyme (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykfC ykfC Bacillus subtilis 1423 -11530641 7000694437 ykfc polysugar degrading enzyme homolog ykfc (db:pir2.dat) A69856 A69856 Bacillus subtilis 1423 -11530641 6000689746 ykfc ykfc (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to an invasion associated protein from) (le:20066) (re:20956) (di:direct) BSAJ2571 AJ002571 g2632020 Bacillus subtilis 1423 -11530641 7500965092 ykfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to polysugar degrading enzyme) (le:173015) (re:173905) (di:direct) BSUB0007 Z99110 g2633653 Bacillus subtilis 1423 -11530641

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788797	3892	26048	459	152

Description

6500726784 hypothetical protein:similar to oligopeptide abc transporter:permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykfD ykfD Bacillus subtilis 1423 -11530642 7000694340 ykfd oligopeptide transport atp-binding protein homolog ykfd (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B69856 B69856 Bacillus subtilis 1423 -11530642 6000689748 ykfd ykfd (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to atp-binding proteins of abc-type) (le:20969) (re:21952) (di:direct) BSAJ2571 AJ002571 g2632021 Bacillus subtilis 1423 -11530642 7500955196 ykfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to oligopeptide abc transporter (permease)) (le:173918) (re:174901) (di:direct) BSUB0007 Z99110 g2633654 Bacillus subtilis 1423 -11530642

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788802	3893	26049	447	148

Description

6500726785 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykgB ykgB Bacillus subtilis 1423 -11530643 7000692577 ykgb conserved hypothetical protein ykgb (db:pir2.dat) D69856 D69856 Bacillus subtilis 1423 -11530643 6000689750 ykgb ykgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:22000) (re:23049) (di:complement) BSAJ2571 AJ002571 g2632022 Bacillus subtilis 1423 -11530643 7500963698 ykgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:174949) (re:175998) (di:complement) BSUB0007 Z99110 g2633655 Bacillus subtilis 1423 -11530643

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788803	3894	26050	747	248

Description

6500726786 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykgA ykgA Bacillus subtilis 1423 -11530644 7000692576 ykga conserved hypothetical protein ykga (db:pir2.dat) C69856 C69856 Bacillus subtilis 1423 -11530644 6000689752 ykga ykga (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to streptococcal acid glycoprotein) (le:23209) (re:24000) (di:complement) BSAJ2571 AJ002571 g2632023 Bacillus subtilis 1423 -11530644 7500963697 ykga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:176158) (re:176949) (di:complement) BSUB0007 Z99110 g2633656 Bacillus subtilis 1423 -11530644

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788806	3895	26051	699	232

Description

6500726787 hypothetical protein:similar to acyl-coa hydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykhA ykhA Bacillus subtilis 1423 -11530645 7000692151 ykha acyl-coa hydrolase homolog ykha (db:pir2.dat) E69856 E69856 Bacillus subtilis 1423 -11530645 6000689754 ykha ykha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:24267) (re:24677) (di:direct) BSAJ2571 AJ002571 g2632024 Bacillus subtilis 1423 -11530645 7500963378 ykha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to acyl-coa hydrolase) (le:177216) (re:177626) (di:direct) BSUB0007 Z99110 g2633657 Bacillus subtilis 1423 -11530645

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788810	3896	26052	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788812	3897	26053	297	98

Description

6500726788 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzH ykzH Bacillus subtilis 1423 -11530646 7000693452 ykzh hypothetical protein ykzh (db:pir2.dat) E69871 E69871 Bacillus subtilis 1423 -11530646 7500964407 ykzh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:179141) (re:179365) (di:complement) BSUB0007 Z99110 g2633659 Bacillus subtilis 1423 -11530646

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788813	3898	26054	768	255

Description

6500726789 hypothetical protein:hypothetical 27.3 kd protein in hmp 3region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykjA ykjA Bacillus subtilis 1423 -11530647 7000692578 ykja probable membrane protein ykja (cl:probable membrane protein ycap) (db:pir2.dat) F69856 F69856 Bacillus subtilis 1423 -11530647 6000689756 ykja ykja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:26561) (re:27292) (di:direct) BSAJ2571 AJ002571 g2632026 Bacillus subtilis 1423 -11530647 7500955870 ykja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:179510) (re:180241) (di:direct) BSUB0007 Z99110 g2633660 Bacillus subtilis 1423 -11530647

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788817	3899	26055	420	139

Description

5000689190 hypothetical protein:hypothetical 20.5 kd protein in hmp 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkA ykkA Bacillus subtilis 1423 -11530648 114165 ykka (de:hypothetical 20.5 kd protein in hmp 3'region) (db:swissprot) YKKA_BACSU P49854 BACILLUS SUBTILIS 1423 -11530648 7000688107 ykka hypothetical protein ykka (db:pir2.dat) G69856 G69856 Bacillus subtilis 1423 -11530648 214922 (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis hmp dna for 7 orfs, complete cds.) (nt:unnamed protein product) (le:3467) (re:3994) (di:direct) BAC168TRP2 D78189 g1063249 Bacillus subtilis 1423 -11530648 301705 ykka ykka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:27384) (re:27911) (di:direct) BSAJ2571 AJ002571 g2632027 Bacillus subtilis 1423 -11530648 6000685476 ykka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:180333) (re:180860) (di:direct) BSUB0007 Z99110 g2633661 Bacillus subtilis 1423 -11530648 6500726790 hypothetical protein:hypothetical 20.5 kd protein in hmp 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkA ykkA Bacillus subtilis 1423 -11530648

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788826	3900	26056	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788827	3901	26057	444	147

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788830	3902	26058	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788838	3903	26059	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788844	3904	26060	687	228

Description

5000689191 hypothetical protein:hypothetical 20.1 kd protein in hmp 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkB ykkB Bacillus subtilis 1423 -11530649 114166 ykkb (de:hypothetical 20.1 kd protein in hmp 3'region) (db:swissprot) YKKB_BACSU P49855 BACILLUS SUBTILIS 1423 -11530649 7000688108 ykkb n-acetyltransferase homolog ykkb (cl:hypothetical protein yoaa) (db:pir2.dat) H69856 H69856 Bacillus subtilis 1423 -11530649 214923 (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis hmp dna for 7 orfs, complete cds.) (nt:low homology to p20 protein of bacillus) (le:3984) (re:4502) (di:direct) BAC168TRP2 D78189 g1063250 Bacillus subtilis 1423 -11530649 301706 ykkb ykkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:27901) (re:28419) (di:direct) BSAJ2571 AJ002571 g2632028 Bacillus subtilis 1423 -11530649 6000685478 ykkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to n-acetyltransferase) (le:180850) (re:181368) (di:direct) BSUB0007 Z99110 g2633662 Bacillus subtilis 1423 -11530649 6500726791 hypothetical protein:hypothetical 20.1 kd protein in hmp 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkB ykkB Bacillus subtilis 1423 -11530649

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788850	3905	26061	462	153

Description

5000689192 hypothetical protein:hypothetical 11.9 kd protein in hmp 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkC ykkC Bacillus subtilis 1423 -11530650 114167 ykkc (de:hypothetical 11.9 kd protein in hmp 3'region) (db:swissprot) YKKC_BACSU P49856 BACILLUS SUBTILIS 1423 -11530650 7000688109 ykkc chaperonin homolog ykkc (cl:suge protein) (db:pir2.dat) A69857 A69857 Bacillus subtilis 1423 -11530650 214924 (sr:bacillus subtilis (strain:168trpc2) dna) (db:genpept-bct1) (de:bacillus subtilis hmp dna for 7 orfs, complete cds.) (nt:unnamed protein product) (le:4724) (re:5062) (di:direct) BAC168TRP2 D78189 g1063251 Bacillus subtilis 1423 -11530650 301707 ykkc ykkc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:28642) (re:28980) (di:direct) BSAJ2571 AJ002571 g2632029 Bacillus subtilis 1423 -11530650 6000685480 ykkc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to chaperonin) (le:181591) (re:181929) (di:direct) BSUB0007 Z99110 g2633663 Bacillus subtilis 1423 -11530650 6500726792 hypothetical protein:hypothetical 11.9 kd protein in hmp 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkC ykkC Bacillus subtilis 1423 -11530650

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788863	3906	26062	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788864	3907	26063	474	157

Description

6500726793 hypothetical protein:hypothetical 12.5 kd protein in hmp 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkD ykkD Bacillus subtilis 1423 -11530651 7000692356 ykkd chaperonin homolog ykkd (cl:suge protein) (db:pir2.dat) B69857 B69857 Bacillus subtilis 1423 -11530651 6000689758 ykkd ykkd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:28980) (re:29297) (di:direct) BSAJ2571 AJ002571 g2632030 Bacillus subtilis 1423 -11530651 7500963520 ykkd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to chaperonin) (le:181929) (re:182246) (di:direct) BSUB0007 Z99110 g2633664 Bacillus subtilis 1423 -11530651

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788870	3908	26064	1521	506

Description

6500726794 hypothetical protein:similar to formyltetrahydrofolate deformylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykkE ykkE Bacillus subtilis 1423 -11530652 7000693005 ykke formyltetrahydrofolate deformylase homolog ykke (cl:phosphoribosylglycinamide formyltransferase:phosphoribosylglycinamide formyltransferase homology) (db:pir2.dat) C69857 C69857 Bacillus subtilis 1423 -11530652 6000689760 ykke ykke (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to formyltetrahydrofolate deformylase) (le:29368) (re:30270) (di:direct) BSAJ2571 AJ002571 g2632031 Bacillus subtilis 1423 -11530652 7500963994 ykke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to formyltetrahydrofolate deformylase) (le:182317) (re:183219) (di:direct) BSUB0007 Z99110 g2633665 Bacillus subtilis 1423 -11530652

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788899	3909	26065	414	137

Description

6500726795 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yklA yklA Bacillus subtilis 1423 -11530653 7000692579 ykla conserved hypothetical protein ykla (cl:hypothetical protein ykla) (db:pir2.dat) D69857 D69857 Bacillus subtilis 1423 -11530653 6000689766 ykla ykla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to osmc from escherichia coli) (le:33103) (re:33528) (di:direct) BSAJ2571 AJ002571 g2632034 Bacillus subtilis 1423 -11530653 7500955921 ykla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:186052) (re:186477) (di:direct) BSUB0007 Z99110 g2633668 Bacillus subtilis 1423 -11530653

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788914	3910	26066	405	135

Description

6500726796 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykmA ykmA Bacillus subtilis 1423 -11530654 7000692580 ykma conserved hypothetical protein ykma (db:pir2.dat) E69857 E69857 Bacillus subtilis 1423 -11530654 6000689768 ykma ykma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:33559) (re:34002) (di:complement) BSAJ2571 AJ002571 g2632035 Bacillus subtilis 1423 -11530654 7500963699 ykma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:186508) (re:186951) (di:complement) BSUB0007 Z99110 g2633669 Bacillus subtilis 1423 -11530654

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788915	3911	26067	348	115

Description

6500726797 yzze:ykza hypothetical protein:similar to general stress protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzA ykzA Bacillus subtilis 1423 -11530655 7000693019 ykza general stress protein homolog ykza (cl:hypothetical protein ykla) (db:pir2.dat) F69870 F69870 Bacillus subtilis 1423 -11530655 6000689770 ykna ykna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to osmc from escherichia coli) (le:34145) (re:34555) (di:direct) BSAJ2571 AJ002571 g2632036 Bacillus subtilis 1423 -11530655 7500955920 ykza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: yzze; similar to general) (le:187094) (re:187504) (di:direct) BSUB0007 Z99110 g2633670 Bacillus subtilis 1423 -11530655

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788917	3912	26068	1266	422

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788929	3913	26069	684	227

Description

6500726798 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknA yknA Bacillus subtilis 1423 -11530656 7000692581 ykna conserved hypothetical protein ykna (cl:hypothetical protein yaaj) (db:pir2.dat) F69857 F69857 Bacillus subtilis 1423 -11530656 6000689772 ykoa ykoa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:34802) (re:35272) (di:complement) BSAJ2571 AJ002571 g2632037 Bacillus subtilis 1423 -11530656 7500955918 ykna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:187751) (re:188221) (di:complement) BSUB0007 Z99110 g2633671 Bacillus subtilis 1423 -11530656

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788936	3914	26070	669	222

Description

6500726799 ykob:ispu hypothetical protein:related to the activation of sigma-h (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ispU ispU Bacillus subtilis 1423 -11530657 7000692148 ispu sigma-h activator ispu (cl:sigma-h activator ispu) (db:pir2.dat) G69646 G69646 Bacillus subtilis 1423 -11530657 6000689778 ykob ykob (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:39331) (re:40164) (di:direct) BSAJ2571 AJ002571 g2632040 Bacillus subtilis 1423 -11530657 7500963376 ispu (fn:related to the activation of sigma-h) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykob) (le:192280) (re:193113) (di:direct) BSUB0007 Z99110 g2633674 Bacillus subtilis 1423 -11530657

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788938	3915	26071	567	188

Description

6500726800 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoC ykoC Bacillus subtilis 1423 -11530658 7000693422 ykoc hypothetical protein ykoc (db:pir2.dat) G69858 G69858 Bacillus subtilis 1423 -11530658 6000689780 ykoc ykoc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:40195) (re:40959) (di:complement) BSAJ2571 AJ002571 g2632041 Bacillus subtilis 1423 -11530658 7500964377 ykoc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:193144) (re:193908) (di:complement) BSUB0007 Z99110 g2633675 Bacillus subtilis 1423 -11530658

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788945	3916	26072	1068	355

Description

6500726801 hypothetical protein:similar to cation abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoD ykoD Bacillus subtilis 1423 -11530659 7000692329 ykod cation abc transporter atp-binding protei homolog ykod (cl:atp-binding cassette homology) (db:pir2.dat) H69858 H69858 Bacillus subtilis 1423 -11530659 6000689782 ykod ykod (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to cobalt transport atp binding protein) (le:41106) (re:42578) (di:complement) BSAJ2571 AJ002571 g2632042 Bacillus subtilis 1423 -11530659 7500963497 ykod (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to cation abc transporter (atp-binding) (le:194055) (re:195527) (di:complement) BSUB0007 Z99110 g2633676 Bacillus subtilis 1423 -11530659

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788949	3917	26073	954	318

Description

6500726802 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoE ykoE Bacillus subtilis 1423 -11530660 7000693423 ykoe hypothetical protein ykoe (db:pir2.dat) A69859 A69859 Bacillus subtilis 1423 -11530660 6000689784 ykoe ykoe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:42565) (re:43164) (di:complement) BSAJ2571 AJ002571 g2632043 Bacillus subtilis 1423 -11530660 7500964378 ykoe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:195514) (re:196113) (di:complement) BSUB0007 Z99110 g2633677 Bacillus subtilis 1423 -11530660

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788958	3918	26074	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788960	3919	26075	867	289

Description

6500726803 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoF ykoF Bacillus subtilis 1423 -11530661 7000693424 ykof hypothetical protein ykof (db:pir2.dat) B69859 B69859 Bacillus subtilis 1423 -11530661 6000689786 ykof ykof (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:43166) (re:43768) (di:complement) BSAJ2571 AJ002571 g2632044 Bacillus subtilis 1423 -11530661 7500964379 ykof (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:196115) (re:196717) (di:complement) BSUB0007 Z99110 g2633678 Bacillus subtilis 1423 -11530661

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788968	3920	26076	534	177

Description

6500726804 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoG ykoG Bacillus subtilis 1423 -11530662 7000694846 ykog two-component response regulator ykoh homolog ykog) (cl:ompr protein:response regulator homology) (db:pir2.dat) C69859 C69859 Bacillus subtilis 1423 -11530662 6000689788 ykog ykog (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to response regulators) (le:44079) (re:44765) (di:direct) BSAJ2571 AJ002571 g2632045 Bacillus subtilis 1423 -11530662 7500965395 ykog (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to two-component response regulator (ykoh)) (le:197028) (re:197714) (di:direct) BSUB0007 Z99110 g2633679 Bacillus subtilis 1423 -11530662

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788969	3921	26077	576	191

Description

6500726805 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoH ykoH Bacillus subtilis 1423 -11530663 7000694875 ykoh two-component sensor histidine kinase homolog ykoh (db:pir2.dat) D69859 D69859 Bacillus subtilis 1423 -11530663 6000689790 ykoh ykoh (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to sensor kinases) (le:44769) (re:46133) (di:direct) BSAJ2571 AJ002571 g2632046 Bacillus subtilis 1423 -11530663 7500965412 ykoh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to two-component sensor histidine kinase) (le:197718) (re:199082) (di:direct) BSUB0007 Z99110 g2633680 Bacillus subtilis 1423 -11530663

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788977	3922	26078	777	258

Description

6500726806 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoI ykoI Bacillus subtilis 1423 -11530664 7000692584 ykoi conserved hypothetical protein ykoi (db:pir2.dat) E69859 E69859 Bacillus subtilis 1423 -11530664 6000689792 ykoi ykoi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:46130) (re:46810) (di:direct) BSAJ2571 AJ002571 g2632047 Bacillus subtilis 1423 -11530664 7500963704 ykoi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:199079) (re:199759) (di:direct) BSUB0007 Z99110 g2633681 Bacillus subtilis 1423 -11530664

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788982	3923	26079	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501788988	3924	26080	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789004	3925	26081	555	184

Description

6500726807 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoJ ykoJ Bacillus subtilis 1423 -11530665 7000692585 ykoj conserved hypothetical protein ykoj (db:pir2.dat) F69859 F69859 Bacillus subtilis 1423 -11530665 6000689794 ykoj ykoj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:46902) (re:47414) (di:direct) BSAJ2571 AJ002571 g2632048 Bacillus subtilis 1423 -11530665 7500963705 ykoj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:199851) (re:200363) (di:direct) BSUB0007 Z99110 g2633682 Bacillus subtilis 1423 -11530665

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789007	3926	26082	657	219

Description

6500726808 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzD ykzD Bacillus subtilis 1423 -11530666 7000692610 ykzd conserved hypothetical protein ykzd (db:pir2.dat) A69871 A69871 Bacillus subtilis 1423 -11530666 6000690693 ykzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:200446) (re:200583) (di:direct) BSUB0007 Z99110 g2633683 Bacillus subtilis 1423 -11530666 7500963727 ykzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:46) (re:183) (di:direct) BSUB0008 Z99111 g2633700 Bacillus subtilis 1423 -11530666

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789013	3927	26083	810	270

Description

6500726809 hypothetical protein:similar to mg2+ transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoK ykoK Bacillus subtilis 1423 -11530667 7000694219 ykok mg2+ transporter homolog ykok (cl:magnesium transport protein mgte) (db:pir2.dat) G69859 G69859 Bacillus subtilis 1423 -11530667 6000689796 ykok ykok (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:homologous to magnesium transporters) (le:48140) (re:49495) (di:direct) BSAJ2571 AJ002571 g2632049 Bacillus subtilis 1423 -11530667 6000689798 ykok (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to mg2+ transporter) (le:201089) (re:202444) (di:direct) BSUB0007 Z99110 g2633684 Bacillus subtilis 1423 -11530667 7500964944 ykok (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to mg2+ transporter) (le:689) (re:2044) (di:direct) BSUB0008 Z99111 g2633701 Bacillus subtilis 1423 -11530667

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789019	3928	26084	330	109

Description

6500726810 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzB ykzB Bacillus subtilis 1423 -11530668 7000693447 ykzb hypothetical protein ykzb (db:pir2.dat) G69870 G69870 Bacillus subtilis 1423 -11530668 6000690695 ykzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:203014) (re:203169) (di:direct) BSUB0007 Z99110 g2633686 Bacillus subtilis 1423 -11530668 7500964402 ykzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:2614) (re:2769) (di:direct) BSUB0008 Z99111 g2633703 Bacillus subtilis 1423 -11530668

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789020	3929	26085	525	175

Description

GTC ORF with score 239 to: (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae putative transmembrane protein (ptm1)gene, complete cds.) (nt:contains putative signal sequence and seven) (le:1169) (re:2740) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789036	3930	26086	1254	417

Description

GTC ORF with score 244 to: (or:Mus musculus) (sr:mouse (strain cd-1) dna, library of o.smithies, clone pump-3 hb) (db:genpept-rod) (de:mouse prp gene encoding proline-rich protein mp-3, exon 2.) (nt:proline-rich protein mp-3) (le:<1) (re:893) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789041	3931	26087	186	61

Description

6500726811 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoL ykoL Bacillus subtilis 1423 -11530669 7000693425 ykol hypothetical protein ykol (db:pir2.dat) H69859 H69859 Bacillus subtilis 1423 -11530669 6000689802 ykol ykol (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:50308) (re:50490) (di:direct) BSAJ2571 AJ002571 g2632051 Bacillus subtilis 1423 -11530669 6000689804 ykol (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:203257) (re:203439) (di:direct) BSUB0007 Z99110 g2633687 Bacillus subtilis 1423 -11530669 7500964380 ykol (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:2857) (re:3039) (di:direct) BSUB0008 Z99111 g2633704 Bacillus subtilis 1423 -11530669

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789042	3932	26088	453	150

Description

6500726812 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoM ykoM Bacillus subtilis 1423 -11530670 7000694769 ykom transcription regulator marr family homolog ykom (cl:regulatory protein mpra) (db:pir2.dat) A69860 A69860 Bacillus subtilis 1423 -11530670 6000689805 ykom ykom (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:putative transcriptional regulator; product) (le:50623) (re:51087) (di:direct) BSAJ2571 AJ002571 g2632052 Bacillus subtilis 1423 -11530670 6000689807 ykom (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to transcriptional regulator (marr family)) (le:203572) (re:204036) (di:direct) BSUB0007 Z99110 g2633688 Bacillus subtilis 1423 -11530670 7500955823 ykom (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to transcriptional regulator (marr family)) (le:3172) (re:3636) (di:direct) BSUB0008 Z99111 g2633705 Bacillus subtilis 1423 -11530670

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789044	3933	26089	390	129

Description

6500726813 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoN ykoN Bacillus subtilis 1423 -11530671 7000692586 ykon conserved hypothetical protein ykon (db:pir2.dat) B69860 B69860 Bacillus subtilis 1423 -11530671 6000689808 ykon ykon (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:51102) (re:52223) (di:complement) BSAJ2571 AJ002571 g2632053 Bacillus subtilis 1423 -11530671 6000689810 ykon (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins from b. subtilis) (le:204051) (re:205172) (di:complement) BSUB0007 Z99110 g2633689 Bacillus subtilis 1423 -11530671 7500963706 ykon (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:3651) (re:4772) (di:complement) BSUB0008 Z99111 g2633706 Bacillus subtilis 1423 -11530671

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789047	3934	26090	279	92

Description

6500726814 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoP ykoP Bacillus subtilis 1423 -11530672 7000693426 ykop hypothetical protein ykop (db:pir2.dat) C69860 C69860 Bacillus subtilis 1423 -11530672 6000689811 ykop ykop (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:52315) (re:52866) (di:direct) BSAJ2571 AJ002571 g2632054 Bacillus subtilis 1423 -11530672 6000689813 ykop (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:205264) (re:205815) (di:direct) BSUB0007 Z99110 g2633690 Bacillus subtilis 1423 -11530672 7500964381 ykop (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:4864) (re:5415) (di:direct) BSUB0008 Z99111 g2633707 Bacillus subtilis 1423 -11530672

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789048	3935	26091	228	76

Description

GTC ORF with score 113 to: (db:genpept-bct1) (de:rhodococcus globerulus hpp operon, 3-(3-hydroxyphenyl) propionatehydroxylase (hppa), 2-hydroxy-6-ketonona-2,4-dienoate hydrolase(hppc), 2,3-dihydroxyphenylpropionate 1,2-dioxygenase (hppb),putative ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789056	3936	26092	738	245

Description

6500726815 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoQ ykoQ Bacillus subtilis 1423 -11530673 7000692587 ykoq probable phosphoesterase:ykoq (cl:probable phosphoesterase yaei:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) D69860 D69860 Bacillus subtilis 1423 -11530673 6000689814 ykoq ykoq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (nt:product homologous to p37049) (le:52894) (re:53706) (di:complement) BSAJ2571 AJ002571 g2632055 Bacillus subtilis 1423 -11530673 6000689816 ykoq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:205843) (re:206655) (di:complement) BSUB0007 Z99110 g2633691 Bacillus subtilis 1423 -11530673 7500954196 ykoq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:5443) (re:6255) (di:complement) BSUB0008 Z99111 g2633708 Bacillus subtilis 1423 -11530673

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789057	3937	26093	351	117

Description

6500726816 ykor:ykos hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoS ykoS Bacillus subtilis 1423 -11530674 7000693427 ykos hypothetical protein ykos (db:pir2.dat) E69860 E69860 Bacillus subtilis 1423 -11530674 6000689817 ykor ykor (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 56 kb dna fragment between xlya and ykor.) (le:53899) (re:55593) (di:direct) BSAJ2571 AJ002571 g2632056 Bacillus subtilis 1423 -11530674 6000689819 ykos (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:alternate gene name: ykor) (le:206848) (re:208542) (di:direct) BSUB0007 Z99110 g2633692 Bacillus subtilis 1423 -11530674 7500964382 ykos (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ykor) (le:6448) (re:8142) (di:direct) BSUB0008 Z99111 g2633709 Bacillus subtilis 1423 -11530674

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789058	3938	26094	339	112

Description

6500726817 hypothetical protein:similar to dolichol phosphate mannose synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoT ykoT Bacillus subtilis 1423 -11530675 7500938583 ykot (de:hypothetical 38.5 kd protein in tnra-sspd intergenic region) (db:swissprot) YKOT_BACSU O34755 BACILLUS SUBTILIS 1423 -11530675 7000692955 ykot dolichol phosphate mannose synthase homolog ykot (cl:stress response protein csbb) (db:pir2.dat) F69860 F69860 Bacillus subtilis 1423 -11530675 7500938585 ykot (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to dolichol phosphate mannose synthase) (le:208555) (re:209568) (di:direct) BSUB0007 Z99110 g2633693 Bacillus subtilis 1423 -11530675 6000690697 ykot (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to dolichol phosphate mannose synthase) (le:8155) (re:9168) (di:direct) BSUB0008 Z99111 g2633710 Bacillus subtilis 1423 -11530675

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789062	3939	26095	750	249

Description

6500726818 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoU ykoU Bacillus subtilis 1423 -11530676 7000693428 ykou hypothetical protein ykou (db:pir2.dat) G69860 G69860 Bacillus subtilis 1423 -11530676 6000690699 ykou (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (le:209594) (re:211429) (di:complement) BSUB0007 Z99110 g2633694 Bacillus subtilis 1423 -11530676 7500964383 ykou (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:9194) (re:11029) (di:complement) BSUB0008 Z99111 g2633711 Bacillus subtilis 1423 -11530676

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789063	3940	26096	360	120

Description

6500726819 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoV ykoV Bacillus subtilis 1423 -11530677 7000692588 ykov conserved hypothetical protein ykov (cl:bacillus subtilis conserved hypothetical protein ykov) (db:pir2.dat) H69860 H69860 Bacillus subtilis 1423 -11530677 6000690701 ykov (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:211433) (re:212368) (di:complement) BSUB0007 Z99110 g2633695 Bacillus subtilis 1423 -11530677 7500963707 ykov (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:11033) (re:11968) (di:complement) BSUB0008 Z99111 g2633712 Bacillus subtilis 1423 -11530677

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789064	3941	26097	627	208

Description

GTC ORF with score 117 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789068	3942	26098	711	236

Description

6500726820 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoW ykoW Bacillus subtilis 1423 -11530678 7000692589 ykow conserved hypothetical protein ykow (db:pir2.dat) A69861 A69861 Bacillus subtilis 1423 -11530678 6000690703 ykow (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to hypothetical proteins) (le:212405) (re:214654) (di:complement) BSUB0007 Z99110 g2633696 Bacillus subtilis 1423 -11530678 7500963708 ykow (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:12005) (re:14254) (di:complement) BSUB0008 Z99111 g2633713 Bacillus subtilis 1423 -11530678

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789069	3943	26099	1035	345

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789073	3944	26100	561	186

Description

GTC ORF with score 309 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f08f1.) (nt:strong similarity to saccharomyces cerevisiae) (le:12974:13463:13738) (re:13105:13682:14227) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789087	3945	26101	648	215

Description

GTC ORF with score 161 to: (fn:possibly involved in regulating granaticin) (db:genpept) (de:streptomyces violaceoruber tu22 granaticin biosynthetic genecluster.) (nt:contains possible cxxc motif) (le:15846) (re:16508) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789536	3946	26102	396	131

Description

6500726821 hypothetical protein:similar to alkaline phosphatase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoX ykoX Bacillus subtilis 1423 -11530679 7000692173 ykox alkaline phosphatase homolog ykox (cl:probable alkaline phosphatase yngc) (db:pir2.dat) B69861 B69861 Bacillus subtilis 1423 -11530679 6000690705 ykox (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to alkaline phosphatase) (le:214988) (re:215653) (di:direct) BSUB0007 Z99110 g2633697 Bacillus subtilis 1423 -11530679 7500963392 ykox (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to alkaline phosphatase) (le:14588) (re:15253) (di:direct) BSUB0008 Z99111 g2633714 Bacillus subtilis 1423 -11530679

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789539	3947	26103	411	136

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789542	3948	26104	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789544	3949	26105	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789546	3950	26106	978	325

Description

GTC ORF with score 208 to: (or:Glomerella cingulata) (db:genpept-pln1) (de:colletotrichum gloeosporioides nitrogen starvation-inducedglutamine rich protein mrna, complete cds.) (nt:glutamine rich protein similar to glutenins;) (le:74) (re:721) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789561	3951	26107	369	122

Description

6500726822 hypothetical protein:similar to toxic anion resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoY ykoY Bacillus subtilis 1423 -11530680 7000694695 ykoy toxic anion resistance protein homolog ykoy (cl:hypothetical protein sll1022) (db:pir2.dat) C69861 C69861 Bacillus subtilis 1423 -11530680 6000690707 ykoy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.) (nt:similar to toxic anion resistance protein) (le:215730) (re:216704) (di:direct) BSUB0007 Z99110 g2633698 Bacillus subtilis 1423 -11530680 7500955960 ykoy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to toxic anion resistance protein) (le:15330) (re:16304) (di:direct) BSUB0008 Z99111 g2633715 Bacillus subtilis 1423 -11530680

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789563	3952	26108	657	218

Description

6500726823 hypothetical protein:similar to rna polymerase sigma factor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoZ ykoZ Bacillus subtilis 1423 -11530681 7000694563 ykoz rna polymerase sigma factor homolog ykoz (db:pir2.dat) D69861 D69861 Bacillus subtilis 1423 -11530681 7500965168 ykoz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to rna polymerase sigma factor) (le:16568) (re:17323) (di:direct) BSUB0008 Z99111 g2633716 Bacillus subtilis 1423 -11530681

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789565	3953	26109	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789567	3954	26110	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789568	3955	26111	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789570	3956	26112	624	207

Description

6500726824 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrI ykrI Bacillus subtilis 1423 -11530682 7000693429 ykri hypothetical protein ykri (db:pir2.dat) E69862 E69862 Bacillus subtilis 1423 -11530682 7500964384 ykri (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:17320) (re:18465) (di:direct) BSUB0008 Z99111 g2633717 Bacillus subtilis 1423 -11530682

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789575	3957	26113	327	108

Description

6500726825 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrK ykrK Bacillus subtilis 1423 -11530683 7000693430 ykrk hypothetical protein ykrk (db:pir2.dat) F69862 F69862 Bacillus subtilis 1423 -11530683 7500964385 ykrk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:18801) (re:19502) (di:complement) BSUB0008 Z99111 g2633719 Bacillus subtilis 1423 -11530683

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789579	3958	26114	381	126

Description

6500726826 hypothetical protein:similar to heat-shock protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrL ykrL Bacillus subtilis 1423 -11530684 7000693084 ykrl heat-shock protein homolog ykrl (cl:heat-shock protein htpx) (db:pir2.dat) G69862 G69862 Bacillus subtilis 1423 -11530684 7500955127 ykrl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to heat-shock protein) (le:19673) (re:20569) (di:direct) BSUB0008 Z99111 g2633720 Bacillus subtilis 1423 -11530684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789586	3959	26115	276	91

Description

6500726827 hypothetical protein:similar to na+-transporting atp synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrM ykrM Bacillus subtilis 1423 -11530685 7000694289 ykrm na+-transporting atp synthase homolog ykrm (cl:na+-atp synthase chain j) (db:pir2.dat) H69862 H69862 Bacillus subtilis 1423 -11530685 7500964998 ykrm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to na+-transporting atp synthase) (le:20743) (re:22092) (di:direct) BSUB0008 Z99111 g2633721 Bacillus subtilis 1423 -11530685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789587	3960	26116	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789588	3961	26117	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789599	3962	26118	366	121

Description

6500726828 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzE ykzE Bacillus subtilis 1423 -11530686 7000693449 ykze hypothetical protein ykze (db:pir2.dat) B69871 B69871 Bacillus subtilis 1423 -11530686 7500964404 ykze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:22395) (re:22571) (di:direct) BSUB0008 Z99111 g2633722 Bacillus subtilis 1423 -11530686

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789604	3963	26119	918	306

Description

6500726829 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrP ykrP Bacillus subtilis 1423 -11530687 7000692592 ykrp conserved hypothetical protein ykrp (db:pir2.dat) A69863 A69863 Bacillus subtilis 1423 -11530687 7500963711 ykrp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:22614) (re:23636) (di:complement) BSUB0008 Z99111 g2633723 Bacillus subtilis 1423 -11530687

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789606	3964	26120	264	87

Description

GTC ORF with score 104 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f11g11.) (nt:contains strong similarity to a dnaj-like domain) (le:1746:1902:2480:2849) (re:1853:2432:2702:3609) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789613	3965	26121	201	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789618	3966	26122	1140	380

Description

6500726830 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrQ ykrQ Bacillus subtilis 1423 -11530688 7000694860 ykrq two-component sensor histidine kinase homolog ykrq (db:pir2.dat) B69863 B69863 Bacillus subtilis 1423 -11530688 7500965413 ykrq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to two-component sensor histidine kinase) (le:23889) (re:26105) (di:direct) BSUB0008 Z99111 g2633724 Bacillus subtilis 1423 -11530688

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789622	3967	26123	546	181

Description

6500726831 hypothetical protein:similar to initiation factor eif-2b:alpha subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrS ykrS Bacillus subtilis 1423 -11530689 7500950824 ykrs (de:hypothetical 38.9 kd protein in dat-spo0e intergenic region) (db:swissprot) YKRS_BACSU O31662 BACILLUS SUBTILIS 1423 -11530689 7000694107 ykrs initiation factor eif-2b alpha subunit homolog ykrs (cl:translation initiation factor eif-2b) (db:pir2.dat) C69863 C69863 Bacillus subtilis 1423 -11530689 7500950826 ykrs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to initiation factor eif-2b (alpha) (le:26848) (re:27909) (di:complement) BSUB0008 Z99111 g2633726 Bacillus subtilis 1423 -11530689

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789639	3968	26124	927	308

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789640	3969	26125	936	311

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789649	3970	26126	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789651	3971	26127	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789655	3972	26128	783	260

Description

6500726832 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrT ykrT Bacillus subtilis 1423 -11530690 7000693431 ykrt hypothetical protein ykrt (db:pir2.dat) D69863 D69863 Bacillus subtilis 1423 -11530690 7500964386 ykrt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:27917) (re:29116) (di:complement) BSUB0008 Z99111 g2633727 Bacillus subtilis 1423 -11530690

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789670	3973	26129	573	191

Description

6500726833 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrU ykrU Bacillus subtilis 1423 -11530691 7000692593 ykru conserved hypothetical protein ykru (cl:hypothetical protein ylr351c) (db:pir2.dat) E69863 E69863 Bacillus subtilis 1423 -11530691 7500963712 ykru (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:29443) (re:30222) (di:complement) BSUB0008 Z99111 g2633728 Bacillus subtilis 1423 -11530691

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789672	3974	26130	216	71

Description

GTC ORF with score 210 to: (sr:candida tropicalis (strain:ifo 0618) dna) (db:genpept-pln1) (de:candida tropicalis dna for d-xylose reductase ii,iii, complete cds.) (nt:xrii is xyra and xyrb hetero-dimer. ; xriii is) (le:148) (re:1122) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789674	3975	26131	381	126

Description

6500726834 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrX ykrX Bacillus subtilis 1423 -11530692 7000692594 ykrx conserved hypothetical protein ykrx (db:pir2.dat) H69863 H69863 Bacillus subtilis 1423 -11530692 7500963713 ykrx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:32951) (re:33658) (di:direct) BSUB0008 Z99111 g2633731 Bacillus subtilis 1423 -11530692

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789697	3976	26132	531	177

Description

6500726835 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrY ykrY Bacillus subtilis 1423 -11530693 7000692595 ykry conserved hypothetical protein ykry (db:pir2.dat) A69864 A69864 Bacillus subtilis 1423 -11530693 7500963714 ykry (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:33616) (re:34245) (di:direct) BSUB0008 Z99111 g2633732 Bacillus subtilis 1423 -11530693

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789705	3977	26133	690	230

Description

6500726836 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrZ ykrZ Bacillus subtilis 1423 -11530694 7000692596 ykrz conserved hypothetical protein ykrz (db:pir2.dat) B69864 B69864 Bacillus subtilis 1423 -11530694 7500963715 ykrz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:34260) (re:34796) (di:direct) BSUB0008 Z99111 g2633733 Bacillus subtilis 1423 -11530694

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789726	3978	26134	339	113

Description

6500726837 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvA ykvA Bacillus subtilis 1423 -11530695 7000693442 ykva hypothetical protein ykva (db:pir2.dat) E69867 E69867 Bacillus subtilis 1423 -11530695 7500964397 ykva (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:34837) (re:35157) (di:complement) BSUB0008 Z99111 g2633734 Bacillus subtilis 1423 -11530695

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789727	3979	26135	1191	396

Description

6500726838 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvD ykvD Bacillus subtilis 1423 -11530696 7000694861 ykvd two-component sensor histidine kinase homolog ykvd (db:pir2.dat) F69867 F69867 Bacillus subtilis 1423 -11530696 7500965414 ykvd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to two-component sensor histidine kinase) (le:36162) (re:37682) (di:complement) BSUB0008 Z99111 g2633737 Bacillus subtilis 1423 -11530696

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789745	3980	26136	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789755	3981	26137	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789759	3982	26138	465	154

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789771	3983	26139	1251	416

Description

6500726839 hypothetical protein:similar to transcriptional regulator:marr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvE ykvE Bacillus subtilis 1423 -11530697 7000694770 ykve transcription regulator marr family homolog ykve (cl:regulatory protein mpra) (db:pir2.dat) G69867 G69867 Bacillus subtilis 1423 -11530697 7500955822 ykve (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to transcriptional regulator (marr family)) (le:37875) (re:38312) (di:direct) BSUB0008 Z99111 g2633738 Bacillus subtilis 1423 -11530697

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789778	3984	26140	426	141

Description

6500726840 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvI ykvI Bacillus subtilis 1423 -11530698 7000692603 ykvi conserved hypothetical protein ykvi (db:pir2.dat) H69867 H69867 Bacillus subtilis 1423 -11530698 7500963721 ykvi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:42768) (re:43811) (di:direct) BSUB0008 Z99111 g2633742 Bacillus subtilis 1423 -11530698

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789784	3985	26141	1500	500

Description

6500726841 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvJ ykvJ Bacillus subtilis 1423 -11530699 7000692604 ykvj ykvj protein (cl:conserved hypothetical protein hi1191) (db:pir2.dat) A69868 A69868 Bacillus subtilis 1423 -11530699 7500963722 ykvj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:44124) (re:44783) (di:direct) BSUB0008 Z99111 g2633743 Bacillus subtilis 1423 -11530699

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789788	3986	26142	900	299

Description

6500726842 hypothetical protein:similar to 6-pyruvoyl tetrahydrobiopterin synthase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvK ykvK Bacillus subtilis 1423 -11530700 7000692071 ykvk 6-pyruvoyl tetrahydrobiopterin synthase homolog ykvk (db:pir2.dat) B69868 B69868 Bacillus subtilis 1423 -11530700 7500963314 ykvk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to 6-pyruvoyl tetrahydrobiopterin synthase) (le:44776) (re:45225) (di:direct) BSUB0008 Z99111 g2633744 Bacillus subtilis 1423 -11530700

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789793	3987	26143	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789797	3988	26144	687	228

Description

6500726843 hypothetical protein:similar to coenzyme pqq synthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvL ykvL Bacillus subtilis 1423 -11530701 7000692380 ykvl coenzyme pqq synthesis homolog ykvl (db:pir2.dat) C69868 C69868 Bacillus subtilis 1423 -11530701 7500963542 ykvl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to coenzyme pqq synthesis) (le:45218) (re:45949) (di:direct) BSUB0008 Z99111 g2633745 Bacillus subtilis 1423 -11530701

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789802	3989	26145	399	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789803	3990	26146	360	120

Description

6500726844 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvM ykvM Bacillus subtilis 1423 -11530702 7000692605 ykvm conserved hypothetical protein ykvm (cl:hypothetical protein ykvm) (db:pir2.dat) D69868 D69868 Bacillus subtilis 1423 -11530702 7500955893 ykvm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:45967) (re:46464) (di:direct) BSUB0008 Z99111 g2633746 Bacillus subtilis 1423 -11530702

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789814	3991	26147	387	128

Description

6500726845 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvN ykvN Bacillus subtilis 1423 -11530703 7000692606 ykvn conserved hypothetical protein ykvn (cl:conserved hypothetical protein mth1285) (db:pir2.dat) E69868 E69868 Bacillus subtilis 1423 -11530703 7500963723 ykvn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:47023) (re:47379) (di:complement) BSUB0008 Z99111 g2633747 Bacillus subtilis 1423 -11530703

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789821	3992	26148	489	162

Description

6500726846 hypothetical protein:similar to glucose 1-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvO ykvO Bacillus subtilis 1423 -11530704 7000693037 ykvo glucose 1-dehydrogenase homolog ykvo (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) F69868 F69868 Bacillus subtilis 1423 -11530704 7500964017 ykvo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to glucose 1-dehydrogenase) (le:47548) (re:48294) (di:direct) BSUB0008 Z99111 g2633748 Bacillus subtilis 1423 -11530704

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789831	3993	26149	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789841	3994	26150	1041	346

Description

6500726847 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvP ykvP Bacillus subtilis 1423 -11530705 7000693443 ykvp hypothetical protein ykvp (db:pir2.dat) G69868 G69868 Bacillus subtilis 1423 -11530705 7500964398 ykvp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:48775) (re:49974) (di:direct) BSUB0008 Z99111 g2633749 Bacillus subtilis 1423 -11530705

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789845	3995	26151	510	169

Description

6500726848 hypothetical protein:similar to chitinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvQ ykvQ Bacillus subtilis 1423 -11530706 7000692362 ykvq chitinase homolog ykvq (db:pir2.dat) H69868 H69868 Bacillus subtilis 1423 -11530706 7500963524 ykvq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to chitinase) (le:50314) (re:51012) (di:direct) BSUB0008 Z99111 g2633750 Bacillus subtilis 1423 -11530706

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789868	3996	26152	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789876	3997	26153	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789898	3998	26154	690	229

Description

6500726849 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvR ykvR Bacillus subtilis 1423 -11530707 7000693444 ykvr hypothetical protein ykvr (db:pir2.dat) A69869 A69869 Bacillus subtilis 1423 -11530707 7500964399 ykvr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:51927) (re:52217) (di:direct) BSUB0008 Z99111 g2633751 Bacillus subtilis 1423 -11530707

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789899	3999	26155	321	106

Description

6500726850 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvS ykvS Bacillus subtilis 1423 -11530708 7000693445 ykvs hypothetical protein ykvs (db:pir2.dat) B69869 B69869 Bacillus subtilis 1423 -11530708 7500964400 ykvs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:52338) (re:52769) (di:complement) BSUB0008 Z99111 g2633752 Bacillus subtilis 1423 -11530708

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789903	4000	26156	405	135

Description

6500726851 hypothetical protein:similar to spore cortex-lytic enzyme (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvT ykvT Bacillus subtilis 1423 -11530709 7000694622 ykvt spore cortex-lytic enzyme homolog ykvt (db:pir2.dat) C69869 C69869 Bacillus subtilis 1423 -11530709 7500965217 ykvt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to spore cortex-lytic enzyme) (le:53182) (re:53808) (di:direct) BSUB0008 Z99111 g2633753 Bacillus subtilis 1423 -11530709

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789907	4001	26157	207	68

Description

6500726852 hypothetical protein:similar to spore cortex membrane protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvU ykvU Bacillus subtilis 1423 -11530710 7000694620 ykvu spore cortex membrane protein homolog ykvu (db:pir2.dat) D69869 D69869 Bacillus subtilis 1423 -11530710 7500965215 ykvu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to spore cortex membrane protein) (le:53926) (re:55263) (di:direct) BSUB0008 Z99111 g2633754 Bacillus subtilis 1423 -11530710

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501789913	4002	26158	228	75

Description

6500726853 hypothetical protein:similar to thioredoxin (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvV ykvV Bacillus subtilis 1423 -11530711 7000694682 ykvv thioredoxin related protein ykvv (cl:bacillus subtilis thioredoxin related protein ykvv) (db:pir2.dat) E69869 E69869 Bacillus subtilis 1423 -11530711 7500965267 ykvv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to thioredoxin) (le:55314) (re:55811) (di:direct) BSUB0008 Z99111 g2633755 Bacillus subtilis 1423 -11530711

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790338	4003	26159	600	199

Description

6500726854 hypothetical protein:similar to heavy metal-transporting atpase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvW ykvW Bacillus subtilis 1423 -11530712 7000693085 ykvw heavy metal-transporting atpase homolog ykvw (cl:atpase nucleotide-binding domain homology) (db:pir2.dat) F69869 F69869 Bacillus subtilis 1423 -11530712 7500964048 ykvw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to heavy metal-transporting atpase) (le:56047) (re:57960) (di:direct) BSUB0008 Z99111 g2633756 Bacillus subtilis 1423 -11530712

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790339	4004	26160	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790347	4005	26161	606	202

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790351	4006	26162	399	133

Description

6500726855 hypothetical protein:similar to xaa-pro dipeptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvY ykvY Bacillus subtilis 1423 -11530713 7000694903 ykvy xaa-pro dipeptidase homolog ykvy (cl:x-pro aminopeptidase) (db:pir2.dat) G69869 G69869 Bacillus subtilis 1423 -11530713 7500965436 ykvy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to xaa-pro dipeptidase) (le:58367) (re:59458) (di:direct) BSUB0008 Z99111 g2633757 Bacillus subtilis 1423 -11530713

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790357	4007	26163	219	72

Description

6500726856 hypothetical protein:similar to transcriptional regulator:laci family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykvZ ykvZ Bacillus subtilis 1423 -11530714 7000694747 ykvz transcription regulator laci family homolog ykvz (cl:lac repressor) (db:pir2.dat) H69869 H69869 Bacillus subtilis 1423 -11530714 7500965319 ykvz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to transcriptional regulator (laci family)) (le:59740) (re:60705) (di:direct) BSUB0008 Z99111 g2633758 Bacillus subtilis 1423 -11530714

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790359	4008	26164	762	253

Description

6500726857 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykwB ykwB Bacillus subtilis 1423 -11530715 7000692607 ykwb conserved hypothetical protein ykwb (db:pir2.dat) A69870 A69870 Bacillus subtilis 1423 -11530715 7500963724 ykwb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:67588) (re:68109) (di:complement) BSUB0008 Z99111 g2633765 Bacillus subtilis 1423 -11530715

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790366	4009	26165	837	278

Description

6500726858 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykwD ykwD Bacillus subtilis 1423 -11530716 7000692608 ykwd conserved hypothetical protein ykwd (db:pir2.dat) C69870 C69870 Bacillus subtilis 1423 -11530716 7500963725 ykwd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:71250) (re:72023) (di:complement) BSUB0008 Z99111 g2633768 Bacillus subtilis 1423 -11530716

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790375	4010	26166	1314	438

Description

GTC ORF with score 146 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c31g5.) (nt:spac31g5.15, anomoly: splicing may be incorrectly) (le:24696:24950:25237:25745) (re:24893:25177:25702:26790) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790380	4011	26167	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790386	4012	26168	552	183

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790396	4013	26169	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790410	4014	26170	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790413	4015	26171	783	261

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790417	4016	26172	975	324

Description

6500726859 hypothetical protein:similar to penicillin-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuA ykuA Bacillus subtilis 1423 -11530717 7000694354 ykua penicillin-binding protein homolog ykua:hypothetical protein kina 5 region (cl:penicillin-binding protein 2b) (db:pir2.dat) G69864 G69864 Bacillus subtilis 1423 -11530717 7500965044 ykua (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to penicillin-binding protein) (le:72417) (re:74474) (di:direct) BSUB0008 Z99111 g2633769 Bacillus subtilis 1423 -11530717

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790423	4017	26173	252	83

Description

6500726860 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykyB ykyB Bacillus subtilis 1423 -11530718 7000693446 ykyb hypothetical protein chev 3 region:hypothetical protein ykyb (db:pir2.dat) E69870 E69870 Bacillus subtilis 1423 -11530718 6000689645 ykub ykub protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:8913) (re:9377) (di:complement) BS16829KB AJ222587 g2632223 Bacillus subtilis 1423 -11530718 7500964401 ykyb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:79169) (re:79633) (di:complement) BSUB0008 Z99111 g2633773 Bacillus subtilis 1423 -11530718

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790428	4018	26174	939	312

Description

6500726861 hypothetical protein:similar to macrolide-efflux protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuC ykuC Bacillus subtilis 1423 -11530719 7000694180 ykuc macrolide-efflux protein homolog ykuc (db:pir2.dat) H69864 H69864 Bacillus subtilis 1423 -11530719 7500964907 ykuc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to macrolide-efflux protein) (le:79759) (re:81051) (di:complement) BSUB0008 Z99111 g2633774 Bacillus subtilis 1423 -11530719

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790453	4019	26175	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790456	4020	26176	987	328

Description

6500726862 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuD ykuD Bacillus subtilis 1423 -11530720 7000692597 ykud conserved hypothetical protein ykud (db:pir2.dat) A69865 A69865 Bacillus subtilis 1423 -11530720 6000689648 ykud ykud protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:10871) (re:11365) (di:complement) BS16829KB AJ222587 g2632225 Bacillus subtilis 1423 -11530720 7500963716 ykud (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:81127) (re:81621) (di:complement) BSUB0008 Z99111 g2633775 Bacillus subtilis 1423 -11530720

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790474	4021	26177	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790477	4022	26178	558	185

Description

6500726863 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuE ykuE Bacillus subtilis 1423 -11530721 7000692598 ykue probable phosphoesterase:ykue (cl:probable phosphoesterase yaei:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) B69865 B69865 Bacillus subtilis 1423 -11530721 6000689650 ykue ykue protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:11422) (re:12285) (di:complement) BS16829KB AJ222587 g2632226 Bacillus subtilis 1423 -11530721 7500954195 ykue (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:81678) (re:82541) (di:complement) BSUB0008 Z99111 g2633776 Bacillus subtilis 1423 -11530721

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790479	4023	26179	432	143

Description

6500726864 hypothetical protein:similar to glucose 1-dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuF ykuF Bacillus subtilis 1423 -11530722 7502851678 ykuf (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YKUF_BACSU O34717 BACILLUS SUBTILIS 1423 -11530722 7000693036 ykuf glucose 1-dehydrogenase homolog ykuf (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) C69865 C69865 Bacillus subtilis 1423 -11530722 6000689652 ykuf ykuf protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to glucose dehydrogenases) (le:12428) (re:13192) (di:direct) BS16829KB AJ222587 g2632227 Bacillus subtilis 1423 -11530722 7500964016 ykuf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to glucose 1-dehydrogenase) (le:82684) (re:83448) (di:direct) BSUB0008 Z99111 g2633777 Bacillus subtilis 1423 -11530722

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790497	4024	26180	900	299

Description

6500726865 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuG ykuG Bacillus subtilis 1423 -11530723 7000692599 ykug conserved hypothetical protein ykug (db:pir2.dat) D69865 D69865 Bacillus subtilis 1423 -11530723 6000689654 ykug ykug protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:13493) (re:15775) (di:direct) BS16829KB AJ222587 g2632228 Bacillus subtilis 1423 -11530723 7500963717 ykug (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:83749) (re:86031) (di:direct) BSUB0008 Z99111 g2633778 Bacillus subtilis 1423 -11530723

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790499	4025	26181	642	213

Description

6500726866 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuH ykuH Bacillus subtilis 1423 -11530724 7000693435 ykuh hypothetical protein ykuh (db:pir2.dat) E69865 E69865 Bacillus subtilis 1423 -11530724 7500964390 ykuh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:86161) (re:86709) (di:direct) BSUB0008 Z99111 g2633779 Bacillus subtilis 1423 -11530724

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790501	4026	26182	1071	356

Description

6500726867 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuI ykuI Bacillus subtilis 1423 -11530725 7000692600 ykui conserved hypothetical protein ykui (db:pir2.dat) F69865 F69865 Bacillus subtilis 1423 -11530725 6000689657 ykui ykui protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:16606) (re:17829) (di:direct) BS16829KB AJ222587 g2632230 Bacillus subtilis 1423 -11530725 7500963718 ykui (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:86862) (re:88085) (di:direct) BSUB0008 Z99111 g2633780 Bacillus subtilis 1423 -11530725

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790508	4027	26183	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790509	4028	26184	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790514	4029	26185	339	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790522	4030	26186	579	193

Description

6500726868 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuJ ykuJ Bacillus subtilis 1423 -11530726 7000693436 ykuj hypothetical protein ykuj (db:pir2.dat) G69865 G69865 Bacillus subtilis 1423 -11530726 6000689659 ykuj ykuj protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:18475) (re:18714) (di:direct) BS16829KB AJ222587 g2632231 Bacillus subtilis 1423 -11530726 7500964391 ykuj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:88731) (re:88970) (di:direct) BSUB0008 Z99111 g2633781 Bacillus subtilis 1423 -11530726

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790527	4031	26187	234	78

Description

6500726869 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuK ykuK Bacillus subtilis 1423 -11530727 7000693437 ykuk hypothetical protein ykuk (db:pir2.dat) H69865 H69865 Bacillus subtilis 1423 -11530727 6000689661 ykuk ykuk protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:18824) (re:19342) (di:direct) BS16829KB AJ222587 g2632232 Bacillus subtilis 1423 -11530727 7500964392 ykuk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:89080) (re:89598) (di:direct) BSUB0008 Z99111 g2633782 Bacillus subtilis 1423 -11530727

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790529	4032	26188	216	71

Description

6500726870 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzF ykzF Bacillus subtilis 1423 -11530728 7000693450 ykzf hypothetical protein ykzf (db:pir2.dat) C69871 C69871 Bacillus subtilis 1423 -11530728 7500964405 ykzf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:89732) (re:89929) (di:direct) BSUB0008 Z99111 g2633783 Bacillus subtilis 1423 -11530728

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790530	4033	26189	369	122

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790547	4034	26190	291	97

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790566	4035	26191	1473	490

Description

6500726871 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuL ykuL Bacillus subtilis 1423 -11530729 7000693438 ykul hypothetical protein ykul (db:pir2.dat) A69866 A69866 Bacillus subtilis 1423 -11530729 7500964393 ykul (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:90067) (re:90510) (di:direct) BSUB0008 Z99111 g2633784 Bacillus subtilis 1423 -11530729

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790572	4036	26192	639	212

Description

6500726872 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuM ykuM Bacillus subtilis 1423 -11530730 7000694754 ykum transcription regulator lysr family homolog ykum (db:pir2.dat) B69866 B69866 Bacillus subtilis 1423 -11530730 6000689664 ykum ykum protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to lysr type transcriptional regulators) (le:20403) (re:21284) (di:direct) BS16829KB AJ222587 g2632234 Bacillus subtilis 1423 -11530730 7500965324 ykum (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to transcriptional regulator (lysr family)) (le:90659) (re:91540) (di:direct) BSUB0008 Z99111 g2633785 Bacillus subtilis 1423 -11530730

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790574	4037	26193	861	286

Description

6500726873 hypothetical protein:similar to flavodoxin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuN ykuN Bacillus subtilis 1423 -11530731 7502851679 ykun (de:probable flavodoxin 1) (db:swissprot) FLAV_BACSU O34737 BACILLUS SUBTILIS 1423 -11530731 7000692995 ykun flavodoxin homolog ykun (cl:flavodoxin:flavodoxin homology) (db:pir2.dat) C69866 C69866 Bacillus subtilis 1423 -11530731 6000689666 ykun ykun protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to flavodoxins) (le:21396) (re:21872) (di:direct) BS16829KB AJ222587 g2632235 Bacillus subtilis 1423 -11530731 7500963988 ykun (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to flavodoxin) (le:91652) (re:92128) (di:direct) BSUB0008 Z99111 g2633786 Bacillus subtilis 1423 -11530731

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790587	4038	26194	774	257

Description

6500726874 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuO ykuO Bacillus subtilis 1423 -11530732 7000693439 ykuo hypothetical protein ykuo (db:pir2.dat) D69866 D69866 Bacillus subtilis 1423 -11530732 6000689668 ykuo ykuo protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:21862) (re:22755) (di:direct) BS16829KB AJ222587 g2632236 Bacillus subtilis 1423 -11530732 7500964394 ykuo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:92118) (re:93011) (di:direct) BSUB0008 Z99111 g2633787 Bacillus subtilis 1423 -11530732

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790599	4039	26195	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790609	4040	26196	267	88

Description

6500726875 hypothetical protein:similar to sulfite reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuP ykuP Bacillus subtilis 1423 -11530733 7502851680 ykup (de:probable flavodoxin 2) (db:swissprot) FLAW_BACSU O34589 BACILLUS SUBTILIS 1423 -11530733 7000694656 ykup sulfite reductase homolog ykup (cl:flavodoxin:flavodoxin homology) (db:pir2.dat) E69866 E69866 Bacillus subtilis 1423 -11530733 6000689670 ykup ykup protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to flavodoxins) (le:22771) (re:23307) (di:direct) BS16829KB AJ222587 g2632237 Bacillus subtilis 1423 -11530733 7500965240 ykup (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to sulfite reductase) (le:93027) (re:93563) (di:direct) BSUB0008 Z99111 g2633788 Bacillus subtilis 1423 -11530733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790616	4041	26197	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790618	4042	26198	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790648	4043	26199	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790653	4044	26200	681	226

Description

6500726876 hypothetical protein:similar to hippurate hydrolase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuR ykuR Bacillus subtilis 1423 -11530734 7000693093 ykur hippurate hydrolase homolog ykur (cl:hippurate hydrolase) (db:pir2.dat) G69866 G69866 Bacillus subtilis 1423 -11530734 6000689674 ykur ykur protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to amino acid hydrolases) (le:24112) (re:25236) (di:direct) BS16829KB AJ222587 g2632239 Bacillus subtilis 1423 -11530734 7500964051 ykur (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hippurate hydrolase) (le:94368) (re:95492) (di:direct) BSUB0008 Z99111 g2633790 Bacillus subtilis 1423 -11530734

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790659	4045	26201	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790662	4046	26202	798	265

Description

GTC ORF with score 93 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, essa i ap2 contig fragmentno. 1.) (nt:similarity to ste11 proteine kinase homolog npk1,) (le:143936:144267:144762) (re:144206:144704:144843) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790683	4047	26203	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501790690	4048	26204	1122	374

Description

GTC ORF with score 173 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone t16h5 (essaiiproject).) (nt:similarity to ari protein - drosophila) (le:8984:9652:10521) (re:9392:10418:10943) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791111	4049	26205	411	136

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791112	4050	26206	552	183

Description

6500726877 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuS ykuS Bacillus subtilis 1423 -11530735 7000693440 ykus hypothetical protein ykus (db:pir2.dat) H69866 H69866 Bacillus subtilis 1423 -11530735 6000689676 ykus ykus protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:25298) (re:25543) (di:direct) BS16829KB AJ222587 g2632240 Bacillus subtilis 1423 -11530735 7500964395 ykus (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:95554) (re:95799) (di:direct) BSUB0008 Z99111 g2633791 Bacillus subtilis 1423 -11530735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791117	4051	26207	774	257

Description

6500726878 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuT ykuT Bacillus subtilis 1423 -11530736 7000692601 ykut conserved hypothetical protein ykut (db:pir2.dat) A69867 A69867 Bacillus subtilis 1423 -11530736 6000689678 ykut ykut protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:25580) (re:26383) (di:complement) BS16829KB AJ222587 g2632241 Bacillus subtilis 1423 -11530736 7500963719 ykut (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:95836) (re:96639) (di:complement) BSUB0008 Z99111 g2633792 Bacillus subtilis 1423 -11530736

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791125	4052	26208	228	75

Description

6500726879 hypothetical protein:similar to 2-cys peroxiredoxin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuU ykuU Bacillus subtilis 1423 -11530737 7000692036 ykuu 2-cys peroxiredoxin homolog ykuu (cl:alkyl hydroperoxide reductase c22 protein:alkyl hydroperoxidase c22 protein homology) (db:pir2.dat) B69867 B69867 Bacillus subtilis 1423 -11530737 6000689680 ykuu ykuu protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (nt:homologous to thiol-specific antioxidant proteins) (le:26620) (re:27162) (di:direct) BS16829KB AJ222587 g2632242 Bacillus subtilis 1423 -11530737 7500963288 ykuu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to 2-cys peroxiredoxin) (le:96876) (re:97418) (di:direct) BSUB0008 Z99111 g2633793 Bacillus subtilis 1423 -11530737

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791129	4053	26209	705	234

Description

6500726880 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuV ykuV Bacillus subtilis 1423 -11530738 7000692602 ykuv conserved hypothetical protein ykuv (db:pir2.dat) C69867 C69867 Bacillus subtilis 1423 -11530738 7500963720 ykuv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:97490) (re:97951) (di:direct) BSUB0008 Z99111 g2633794 Bacillus subtilis 1423 -11530738

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791140	4054	26210	1026	341

Description

GTC ORF with score 316 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid b0252.) (nt:similar to sphingomyelin phosphodiesterase) (le:10366:10610:10737:11041) (re:10558:10694:10854:11596) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791155	4055	26211	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791161	4056	26212	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791172	4057	26213	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791194	4058	26214	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791195	4059	26215	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791211	4060	26216	747	248

Description

6500726881 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykuW ykuW Bacillus subtilis 1423 -11530739 7000693441 ykuw hypothetical protein ykuw (db:pir2.dat) D69867 D69867 Bacillus subtilis 1423 -11530739 6000689683 ykuw ykuw protein (db:genpept-bct1) (de:bacillus subtilis 29kb dna fragment from ykwc gene to cse15 gene.) (le:28145) (re:28720) (di:direct) BS16829KB AJ222587 g2632244 Bacillus subtilis 1423 -11530739 7500964396 ykuw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:98402) (re:98977) (di:direct) BSUB0008 Z99111 g2633795 Bacillus subtilis 1423 -11530739

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791218	4061	26217	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791229	4062	26218	1269	423

Description

6500726882 cse15:yknt hypothetical protein:similar to sporulation protein sigma-e-controlled (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknT yknT Bacillus subtilis 1423 -11530740 7000693419 yknt hypothetical protein yknt (db:pir2.dat) G69857 G69857 Bacillus subtilis 1423 -11530740 7500964372 yknt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: cse15; similar to sporulation) (le:99018) (re:99983) (di:complement) BSUB0008 Z99111 g2633796 Bacillus subtilis 1423 -11530740

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791247	4063	26219	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791267	4064	26220	444	148

Description

6500726883 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknU yknU Bacillus subtilis 1423 -11530741 7000692091 yknu abc transporter atp-binding protein homolog yknu (cl:atp-binding cassette homology) (db:pir2.dat) H69857 H69857 Bacillus subtilis 1423 -11530741 7500963331 yknu yknu (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to hypothetical abc transporter ywja from) (le:4992) (re:6749) (di:direct) AF012285 AF012285 g3282116 Bacillus subtilis 1423 -11530741 7500963330 yknu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to abc transporter (atp-binding protein)) (le:104504) (re:106261) (di:direct) BSUB0008 Z99111 g2633803 Bacillus subtilis 1423 -11530741

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791271	4065	26221	846	281

Description

6500726884 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknV yknV Bacillus subtilis 1423 -11530742 7000692092 yknv abc transporter atp-binding protein homolog yknv (cl:atp-binding cassette homology) (db:pir2.dat) A69858 A69858 Bacillus subtilis 1423 -11530742 7500963333 yknv yknv (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to hypothetical abc transporter ywja from) (le:6761) (re:8575) (di:direct) AF012285 AF012285 g3282117 Bacillus subtilis 1423 -11530742 7500963332 yknv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to abc transporter (atp-binding protein)) (le:106273) (re:108087) (di:direct) BSUB0008 Z99111 g2633804 Bacillus subtilis 1423 -11530742

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791285	4066	26222	258	85

Description

6500726885 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknW yknW Bacillus subtilis 1423 -11530743 7000693420 yknw hypothetical protein yknw (db:pir2.dat) B69858 B69858 Bacillus subtilis 1423 -11530743 7500964374 yknw yknw (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (le:8685) (re:9380) (di:direct) AF012285 AF012285 g3282118 Bacillus subtilis 1423 -11530743 7500964373 yknw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:108197) (re:108892) (di:direct) BSUB0008 Z99111 g2633805 Bacillus subtilis 1423 -11530743

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791286	4067	26223	1128	375

Description

GTC ORF with score 172 to: (sr:streptomyces hygroscopicus (tissue library: atcc 21705) dna) (db:genpept-bct1) (de:streptomyces hygroscopicus acetyl-hydrolase (bah), thioesterase(orf1 and 2), transport protein (orf3), and regulatory protein(brpa) genes,...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791297	4068	26224	312	103

Description

6500726886 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknX yknX Bacillus subtilis 1423 -11530744 7000692582 yknx conserved hypothetical protein yknx (db:pir2.dat) C69858 C69858 Bacillus subtilis 1423 -11530744 7500963701 yknx yknx (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (le:9385) (re:10518) (di:direct) AF012285 AF012285 g3282119 Bacillus subtilis 1423 -11530744 7500963700 yknx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:108897) (re:110030) (di:direct) BSUB0008 Z99111 g2633806 Bacillus subtilis 1423 -11530744

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791301	4069	26225	222	73

Description

6500726887 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknY yknY Bacillus subtilis 1423 -11530745 7000692093 ykny abc transporter atp-binding protein homolog ykny (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) D69858 D69858 Bacillus subtilis 1423 -11530745 7500955272 ykny ykny (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to glutamine transport atp-binding protein) (le:10519) (re:11211) (di:direct) AF012285 AF012285 g3282120 Bacillus subtilis 1423 -11530745 7500955271 ykny (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to abc transporter (atp-binding protein)) (le:110031) (re:110723) (di:direct) BSUB0008 Z99111 g2633807 Bacillus subtilis 1423 -11530745

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791321	4070	26226	408	135

Description

6500726888 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yknZ yknZ Bacillus subtilis 1423 -11530746 7000692583 yknz conserved hypothetical protein yknz (db:pir2.dat) E69858 E69858 Bacillus subtilis 1423 -11530746 7500963703 yknz yknz (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to b. subtilus yzib, swiss-prot accession) (le:11208) (re:12401) (di:direct) AF012285 AF012285 g3282122 Bacillus subtilis 1423 -11530746 7500963702 yknz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:110720) (re:111913) (di:direct) BSUB0008 Z99111 g2633808 Bacillus subtilis 1423 -11530746

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791322	4071	26227	375	125

Description

6500726889 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykoA ykoA Bacillus subtilis 1423 -11530747 7000693421 ykoa hypothetical protein ykoa (db:pir2.dat) F69858 F69858 Bacillus subtilis 1423 -11530747 7500964376 ykoa ykoa (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to orfs in b. amyloliquifaciens, encoded by) (le:17026) (re:17295) (di:complement) AF012285 AF012285 g3282127 Bacillus subtilis 1423 -11530747 7500964375 ykoa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:116538) (re:116807) (di:complement) BSUB0008 Z99111 g2633813 Bacillus subtilis 1423 -11530747

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791323	4072	26228	519	172

Description

6500726890 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykpA ykpA Bacillus subtilis 1423 -11530748 7000692094 ykpa abc transporter atp-binding protein homolog ykpa (cl:atp-binding cassette homology) (db:pir2.dat) E69861 E69861 Bacillus subtilis 1423 -11530748 7500963335 ykpa ykpa (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to e. coli hypothetical abc transporter) (le:17476) (re:19098) (di:direct) AF012285 AF012285 g3282128 Bacillus subtilis 1423 -11530748 7500963334 ykpa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to abc transporter (atp-binding protein)) (le:116988) (re:118610) (di:direct) BSUB0008 Z99111 g2633814 Bacillus subtilis 1423 -11530748

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791336	4073	26229	363	120

Description

6500726891 hypothetical protein:similar to thiamin biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykpB ykpB Bacillus subtilis 1423 -11530749 7000694674 ykpb thiamin biosynthesis homolog ykpb (db:pir2.dat) F69861 F69861 Bacillus subtilis 1423 -11530749 7500965259 ykpb ykpb (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to partial orf in 3' flank of) (le:19155) (re:20066) (di:direct) AF012285 AF012285 g3282129 Bacillus subtilis 1423 -11530749 7500965258 ykpb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to thiamin biosynthesis) (le:118667) (re:119578) (di:direct) BSUB0008 Z99111 g2633815 Bacillus subtilis 1423 -11530749

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791364	4074	26230	909	302

Description

6500726892 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykpC ykpC Bacillus subtilis 1423 -11530750 7000692590 ykpc conserved hypothetical protein ykpc (db:pir2.dat) G69861 G69861 Bacillus subtilis 1423 -11530750 7500963709 ykpc unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (le:21442) (re:21576) (di:complement) AF012285 AF012285 g3282131 Bacillus subtilis 1423 -11530750 220070 ykpc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:120954) (re:121088) (di:complement) BSUB0008 Z99111 g2633817 Bacillus subtilis 1423 -11530750

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791367	4075	26231	339	112

Description

5000689590 ylxu:yzab:ykqa hypothetical protein:hypothetical 31.7 kd protein in kinc-adec intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykqA ykqA Bacillus subtilis 1423 -11530751 114491 ykqa (de:hypothetical 31.7 kd protein in kinc-adec intergenic region (orf3)) (db:swissprot) YKQA_BACSU P39759 BACILLUS SUBTILIS 1423 -11530751 7000688110 ykqa conserved hypothetical protein ykqa (db:pir2.dat) I39872 I39872 Bacillus subtilis 1423 -11530751 220074 unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to products of orf3 encoded by genbank) (le:24738) (re:25571) (di:direct) AF012285 AF012285 g3282135 Bacillus subtilis 1423 -11530751 7500938606 orf3 (sr:bacillus subtilis (sub_species:marburg, strain:168) (db:genpept-bct1) (de:bacillus subtilis genes for amps, mrebh, orf1, kinc, orf3, orf4 andorf5.) (le:4279) (re:5112) (di:direct) BACAMOKOOO D37799 g1065988 Bacillus subtilis 1423 -11530751 215165 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:bacillus subtilis sensor kinase (kinc) gene, complete cds andcomplete orf.) (nt:orf) (le:1485) (re:2318) (di:direct) BACKINC L34803 g514331 Bacillus subtilis 1423 -11530751 216264 ykqa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ylxu, yzab; similar to) (le:124250) (re:125083) (di:direct) BSUB0008 Z99111 g2633821 Bacillus subtilis 1423 -11530751 170095 ykqa conserved hypothetical protein ykqa (db:pir) I39872 I39872 Bacillus subtilis 1423 -11530751 6500726893 ylxu:yzab hypothetical protein:hypothetical 31.7 kd protein in kinc-adec intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykqA ykqA Bacillus subtilis 1423 -11530751

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791380	4076	26232	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791404	4077	26233	564	187

Description

5000689591 ylxv:yzac:ykqb hypothetical protein:hypothetical 24.3 kd protein in kinc-adec intergenic region:orf4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykqB ykqB Bacillus subtilis 1423 -11530752 114492 ykqb (de:hypothetical 24.3 kd protein in kinc-adec intergenic region (orf4)) (db:swissprot) YKQB_BACSU P39760 BACILLUS SUBTILIS 1423 -11530752 7000688111 ykqb conserved hypothetical protein ykqb (cl:conserved hypothetical protein mg323) (db:pir2.dat) A69862 A69862 Bacillus subtilis 1423 -11530752 7500938607 ykqa unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to product of orf4 encoded by genbank) (le:25634) (re:26299) (di:direct) AF012285 AF012285 g3282136 Bacillus subtilis 1423 -11530752 215166 orf4 (sr:bacillus subtilis (sub_species:marburg, strain:168) (db:genpept-bct1) (de:bacillus subtilis genes for amps, mrebh, orf1, kinc, orf3, orf4 andorf5.) (le:5175) (re:5840) (di:direct) BACAMOKOOO D37799 g520844 Bacillus subtilis 1423 -11530752 220075 ykqb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ylxv, yzac; similar to) (le:125146) (re:125811) (di:direct) BSUB0008 Z99111 g2633822 Bacillus subtilis 1423 -11530752 6500726894 ylxv:yzac hypothetical protein:hypothetical 24.3 kd protein in kinc-adec intergenic region:orf4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykqB ykqB Bacillus subtilis 1423 -11530752

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791412	4078	26234	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791418	4079	26235	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791431	4080	26236	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791435	4081	26237	693	230

Description

6500726895 hypothetical protein:hypothetical 61.5 kd protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykqC ykqC Bacillus subtilis 1423 -11530753 5500686610 ykqc (de:hypothetical 61.5 kd protein in adec-pdha intergenic region) (db:swissprot) YKQC_BACSU Q45493 BACILLUS SUBTILIS 1423 -11530753 7000688112 ykqc conserved hypothetical protein ykqc (cl:conserved hypothetical protein mg139) (db:pir2.dat) B69862 B69862 Bacillus subtilis 1423 -11530753 7500938608 ykqc unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to aminopeptidase amps with swiss-prot) (le:28221) (re:29888) (di:complement) AF012285 AF012285 g3282138 Bacillus subtilis 1423 -11530753 220077 ykqc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:127733) (re:129400) (di:complement) BSUB0008 Z99111 g2633824 Bacillus subtilis 1423 -11530753

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791442	4082	26238	486	161

Description

6500726896 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzG ykzG Bacillus subtilis 1423 -11530754 7000693451 ykzg hypothetical protein ykzg (db:pir2.dat) D69871 D69871 Bacillus subtilis 1423 -11530754 7500964406 ykzg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:129406) (re:129615) (di:complement) BSUB0008 Z99111 g2633825 Bacillus subtilis 1423 -11530754

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791446	4083	26239	435	144

Description

6500726897 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykrA ykrA Bacillus subtilis 1423 -11530755 7000692591 ykra conserved hypothetical protein ykra (db:pir2.dat) C69862 C69862 Bacillus subtilis 1423 -11530755 7500963710 ykra unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar in c-terminus to partial sequence of orf1) (le:30489) (re:31262) (di:direct) AF012285 AF012285 g3282139 Bacillus subtilis 1423 -11530755 220078 ykra (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:130001) (re:130774) (di:direct) BSUB0008 Z99111 g2633826 Bacillus subtilis 1423 -11530755

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791457	4084	26240	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791465	4085	26241	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791466	4086	26242	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791477	4087	26243	1464	488

Description

6500726898 ykrc:ykya hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykyA ykyA Bacillus subtilis 1423 -11530756 7000692609 ykya conserved hypothetical protein ykya:hypothetical protein acea 5 region (db:pir2.dat) D69870 D69870 Bacillus subtilis 1423 -11530756 7500963726 ykrc unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to orf5 encoded by genbank accession) (le:32388) (re:33005) (di:direct) AF012285 AF012285 g3282141 Bacillus subtilis 1423 -11530756 220080 ykya (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: ykrc; similar to hypothetical) (le:131900) (re:132517) (di:direct) BSUB0008 Z99111 g2633828 Bacillus subtilis 1423 -11530756

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791481	4088	26244	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791484	4089	26245	1125	374

Description

6500726899 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yktA yktA Bacillus subtilis 1423 -11530757 7000693432 ykta hypothetical protein ykta (db:pir2.dat) C69864 C69864 Bacillus subtilis 1423 -11530757 7500964387 ykta unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (le:41039) (re:41305) (di:direct) AF012285 AF012285 g3282148 Bacillus subtilis 1423 -11530757 220087 ykta (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:140551) (re:140817) (di:direct) BSUB0008 Z99111 g2633835 Bacillus subtilis 1423 -11530757

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791489	4090	26246	579	192

Description

6500726900 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yktB yktB Bacillus subtilis 1423 -11530758 7000693433 yktb hypothetical protein yktb (db:pir2.dat) D69864 D69864 Bacillus subtilis 1423 -11530758 7500964388 yktb unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (le:41338) (re:41976) (di:complement) AF012285 AF012285 g3282149 Bacillus subtilis 1423 -11530758 220088 yktb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:140850) (re:141488) (di:complement) BSUB0008 Z99111 g2633836 Bacillus subtilis 1423 -11530758

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791496	4091	26247	477	158

Description

6500726901 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzI ykzI Bacillus subtilis 1423 -11530759 7000693453 ykzi hypothetical protein ykzi (db:pir2.dat) F69871 F69871 Bacillus subtilis 1423 -11530759 7500964408 ykzi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:141728) (re:141916) (di:direct) BSUB0008 Z99111 g2633837 Bacillus subtilis 1423 -11530759

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791501	4092	26248	195	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791971	4093	26249	513	170

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791974	4094	26250	276	91

Description

6500726902 hypothetical protein:similar to myo-inositol-1:or 4-monophosphatase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yktC yktC Bacillus subtilis 1423 -11530760 7502851681 suhb (de:extragenic suppressor protein suhb homolog) (db:swissprot) SUHB_BACSU Q45499 BACILLUS SUBTILIS 1423 -11530760 7000694273 yktc myo-inositol-1 or 4 -monophosphatase homolog yktc (cl:suppressor protein suhb) (db:pir2.dat) E69864 E69864 Bacillus subtilis 1423 -11530760 7500964989 yktc unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (nt:similar to e. coli extragenic suppressor protein) (le:42544) (re:43341) (di:direct) AF012285 AF012285 g3282150 Bacillus subtilis 1423 -11530760 220089 yktc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to myo-inositol-1(or 4)-monophosphatase) (le:142056) (re:142853) (di:direct) BSUB0008 Z99111 g2633838 Bacillus subtilis 1423 -11530760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791979	4095	26251	357	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791982	4096	26252	774	258

Description

6500726903 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ykzC ykzC Bacillus subtilis 1423 -11530761 7000693448 ykzc hypothetical protein ykzc (db:pir2.dat) H69870 H69870 Bacillus subtilis 1423 -11530761 7500964403 ykzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:142879) (re:143307) (di:direct) BSUB0008 Z99111 g2633839 Bacillus subtilis 1423 -11530761

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501791992	4097	26253	507	168

Description

GTC ORF with score 605 to: (sr:aspergillus terreus (strain:imi16043) dna, clone_lib:lamda zapii) (db:genpept-pln1) (de:aspergillus terreus dhgo gene for dihydrogeodin oxidase, completecds (exon1-7).) (nt:copper binding site: 1224..1238, 1414..1431,) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792007	4098	26254	1281	427

Description

6500726904 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yktD yktD Bacillus subtilis 1423 -11530762 7000693434 yktd hypothetical protein yktd (db:pir2.dat) F69864 F69864 Bacillus subtilis 1423 -11530762 7500964389 yktd unknown (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis moba-npre gene region.) (le:43873) (re:44787) (di:complement) AF012285 AF012285 g3282151 Bacillus subtilis 1423 -11530762 220090 yktd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:143385) (re:144299) (di:complement) BSUB0008 Z99111 g2633840 Bacillus subtilis 1423 -11530762

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792013	4099	26255	660	219

Description

6500726905 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaA ylaA Bacillus subtilis 1423 -11530763 7000693454 ylaa hypothetical protein ylaa (db:pir2.dat) G69871 G69871 Bacillus subtilis 1423 -11530763 4000714666 ylaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:146501) (re:148441) (di:direct) BSUB0008 Z99111 g2633842 Bacillus subtilis 1423 -11530763 7500964409 ylaa (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:760) (re:2700) (di:direct) BSZ97025 Z97025 g2224760 Bacillus subtilis 1423 -11530763

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792016	4100	26256	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792020	4101	26257	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792024	4102	26258	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792025	4103	26259	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792039	4104	26260	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792043	4105	26261	519	173

Description

6500726906 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaB ylaB Bacillus subtilis 1423 -11530764 7000693455 ylab hypothetical protein ylab (db:pir2.dat) H69871 H69871 Bacillus subtilis 1423 -11530764 4000714667 ylab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:148431) (re:148700) (di:direct) BSUB0008 Z99111 g2633843 Bacillus subtilis 1423 -11530764 7500964410 ylab (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:2690) (re:2959) (di:direct) BSZ97025 Z97025 g2224761 Bacillus subtilis 1423 -11530764

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792055	4106	26262	207	68

Description

6500726907 hypothetical protein:similar to rna polymerase ecf-type sigma factor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaC ylaC Bacillus subtilis 1423 -11530765 7000694555 ylac rna polymerase ecf-type sigma factor homolog ylac (db:pir2.dat) A69872 A69872 Bacillus subtilis 1423 -11530765 4000714668 ylac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to rna polymerase ecf-type sigma factor) (le:148700) (re:149221) (di:direct) BSUB0008 Z99111 g2633844 Bacillus subtilis 1423 -11530765 7500965167 ylac (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (nt:encodes putative rna polymerase sigma factor,) (le:2959) (re:3480) (di:direct) BSZ97025 Z97025 g2224762 Bacillus subtilis 1423 -11530765

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792058	4107	26263	213	70

Description

6500726908 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaD ylaD Bacillus subtilis 1423 -11530766 7000693456 ylad hypothetical protein ylad (db:pir2.dat) B69872 B69872 Bacillus subtilis 1423 -11530766 4000714669 ylad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:149218) (re:149511) (di:direct) BSUB0008 Z99111 g2633845 Bacillus subtilis 1423 -11530766 7500964411 ylad (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (nt:product similar to b. subtilis ybbm gene product) (le:3477) (re:3770) (di:direct) BSZ97025 Z97025 g2224763 Bacillus subtilis 1423 -11530766

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792059	4108	26264	210	69

Description

6500726909 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaE ylaE Bacillus subtilis 1423 -11530767 7000693457 ylae hypothetical protein ylae (db:pir2.dat) C69872 C69872 Bacillus subtilis 1423 -11530767 4000714670 ylae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:149551) (re:150162) (di:complement) BSUB0008 Z99111 g2633846 Bacillus subtilis 1423 -11530767 7500964412 ylae (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:3810) (re:4421) (di:complement) BSZ97025 Z97025 g2224764 Bacillus subtilis 1423 -11530767

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792061	4109	26265	1113	371

Description

6500726910 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaF ylaF Bacillus subtilis 1423 -11530768 7000693458 ylaf hypothetical protein ylaf (db:pir2.dat) D69872 D69872 Bacillus subtilis 1423 -11530768 4000714671 ylaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:150435) (re:150623) (di:complement) BSUB0008 Z99111 g2633847 Bacillus subtilis 1423 -11530768 7500964413 ylaf (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:4694) (re:4882) (di:complement) BSZ97025 Z97025 g2224765 Bacillus subtilis 1423 -11530768

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792062	4110	26266	273	90

Description

6500726911 hypothetical protein:similar to gtp-binding elongation factor (gtcfc:10.7) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaG ylaG Bacillus subtilis 1423 -11530769 4000714672 typa (de:gtp-binding protein typa/bipa homolog) (db:swissprot) TYPA_BACSU O07631 BACILLUS SUBTILIS 1423 -11530769 7000693076 ylag gtp-binding elongation factor homolog ylag (cl:translation elongation factor tu homology) (db:pir2.dat) E69872 E69872 Bacillus subtilis 1423 -11530769 7500893594 ylag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to gtp-binding elongation factor) (le:150736) (re:152574) (di:direct) BSUB0008 Z99111 g2633848 Bacillus subtilis 1423 -11530769 7502851682 ylag (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (nt:product highly similar to elongation factor ef-g) (le:4995) (re:6833) (di:direct) BSZ97025 Z97025 g2224766 Bacillus subtilis 1423 -11530769 7500893592 typa (de:gtp-binding protein typa/bipa homolog) (db:swissprot) TYPA_BACSU O07631 BACILLUS SUBTILIS 1423 -11530769

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792065	4111	26267	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792078	4112	26268	264	87

Description

6500726912 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaH ylaH Bacillus subtilis 1423 -11530770 7000693459 ylah hypothetical protein ylah (db:pir2.dat) F69872 F69872 Bacillus subtilis 1423 -11530770 4000714673 ylah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:152631) (re:152948) (di:direct) BSUB0008 Z99111 g2633849 Bacillus subtilis 1423 -11530770 7500964414 ylah (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:6890) (re:7207) (di:direct) BSZ97025 Z97025 g2224767 Bacillus subtilis 1423 -11530770

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792085	4113	26269	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792090	4114	26270	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792098	4115	26271	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792113	4116	26272	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792129	4117	26273	549	182

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792130	4118	26274	537	178

Description

6500726913 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaI ylaI Bacillus subtilis 1423 -11530771 7000693460 ylai hypothetical protein ylai (db:pir2.dat) G69872 G69872 Bacillus subtilis 1423 -11530771 4000714674 ylai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:153004) (re:153213) (di:complement) BSUB0008 Z99111 g2633850 Bacillus subtilis 1423 -11530771 7500964415 ylai (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:7263) (re:7472) (di:complement) BSZ97025 Z97025 g2224768 Bacillus subtilis 1423 -11530771

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792141	4119	26275	894	297

Description

6500726914 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaJ ylaJ Bacillus subtilis 1423 -11530772 7000692611 ylaj conserved hypothetical protein ylaj (db:pir2.dat) H69872 H69872 Bacillus subtilis 1423 -11530772 4000714675 ylaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:153296) (re:153925) (di:complement) BSUB0008 Z99111 g2633851 Bacillus subtilis 1423 -11530772 7500963728 ylaj (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (nt:product similar to b. subtilis yhcn hypothetical) (le:7555) (re:8184) (di:complement) BSZ97025 Z97025 g2224769 Bacillus subtilis 1423 -11530772

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792142	4120	26276	789	262

Description

6500726915 hypothetical protein:similar to phosphate starvation inducible protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaK ylaK Bacillus subtilis 1423 -11530773 7000694399 ylak phosphate starvation inducible protein homolog ylak (db:pir2.dat) A69873 A69873 Bacillus subtilis 1423 -11530773 4000714676 ylak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to phosphate starvation inducible protein) (le:154080) (re:155408) (di:direct) BSUB0008 Z99111 g2633852 Bacillus subtilis 1423 -11530773 7500965065 ylak (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (nt:product similar to e. coli phoh protein) (le:8339) (re:9667) (di:direct) BSZ97025 Z97025 g2224770 Bacillus subtilis 1423 -11530773

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792168	4121	26277	480	159

Description

6500726916 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaL ylaL Bacillus subtilis 1423 -11530774 7000693461 ylal hypothetical protein ylal (db:pir2.dat) B69873 B69873 Bacillus subtilis 1423 -11530774 4000714677 ylal (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:155412) (re:155897) (di:complement) BSUB0008 Z99111 g2633853 Bacillus subtilis 1423 -11530774 7500964416 ylal (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:9671) (re:10156) (di:complement) BSZ97025 Z97025 g2224771 Bacillus subtilis 1423 -11530774

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792191	4122	26278	774	257

Description

6500726917 hypothetical protein:hypothetical 34.0 kd protein ylam (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaM ylaM Bacillus subtilis 1423 -11530775 7500950933 ylam (de:hypothetical 34.0 kd protein in npre-pyca intergenic region) (db:swissprot) YLAM_BACSU O07637 BACILLUS SUBTILIS 1423 -11530775 7000688116 ylam glutaminase homolog ylam (cl:hypothetical protein b1524) (db:pir2.dat) C69873 C69873 Bacillus subtilis 1423 -11530775 4000714678 ylam (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to glutaminase) (le:156000) (re:156929) (di:direct) BSUB0008 Z99111 g2633854 Bacillus subtilis 1423 -11530775 7502851683 ylam (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (nt:putative glutaminase) (le:10259) (re:11188) (di:direct) BSZ97025 Z97025 g2224772 Bacillus subtilis 1423 -11530775 5500686616 ylam (de:hypothetical 34.0 kd protein in npre-pyca intergenic region) (db:swissprot) YLAM_BACSU O07637 BACILLUS SUBTILIS 1423 -11530775

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792199	4123	26279	705	234

Description

6500726918 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaN ylaN Bacillus subtilis 1423 -11530776 7000693462 ylan hypothetical protein ylan (db:pir2.dat) D69873 D69873 Bacillus subtilis 1423 -11530776 4000714679 ylan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:157027) (re:157308) (di:direct) BSUB0008 Z99111 g2633855 Bacillus subtilis 1423 -11530776 7500964417 ylan (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (le:11286) (re:11567) (di:direct) BSZ97025 Z97025 g2224773 Bacillus subtilis 1423 -11530776

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792212	4124	26280	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792213	4125	26281	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792217	4126	26282	384	128

Description

6500726919 hypothetical protein:hypothetical 43.7 kd protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylaO ylaO Bacillus subtilis 1423 -11530777 7500950934 ylao (de:hypothetical 43.7 kd protein in npre-pyca intergenic region) (db:swissprot) YLAO_BACSU O07639 BACILLUS SUBTILIS 1423 -11530777 7000688117 ylao cell-division protein homolog ylao (cl:rod shape-determining protein) (db:pir2.dat) E69873 E69873 Bacillus subtilis 1423 -11530777 4000714680 ylao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to cell-division protein) (le:157514) (re:158725) (di:direct) BSUB0008 Z99111 g2633856 Bacillus subtilis 1423 -11530777 7502851684 ylao (db:genpept-bct1) (de:bacillus subtilis npre, yla(a,b,c,d,e,f,g,h,i,j,k,l,m,n,o) and pycagenes.) (nt:product similar to b. subtilis spove protein and to) (le:11773) (re:12984) (di:direct) BSZ97025 Z97025 g2224774 Bacillus subtilis 1423 -11530777 5500686617 ylao (de:hypothetical 43.7 kd protein in npre-pyca intergenic region) (db:swissprot) YLAO_BACSU O07639 BACILLUS SUBTILIS 1423 -11530777

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792219	4127	26283	564	187

Description

6500726920 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ctaG ctaG Bacillus subtilis 1423 -11530778 7000693122 ctag hypothetical protein ctag (db:pir2.dat) H69609 H69609 Bacillus subtilis 1423 -11530778 5500687752 ctag ctag protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:9554) (re:10447) (di:direct) BS16823KB Z98682 g2339996 Bacillus subtilis 1423 -11530778 7500964070 ctag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:169037) (re:169930) (di:direct) BSUB0008 Z99111 g2633864 Bacillus subtilis 1423 -11530778

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792229	4128	26284	378	125

Description

GTC ORF with score 189 to: (fn:catalyzes hydroxylation at c-15 of) (db:genpept-pln1) (de:fusarium sporotrichioides isotrichodermin c-15 hydroxylase (tri11)gene, complete cds.) (nt:cytochrome p450 monooxygenase) (le:189:286:1132:1526:1757) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792232	4129	26285	228	75

Description

GTC ORF with score 96 to: (fn:activities of formation of isobutene and) (sr:rhodotorula minuta (strain:ifo1102) dna) (db:genpept-pln1) (de:rhodotorula minuta dna for isobutene-forming enzyme and benzoate4-hydroxylase, complete cds.) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792234	4130	26286	213	70

Description

GTC ORF with score 277 to: (fn:putative regulatory subunit of holoenzyme) (db:genpept-pln1) (de:ajellomyces capsulatus nad(+)-isocitrate dehydrogenase subunit i(idh1) mrna, nuclear gene encoding mitochondrial protein, completecds.) (nt:precursor form; ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792242	4131	26287	579	192

Description

6500726921 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbA ylbA Bacillus subtilis 1423 -11530779 7000693463 ylba hypothetical protein ylba (db:pir2.dat) F69873 F69873 Bacillus subtilis 1423 -11530779 5500687753 ylba ylba protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:10479) (re:10841) (di:complement) BS16823KB Z98682 g2339997 Bacillus subtilis 1423 -11530779 7500964418 ylba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:169962) (re:170324) (di:complement) BSUB0008 Z99111 g2633865 Bacillus subtilis 1423 -11530779

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792250	4132	26288	1437	479

Description

6500726922 hypothetical protein:similar to imp dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbB ylbB Bacillus subtilis 1423 -11530780 7000694104 ylbb yhcv-related protein ylbb:inosine-monophosphate dehydrogenase homolog misnomer (cl:conserved hypothetical protein yhcv:cbs homology) (db:pir2.dat) G69873 G69873 Bacillus subtilis 1423 -11530780 5500687754 ylbb ylbb protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:10981) (re:11433) (di:direct) BS16823KB Z98682 g2339998 Bacillus subtilis 1423 -11530780 7500953817 ylbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to imp dehydrogenase) (le:170464) (re:170916) (di:direct) BSUB0008 Z99111 g2633866 Bacillus subtilis 1423 -11530780

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792261	4133	26289	597	198

Description

6500726923 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbC ylbC Bacillus subtilis 1423 -11530781 7000692612 ylbc conserved hypothetical protein ylbc (db:pir2.dat) H69873 H69873 Bacillus subtilis 1423 -11530781 5500687755 ylbc ylbc protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:11510) (re:12550) (di:direct) BS16823KB Z98682 g2339999 Bacillus subtilis 1423 -11530781 7500963729 ylbc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:170993) (re:172033) (di:direct) BSUB0008 Z99111 g2633867 Bacillus subtilis 1423 -11530781

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792274	4134	26290	1044	348

Description

6500726924 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbD ylbD Bacillus subtilis 1423 -11530782 7000693464 ylbd hypothetical protein ylbd (db:pir2.dat) A69874 A69874 Bacillus subtilis 1423 -11530782 5500687756 ylbd ylbd protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:12782) (re:13180) (di:direct) BS16823KB Z98682 g2340000 Bacillus subtilis 1423 -11530782 7500964419 ylbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:172265) (re:172663) (di:direct) BSUB0008 Z99111 g2633868 Bacillus subtilis 1423 -11530782

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792280	4135	26291	765	254

Description

6500726925 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbE ylbE Bacillus subtilis 1423 -11530783 7000693465 ylbe hypothetical protein ylbe (db:pir2.dat) B69874 B69874 Bacillus subtilis 1423 -11530783 5500687757 ylbe ylbe protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:13196) (re:13435) (di:direct) BS16823KB Z98682 g2340001 Bacillus subtilis 1423 -11530783 7500964420 ylbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:172679) (re:172918) (di:direct) BSUB0008 Z99111 g2633869 Bacillus subtilis 1423 -11530783

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792291	4136	26292	309	103

Description

GTC ORF with score 145 to: (fn:an activator of nf-kappab and putative signal) (sr:mus musculus (strain:balb/c) female monocyte-macrophag) (db:genpept-rod) (de:mouse mrna for traf5 protein, complete cds.) (nt:traf(tnf receptor associated factor) family)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792294	4137	26293	339	112

Description

GTC ORF with score 112 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid zc13.) (nt:contains similarity to c3hc4-class zinc finger) (le:5218:5389:5611:6329) (re:5331:5512:6011:6436) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792305	4138	26294	414	137

Description

GTC ORF with score 94 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792307	4139	26295	1485	495

Description

6500726926 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbF ylbF Bacillus subtilis 1423 -11530784 7000692613 ylbf conserved hypothetical protein ylbf (db:pir2.dat) C69874 C69874 Bacillus subtilis 1423 -11530784 5500687758 ylbf ylbf protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:13551) (re:14000) (di:direct) BS16823KB Z98682 g2340002 Bacillus subtilis 1423 -11530784 7500963730 ylbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:173034) (re:173483) (di:direct) BSUB0008 Z99111 g2633870 Bacillus subtilis 1423 -11530784

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792330	4140	26296	624	207

Description

6500726927 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbG ylbG Bacillus subtilis 1423 -11530785 7000692614 ylbg conserved hypothetical protein ylbg (db:pir2.dat) D69874 D69874 Bacillus subtilis 1423 -11530785 5500687759 ylbg ylbg protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:14055) (re:14327) (di:direct) BS16823KB Z98682 g2340003 Bacillus subtilis 1423 -11530785 7500963731 ylbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:173538) (re:173810) (di:direct) BSUB0008 Z99111 g2633871 Bacillus subtilis 1423 -11530785

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792333	4141	26297	903	301

Description

6500726928 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbH ylbH Bacillus subtilis 1423 -11530786 7000692615 ylbh conserved hypothetical protein ylbh (db:pir2.dat) E69874 E69874 Bacillus subtilis 1423 -11530786 5500687760 ylbh ylbh protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:14650) (re:15144) (di:direct) BS16823KB Z98682 g2340004 Bacillus subtilis 1423 -11530786 7500963732 ylbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:174133) (re:174627) (di:direct) BSUB0008 Z99111 g2633872 Bacillus subtilis 1423 -11530786

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792334	4142	26298	672	223

Description

6500726929 hypothetical protein:similar to lipopolysaccharide core biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbI ylbI Bacillus subtilis 1423 -11530787 7000694168 ylbi lipopolysaccharide core biosynthesis homolog ylbi (cl:lipopolysaccharide core biosynthesis protein kdtb) (db:pir2.dat) F69874 F69874 Bacillus subtilis 1423 -11530787 5500687761 ylbi ylbi protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:15208) (re:15693) (di:direct) BS16823KB Z98682 g2340005 Bacillus subtilis 1423 -11530787 7500964899 ylbi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to lipopolysaccharide core biosynthesis) (le:174691) (re:175176) (di:direct) BSUB0008 Z99111 g2633873 Bacillus subtilis 1423 -11530787

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792341	4143	26299	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792342	4144	26300	1164	387

Description

6500726930 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbJ ylbJ Bacillus subtilis 1423 -11530788 7000693466 ylbj hypothetical protein ylbj (db:pir2.dat) G69874 G69874 Bacillus subtilis 1423 -11530788 5500687762 ylbj ylbj protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:15704) (re:16930) (di:complement) BS16823KB Z98682 g2340006 Bacillus subtilis 1423 -11530788 7500964421 ylbj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:175187) (re:176413) (di:complement) BSUB0008 Z99111 g2633874 Bacillus subtilis 1423 -11530788

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792360	4145	26301	1368	455

Description

6500726931 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbK ylbK Bacillus subtilis 1423 -11530789 7000692616 ylbk conserved hypothetical protein ylbk (db:pir2.dat) H69874 H69874 Bacillus subtilis 1423 -11530789 5500687763 ylbk ylbk protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:17111) (re:17893) (di:direct) BS16823KB Z98682 g2340007 Bacillus subtilis 1423 -11530789 7500963733 ylbk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:176594) (re:177376) (di:direct) BSUB0008 Z99111 g2633875 Bacillus subtilis 1423 -11530789

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792366	4146	26302	402	133

Description

6500726932 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbL ylbL Bacillus subtilis 1423 -11530790 7000693467 ylbl hypothetical protein ylbl (db:pir2.dat) A69875 A69875 Bacillus subtilis 1423 -11530790 5500687764 ylbl ylbl protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:17895) (re:18947) (di:direct) BS16823KB Z98682 g2340008 Bacillus subtilis 1423 -11530790 7500964422 ylbl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:177378) (re:178430) (di:direct) BSUB0008 Z99111 g2633876 Bacillus subtilis 1423 -11530790

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792368	4147	26303	423	140

Description

GTC ORF with score 151 to: (fn:binds to gtp-bound form of rho and binds to) (sr:house mouse) (db:genpept-rod) (de:mus musculus p140mdia mrna, complete cds.) (nt:a formin related polyproline protein; similar to) (le:94) (re:3861) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792371	4148	26304	267	88

Description

6500726933 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbM ylbM Bacillus subtilis 1423 -11530791 7000692617 ylbm conserved hypothetical protein ylbm (db:pir2.dat) B69875 B69875 Bacillus subtilis 1423 -11530791 5500687765 ylbm ylbm protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:18936) (re:20183) (di:complement) BS16823KB Z98682 g2340009 Bacillus subtilis 1423 -11530791 7500963734 ylbm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:178419) (re:179666) (di:complement) BSUB0008 Z99111 g2633877 Bacillus subtilis 1423 -11530791

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792865	4149	26305	882	294

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792873	4150	26306	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792882	4151	26307	804	267

Description

6500726934 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbN ylbN Bacillus subtilis 1423 -11530792 7000693468 ylbn hypothetical protein ylbn (db:pir2.dat) C69875 C69875 Bacillus subtilis 1423 -11530792 5500687766 ylbn ylbn protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:20393) (re:20911) (di:direct) BS16823KB Z98682 g2340010 Bacillus subtilis 1423 -11530792 7500964423 ylbn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:179876) (re:180394) (di:direct) BSUB0008 Z99111 g2633878 Bacillus subtilis 1423 -11530792

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792886	4152	26308	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792889	4153	26309	495	164

Description

6500726935 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbO ylbO Bacillus subtilis 1423 -11530793 7000692618 ylbo conserved hypothetical protein ylbo (cl:hypothetical protein ylbo) (db:pir2.dat) D69875 D69875 Bacillus subtilis 1423 -11530793 5500687768 ylbo ylbo protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:21258) (re:21839) (di:direct) BS16823KB Z98682 g2340012 Bacillus subtilis 1423 -11530793 7500955896 ylbo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins from b. subtilis) (le:180741) (re:181322) (di:direct) BSUB0008 Z99111 g2633880 Bacillus subtilis 1423 -11530793

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792908	4154	26310	333	111

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792915	4155	26311	1140	380

Description

6500726936 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbP ylbP Bacillus subtilis 1423 -11530794 7000693469 ylbp hypothetical protein ylbp (db:pir2.dat) E69875 E69875 Bacillus subtilis 1423 -11530794 5500687769 ylbp ylbp protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:21896) (re:22378) (di:complement) BS16823KB Z98682 g2340013 Bacillus subtilis 1423 -11530794 7500964424 ylbp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:181379) (re:181861) (di:complement) BSUB0008 Z99111 g2633881 Bacillus subtilis 1423 -11530794

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792934	4156	26312	735	244

Description

6500726937 hypothetical protein:similar to pyrimidine-thiamine biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylbQ ylbQ Bacillus subtilis 1423 -11530795 7502851685 apba (ec:1.1.1.169) (de:reductase) (kpa reductase)) (db:swissprot) APBA_BACSU O34661 BACILLUS SUBTILIS 1423 -11530795 7000694479 ylbq pyrimidine-thiamine biosynthesis homolog ylbq (db:pir2.dat) F69875 F69875 Bacillus subtilis 1423 -11530795 5500687770 ylbq ylbq protein (db:genpept-bct1) (de:bacillus subtilis genomic dna 23.9kb fragment.) (le:22538) (re:23434) (di:direct) BS16823KB Z98682 g2340014 Bacillus subtilis 1423 -11530795 7500965122 ylbq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to pyrimidine-thiamine biosynthesis) (le:182021) (re:182917) (di:direct) BSUB0008 Z99111 g2633882 Bacillus subtilis 1423 -11530795

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792944	4157	26313	243	80

Description

6500726938 hypothetical protein:hypothetical 62.6 kd protein in ftsl 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yllA yllA Bacillus subtilis 1423 -11530796 7000693470 ylla hypothetical protein ylla (db:pir2.dat) G69875 G69875 Bacillus subtilis 1423 -11530796 7500964425 ylla (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (le:182988) (re:184607) (di:direct) BSUB0008 Z99111 g2633883 Bacillus subtilis 1423 -11530796

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792947	4158	26314	471	156

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792964	4159	26315	216	71

Description

5000689195 hypothetical protein:hypothetical 16.6 kd protein in ftsl 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yllB yllB Bacillus subtilis 1423 -11530797 114413 yllb (de:hypothetical 16.6 kd protein in rpmf-ftsl intergenic region) (db:swissprot) YLLB_BACSU P55343 BACILLUS SUBTILIS 1423 -11530797 7000688134 yllb conserved hypothetical protein yllb (cl:hypothetical protein mg221) (db:pir2.dat) H69875 H69875 Bacillus subtilis 1423 -11530797 220245 yllb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:184733) (re:185164) (di:direct) BSUB0008 Z99111 g2633884 Bacillus subtilis 1423 -11530797 7500950990 yllb unknown (db:genpept-bct1) (de:b.subtilis ylla, yllb, yllc, ftsl, pbpb and spovd genes.) (le:1754) (re:2185) (di:direct) BSYLLSPO Z68230 g1122759 Bacillus subtilis 1423 -11530797 6500726939 hypothetical protein:hypothetical 16.6 kd protein in ftsl 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yllB yllB Bacillus subtilis 1423 -11530797

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792965	4160	26316	1146	382

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792974	4161	26317	915	305

Description

6500726940 yllc:ylxa hypothetical protein:hypothetical 35.3 kd protein in ftsl 5region:orfb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxA ylxA Bacillus subtilis 1423 -11530798 114475 ylxa:yllc (de:hypothetical 35.3 kd protein in ftsl 5'region (orfb)) (db:swissprot) YLXA_BACSU Q07876 BACILLUS SUBTILIS 1423 -11530798 7000688138 ylxa yabc protein homolog ylxa:pbpb 5-region hypothetical protein b (cl:escherichia coli yabc protein) (db:pir2.dat) D69881 D69881 Bacillus subtilis 1423 -11530798 220246 ylxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:alternate gene name: yllc; similar to hypothetical) (le:185234) (re:186169) (di:direct) BSUB0008 Z99111 g2633885 Bacillus subtilis 1423 -11530798 7500951008 yllc unknown (db:genpept-bct1) (de:b.subtilis ylla, yllb, yllc, ftsl, pbpb and spovd genes.) (le:2255) (re:3190) (di:direct) BSYLLSPO Z68230 g1122760 Bacillus subtilis 1423 -11530798 5000689577 (de:(ylxa) (pn:hypothetical 35:hypothetical protein in pbpb 5"region:orfb:fragment) (gn:yllc) (gtcfc:13.07) (ec:) (ylxa_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ylxA ylxA Bacillus subtilis 1423 10056201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792975	4162	26318	225	74

Description

6500726941 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxW ylxW Bacillus subtilis 1423 -11530799 170203 ylxw conserved hypothetical protein ylxw (db:pir2.dat) C43727 S26502 Bacillus subtilis 1423 -11530799 7500963748 (sr:bacillus subtilis (clone: lambda-bs1) dna) (db:genpept-bct1) (de:bacillus subtilis (clone lambda-bs1) cell division and sporulationprotein (dds) gene, complete cds.) (nt:orf4; putative) (le:2309) (re:3004) (di:direct) BACDDSA M31827 g1129091 Bacillus subtilis 1423 -11530799 215486 ylxw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:199098) (re:199793) (di:direct) BSUB0008 Z99111 g2633896 Bacillus subtilis 1423 -11530799 7000692636 ylxw conserved hypothetical protein ylxw (db:pir) C43727 C43727 Bacillus subtilis 1423 -11530799

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792976	4163	26319	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792978	4164	26320	264	87

Description

6500726942 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxX ylxX Bacillus subtilis 1423 -11530800 7000692637 ylxx hypothetical protein ylxx (db:pir2.dat) G69882 G69882 Bacillus subtilis 1423 -11530800 7500963749 ylxx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.) (nt:similar to hypothetical proteins) (le:199816) (re:200523) (di:direct) BSUB0008 Z99111 g2633897 Bacillus subtilis 1423 -11530800

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792979	4165	26321	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792981	4166	26322	747	248

Description

6500726943 hypothetical protein:similar to abc transporter:atp-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmA ylmA Bacillus subtilis 1423 -11530801 7000692095 ylma abc transporter atp-binding protein homolog ylma (cl:atp-binding cassette homology) (db:pir2.dat) A69876 A69876 Bacillus subtilis 1423 -11530801 7500963336 ylma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to abc transporter (atp-binding protein)) (le:7535) (re:8329) (di:direct) BSUB0009 Z99112 g2633907 Bacillus subtilis 1423 -11530801

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792984	4167	26323	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792985	4168	26324	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501792999	4169	26325	297	98

Description

6500726944 hypothetical protein:similar to acetylornithine deacetylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmB ylmB Bacillus subtilis 1423 -11530802 7000692143 ylmb acetylornithine deacetylase homolog ylmb (db:pir2.dat) B69876 B69876 Bacillus subtilis 1423 -11530802 7500963372 ylmb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to acetylornithine deacetylase) (le:8531) (re:9811) (di:direct) BSUB0009 Z99112 g2633908 Bacillus subtilis 1423 -11530802

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793000	4170	26326	1869	622

Description

6500726945 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmC ylmC Bacillus subtilis 1423 -11530803 7000692619 ylmc conserved hypothetical protein ylmc (cl:conserved hypothetical protein ymxh) (db:pir2.dat) C69876 C69876 Bacillus subtilis 1423 -11530803 7500963735 ylmc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:9894) (re:10139) (di:direct) BSUB0009 Z99112 g2633909 Bacillus subtilis 1423 -11530803

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793002	4171	26327	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793018	4172	26328	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793028	4173	26329	690	229

Description

GTC ORF with score 441 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 37 kb genomic dna, clone c213.) (nt:similar to s.cerevisiae hypothetical protein) (le:22026) (re:23384) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793029	4174	26330	585	194

Description

GTC ORF with score 305 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 37 kb genomic dna, clone c213.) (nt:similar to s.cerevisiae hypothetical protein) (le:22026) (re:23384) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793033	4175	26331	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793038	4176	26332	1167	389

Description

6500726946 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmD ylmD Bacillus subtilis 1423 -11530804 7000692620 ylmd conserved hypothetical protein ylmd (db:pir2.dat) D69876 D69876 Bacillus subtilis 1423 -11530804 7500963736 ylmd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:10302) (re:11138) (di:direct) BSUB0009 Z99112 g2633910 Bacillus subtilis 1423 -11530804

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793042	4177	26333	363	120

Description

6500726947 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmE ylmE Bacillus subtilis 1423 -11530805 7500950991 ylme (de:hypothetical 25.7 kd protein in sigg-diviva intergenic region) (db:swissprot) YLME_BACSU O31727 BACILLUS SUBTILIS 1423 -11530805 7000692621 ylme conserved hypothetical protein ylme (cl:conserved hypothetical protein hi0090) (db:pir2.dat) E69876 E69876 Bacillus subtilis 1423 -11530805 7500950993 ylme (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:11151) (re:11843) (di:direct) BSUB0009 Z99112 g2633911 Bacillus subtilis 1423 -11530805

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793047	4178	26334	1002	333

Description

6500726948 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmF ylmF Bacillus subtilis 1423 -11530806 7000692622 ylmf conserved hypothetical protein ylmf (db:pir2.dat) F69876 F69876 Bacillus subtilis 1423 -11530806 7500963737 ylmf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:11846) (re:12295) (di:direct) BSUB0009 Z99112 g2633912 Bacillus subtilis 1423 -11530806

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793049	4179	26335	201	66

Description

6500726949 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmG ylmG Bacillus subtilis 1423 -11530807 7000692623 ylmg conserved hypothetical protein ylmg (c1:conserved hypothetical protein ssr2142) (db:pir2.dat) G69876 G69876 Bacillus subtilis 1423 -11530807 7500963738 ylmg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:12302) (re:12574) (di:direct) BSUB0009 Z99112 g2633913 Bacillus subtilis 1423 -11530807

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793051	4180	26336	384	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793061	4181	26337	444	148

Description

6500726950 hypothetical protein:similar to cell-division protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylmH ylmH Bacillus subtilis 1423 -11530808 7000692348 ylmh cell-division protein homolog ylmh (db:pir2.dat) H69876 H69876 Bacillus subtilis 1423 -11530808 220148 (db:genpept-bct1) (de:bacillus subtilis minicell-associated protein (diviva) gene,complete cds, and isoleucyl-trna-synthetase (iles) gene, partialcds.) (nt:orf) (le:306) (re:1079) (di:direct) BSU60901 U60901 g1518679 Bacillus subtilis 1423 -11530808 297578 ylmh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to cell-division protein) (le:12635) (re:13408) (di:direct) BSUB0009 Z99112 g2633914 Bacillus subtilis 1423 -11530808

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793065	4182	26338	285	94

Description

6500726951 ylmk:ylya hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylyA ylyA Bacillus subtilis 1423 -11530809 7500951020 ylya (de:hypothetical 16.8 kd protein in iles-lsp intergenic region (orf-t)) (db:swissprot) YLYA_BACSU Q45478 BACILLUS SUBTILIS 1423 -11530809 7000692638 ylya conserved hypothetical protein ylya (db:pir2.dat) A69883 A69883 Bacillus subtilis 1423 -11530809 7500951022 ylya (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylmk; similar to hypothetical) (le:17181) (re:17624) (di:direct) BSUB0009 Z99112 g2633917 Bacillus subtilis 1423 -11530809

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793066	4183	26339	822	273

Description

6500726952 ylml:ylyb hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylyB ylyB Bacillus subtilis 1423 -11530810 7000692639 ylyb conserved hypothetical protein ylyb (cl:conserved hypothetical protein hi0176) (db:pir2.dat) B69883 B69883 Bacillus subtilis 1423 -11530810 7500963750 ylyb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylml; similar to hypothetical) (le:18193) (re:19014) (di:direct) BSUB0009 Z99112 g2633919 Bacillus subtilis 1423 -11530810

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793077	4184	26340	924	307

Description

6500726953 hypothetical protein:similar to anion permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylnA ylnA Bacillus subtilis 1423 -11530811 7000692208 ylna anion permease homolog ylna (db:pir2.dat) A69877 A69877 Bacillus subtilis 1423 -11530811 5500687775 ylna ylna protein (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (le:1261) (re:2325) (di:direct) BSPYREYLO AJ000974 g2462957 Bacillus subtilis 1423 -11530811 7500963415 ylna (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to anion permease) (le:32074) (re:33138) (di:direct) BSUB0009 Z99112 g2633931 Bacillus subtilis 1423 -11530811

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793094	4185	26341	537	178

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793099	4186	26342	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793102	4187	26343	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793103	4188	26344	300	99

Description

6500726954 hypothetical protein:similar to sulfate adenylyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylnB ylnB Bacillus subtilis 1423 -11530812 7000694654 ylnb sulfate adenylyltransferase homolog ylnb (cl:sulfate adenylyltransferase homology) (db:pir2.dat) B69877 B69877 Bacillus subtilis 1423 -11530812 5500687776 ylnb putative sulfate adenylyltransferase (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (le:2374) (re:3522) (di:direct) BSPYREYLO AJ000974 g2462958 Bacillus subtilis 1423 -11530812 7500965238 ylnb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to sulfate adenylyltransferase) (le:33187) (re:34335) (di:direct) BSUB0009 Z99112 g2633932 Bacillus subtilis 1423 -11530812

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793104	4189	26345	225	74

Description

6500726955 hypothetical protein:similar to adenylylsulfate kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylnC ylnC Bacillus subtilis 1423 -11530813 7000692159 ylnc adenylylsulfate kinase homolog ylnc (cl:adenylylsulfate kinase:adenylylsulfate kinase homology) (db:pir2.dat) C69877 C69877 Bacillus subtilis 1423 -11530813 5500687777 ylnc putative adenosine 5-phosphosulfate kinase (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (le:3535) (re:4128) (di:direct) BSPYREYLO AJ000974 g2462959 Bacillus subtilis 1423 -11530813 7500954076 ylnc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to adenylylsulfate kinase) (le:34348) (re:34941) (di:direct) BSUB0009 Z99112 g2633933 Bacillus subtilis 1423 -11530813

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793125	4190	26346	561	186

Description

6500726956 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylnE ylnE Bacillus subtilis 1423 -11530814 7000692624 ylne conserved hypothetical protein ylne (cl:conserved hypothetical protein ylne) (db:pir2.dat) E69877 E69877 Bacillus subtilis 1423 -11530814 5500687779 ylne ylne protein (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (le:5003) (re:5788) (di:direct) BSPYREYLO AJ000974 g2462961 Bacillus subtilis 1423 -11530814 7500963739 ylne (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:35816) (re:36601) (di:direct) BSUB0009 Z99112 g2633935 Bacillus subtilis 1423 -11530814

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793132	4191	26347	666	221

Description

6500726957 hypothetical protein:similar to uroporphyrin-iii c-methyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylnF ylnF Bacillus subtilis 1423 -11530815 7000694896 ylnf uroporphyrin-iii c-methyltransferase homolog ylnf (db:pir2.dat) F69877 F69877 Bacillus subtilis 1423 -11530815 5500687780 ylnf ylnf protein (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (le:5769) (re:6257) (di:direct) BSPYREYLO AJ000974 g2462962 Bacillus subtilis 1423 -11530815 7500965433 ylnf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to uroporphyrin-iii c-methyltransferase) (le:36582) (re:37070) (di:direct) BSUB0009 Z99112 g2633936 Bacillus subtilis 1423 -11530815

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793134	4192	26348	231	76

Description

6500726958 hypothetical protein:similar to fibronectin-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloA yloA Bacillus subtilis 1423 -11530816 7000692988 yloa fibronectin-binding protein homolog yloa (db:pir2.dat) G69877 G69877 Bacillus subtilis 1423 -11530816 5500687781 yloa putative fibronectin-binding protein (db:genpept-bct1) (de:bacillus subtilis pyre to yloa gene region.) (nt:protein a-like) (le:6297) (re:8015) (di:complement) BSPYREYLO AJ000974 g2462963 Bacillus subtilis 1423 -11530816 7500963982 yloa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to fibronectin-binding protein) (le:37110) (re:38828) (di:complement) BSUB0009 Z99112 g2633937 Bacillus subtilis 1423 -11530816

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793139	4193	26349	204	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793144	4194	26350	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793156	4195	26351	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793161	4196	26352	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793177	4197	26353	222	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793179	4198	26354	1206	402

Description

GTC ORF with score 876 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c23c4.) (nt:spac23c4.17, unknown, len:674aa, similar eg. to) (le:27495:27565:27723:28938) (re:27515:27614:28877:29204) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793181	4199	26355	321	106

Description

6500726959 hypothetical protein:similar to calcium-transporting atpase (gtcfc:14.1) (ec:3.6.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloB yloB Bacillus subtilis 1423 -11530817 7000692303 ylob calcium-transporting atpase homolog ylob (cl:na+/k+-transporting atpase alpha chain:atpase nucleotide-binding domain homology) (db:pir2.dat) H69877 H69877 Bacillus subtilis 1423 -11530817 5500687790 ylob (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to calcium-transporting atpase) (le:38944) (re:41616) (di:direct) BSUB0009 Z99112 g2633938 Bacillus subtilis 1423 -11530817 7500963472 ylob putative pacl protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:716) (re:3388) (di:direct) BSY13937 Y13937 g2337795 Bacillus subtilis 1423 -11530817

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793202	4200	26356	1116	372

Description

6500726960 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloC yloC Bacillus subtilis 1423 -11530818 7000692625 yloc conserved hypothetical protein yloc (cl:hypothetical protein hi0467) (db:pir2.dat) A69878 A69878 Bacillus subtilis 1423 -11530818 5500687791 yloc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:41699) (re:42574) (di:direct) BSUB0009 Z99112 g2633939 Bacillus subtilis 1423 -11530818 7500963740 yloc yloc protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:3471) (re:4346) (di:direct) BSY13937 Y13937 g2337796 Bacillus subtilis 1423 -11530818

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793209	4201	26357	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793220	4202	26358	1377	459

Description

6500726961 hypothetical protein:similar to guanylate kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloD yloD Bacillus subtilis 1423 -11530819 7000693078 ylod guanylate kinase homolog ylod (cl:guanylate kinase:guanylate kinase homology) (db:pir2.dat) B69878 B69878 Bacillus subtilis 1423 -11530819 5500687792 ylod (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to guanylate kinase) (le:42808) (re:43542) (di:direct) BSUB0009 Z99112 g2633940 Bacillus subtilis 1423 -11530819 7500964042 ylod putative gmk protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:4580) (re:5314) (di:direct) BSY13937 Y13937 g2337797 Bacillus subtilis 1423 -11530819

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793226	4203	26359	609	203

Description

GTC ORF with score 198 to: (db:genpept-pln2) (de:emericella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj),(stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793252	4204	26360	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793256	4205	26361	240	79

Description

6500726962 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloH yloH Bacillus subtilis 1423 -11530820 7000693471 yloh hypothetical protein yloh (db:pir2.dat) C69878 C69878 Bacillus subtilis 1423 -11530820 5500687793 yloh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:43546) (re:43749) (di:direct) BSUB0009 Z99112 g2633941 Bacillus subtilis 1423 -11530820 7500964426 yloh putative rpoz protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:5318) (re:5521) (di:direct) BSY13937 Y13937 g2337798 Bacillus subtilis 1423 -11530820

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793257	4206	26362	330	109

Description

6500726963 hypothetical protein:similar to pantothenate metabolism flavoprotein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloI yloI Bacillus subtilis 1423 -11530821 7000694347 yloi pantothenate metabolism flavoprotein homolog yloi (cl:pantothenate metabolism flavoprotein dfp) (db:pir2.dat) D69878 D69878 Bacillus subtilis 1423 -11530821 5500687794 yloi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to pantothenate metabolism flavoprotein) (le:43830) (re:45050) (di:direct) BSUB0009 Z99112 g2633942 Bacillus subtilis 1423 -11530821 7500965037 yloi putative dfp protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:5602) (re:6822) (di:direct) BSY13937 Y13937 g2337799 Bacillus subtilis 1423 -11530821

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793259	4207	26363	522	173

Description

6500726964 sun:ylom hypothetical protein:similar to rna-binding sun protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloM yloM Bacillus subtilis 1423 -11530822 7502851686 sun:fmu (de:sun protein) (db:swissprot) SUN_BACSU P94464 BACILLUS SUBTILIS 1423 -11530822 7000694566 ylom rna-binding sun protein homolog ylom (cl:hypothetical protein hi0624) (db:pir2.dat) E69878 E69878 Bacillus subtilis 1423 -11530822 5500687797 ylom (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: sun; similar to rna-binding) (le:48918) (re:50261) (di:direct) BSUB0009 Z99112 g2633946 Bacillus subtilis 1423 -11530822 7500955898 ylom putative fmu protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:10690) (re:12033) (di:direct) BSY13937 Y13937 g2337803 Bacillus subtilis 1423 -11530822

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793272	4208	26364	954	317

Description

GTC ORF with score 142 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, essa i ap2 contig fragmentno. 2.) (nt:similar to hypothetical protein k02b2.3,) (le:21621:22169) (re:22079:22726) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793286	4209	26365	456	151

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793288	4210	26366	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793289	4211	26367	279	92

Description

6500726965 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloN yloN Bacillus subtilis 1423 -11530823 7500950997 ylon (de:hypothetical 41.6 kd protein in fmt-spovm intergenic region) (db:swissprot) YLON_BACSU O34617 BACILLUS SUBTILIS 1423 -11530823 7000692626 ylon conserved hypothetical protein ylon (cl:conserved hypothetical protein hi0365) (db:pir2.dat) F69878 F69878 Bacillus subtilis 1423 -11530823 7500950999 ylon (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:50265) (re:51356) (di:direct) BSUB0009 Z99112 g2633947 Bacillus subtilis 1423 -11530823 5500687798 ylon ylon protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:12037) (re:13128) (di:direct) BSY13937 Y13937 g2337804 Bacillus subtilis 1423 -11530823

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793290	4212	26368	246	81

Description

6500726966 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloO yloO Bacillus subtilis 1423 -11530824 7000692627 yloo conserved hypothetical protein yloo (cl:conserved hypothetical protein yloo:conserved hypothetical protein yloo homology) (db:pir2.dat) G69878 G69878 Bacillus subtilis 1423 -11530824 5500687799 yloo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:51363) (re:52127) (di:direct) BSUB0009 Z99112 g2633948 Bacillus subtilis 1423 -11530824 7500955966 yloo putative ptc1 protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:13135) (re:13899) (di:direct) BSY13937 Y13937 g2337805 Bacillus subtilis 1423 -11530824

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793306	4213	26369	234	77

Description

6500726967 hypothetical protein:similar to protein kinase (gtcfc:14.1) (ec:2.7.1.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloP yloP Bacillus subtilis 1423 -11530825 7000694457 ylop protein kinase homolog ylop (cl:protein kinase homology) (db:pir2.dat) H69878 H69878 Bacillus subtilis 1423 -11530825 5500687800 ylop (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to protein kinase) (le:52121) (re:54067) (di:direct) BSUB0009 Z99112 g2633949 Bacillus subtilis 1423 -11530825 7500965107 ylop putative pkn2 protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:13893) (re:15839) (di:direct) BSY13937 Y13937 g2337806 Bacillus subtilis 1423 -11530825

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793308	4214	26370	531	176

Description

6500726968 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloQ yloQ Bacillus subtilis 1423 -11530826 7000692628 yloq conserved hypothetical protein yloq (cl:conserved hypothetical protein hi1714) (db:pir2.dat) A69879 A69879 Bacillus subtilis 1423 -11530826 5500687801 yloq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:54082) (re:54978) (di:direct) BSUB0009 Z99112 g2633950 Bacillus subtilis 1423 -11530826 7500963741 yloq yloq protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:15854) (re:16750) (di:direct) BSY13937 Y13937 g2337807 Bacillus subtilis 1423 -11530826

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793309	4215	26371	546	181

Description

6500726969 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloS yloS Bacillus subtilis 1423 -11530827 7000693472 ylos hypothetical protein ylos (db:pir2.dat) C69879 C69879 Bacillus subtilis 1423 -11530827 5500687803 ylos (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:55709) (re:56353) (di:direct) BSUB0009 Z99112 g2633952 Bacillus subtilis 1423 -11530827 7500964427 ylos ylos protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:17481) (re:18125) (di:direct) BSY13937 Y13937 g2337809 Bacillus subtilis 1423 -11530827

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793313	4216	26372	630	210

Description

6500726970 hypothetical protein:similar to alkaline-shock protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloU yloU Bacillus subtilis 1423 -11530828 7000692176 ylou alkaline-shock protein homolog ylou (db:pir2.dat) D69879 D69879 Bacillus subtilis 1423 -11530828 5500687804 ylou (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to alkaline-shock protein) (le:57043) (re:57405) (di:direct) BSUB0009 Z99112 g2633955 Bacillus subtilis 1423 -11530828 7500963394 ylou putative asp23 protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:18815) (re:19177) (di:direct) BSY13937 Y13937 g2337812 Bacillus subtilis 1423 -11530828

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793316	4217	26373	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793857	4218	26374	537	178

Description

6500726971 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloV yloV Bacillus subtilis 1423 -11530829 7000692629 ylov conserved hypothetical protein ylov (cl:mycoplasma genitalium hypothetical protein mg369) (db:pir2.dat) E69879 E69879 Bacillus subtilis 1423 -11530829 5500687805 ylov (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:57421) (re:59082) (di:direct) BSUB0009 Z99112 g2633956 Bacillus subtilis 1423 -11530829 7500963742 ylov ylov protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:19193) (re:20854) (di:direct) BSY13937 Y13937 g2337813 Bacillus subtilis 1423 -11530829

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793858	4219	26375	429	143

Description

6500726972 hypothetical protein:similar to phosphoglycerate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yloW yloW Bacillus subtilis 1423 -11530830 7000694409 ylow phosphoglycerate dehydrogenase homolog ylow (db:pir2.dat) F69879 F69879 Bacillus subtilis 1423 -11530830 5500687806 ylow (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to phosphoglycerate dehydrogenase) (le:59221) (re:59883) (di:direct) BSUB0009 Z99112 g2633957 Bacillus subtilis 1423 -11530830 7500965070 ylow putative yhaq protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:20993) (re:21655) (di:direct) BSY13937 Y13937 g2337814 Bacillus subtilis 1423 -11530830

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793867	4220	26376	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793869	4221	26377	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793881	4222	26378	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793892	4223	26379	219	72

Description

6500726973 hypothetical protein:similar to atp-dependent dna helicase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylpB ylpB Bacillus subtilis 1423 -11530831 7502851687 recg (ec:3.6.1.-) (de:atp-dependent dna helicase recg,) (db:swissprot) RECG_BACSU O34942 BACILLUS SUBTILIS 1423 -11530831 7000692250 ylpb atp-dependent dna helicase homolog ylpb (cl:dna helicase recg:dead/h box helicase homology) (db:pir2.dat) H69879 H69879 Bacillus subtilis 1423 -11530831 5500687808 ylpb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to atp-dependent dna helicase) (le:60789) (re:62837) (di:direct) BSUB0009 Z99112 g2633959 Bacillus subtilis 1423 -11530831 7500954356 ylpb putative recg protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:22561) (re:24609) (di:direct) BSY13937 Y13937 g2337816 Bacillus subtilis 1423 -11530831

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793897	4224	26380	228	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793916	4225	26381	414	138

Description

GTC ORF with score 185 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid y48e1b, complete sequence.) (nt:similar to geranylgeranyl transferase beta subunit;) (le:23560:25706:28843) (re:23686:26196:29020) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793935	4226	26382	489	163

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793940	4227	26383	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793950	4228	26384	969	322

Description

6500726974 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylpC ylpC Bacillus subtilis 1423 -11530832 7000693473 ylpc hypothetical protein ylpc (db:pir2.dat) A69880 A69880 Bacillus subtilis 1423 -11530832 5500687809 ylpc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:62946) (re:63512) (di:direct) BSUB0009 Z99112 g2633960 Bacillus subtilis 1423 -11530832 7500964428 ylpc ylpc protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:24718) (re:25284) (di:direct) BSY13937 Y13937 g2337817 Bacillus subtilis 1423 -11530832

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793957	4229	26385	309	102

Description

GTC ORF with score 149 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completecds.) (nt:similar to salicylate hydroxylase; orf7) (le:10288) (re:11433) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793958	4230	26386	738	245

Description

GTC ORF with score 235 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793962	4231	26387	453	150

Description

GTC ORF with score 238 to: (db:genpept) (de:aureobasidium pullulans multidrug resistance protein 1 (mdr1) gene,promoter region and complete cds.) (nt:atp-binding cassette (abc) transporter protein) (le:542) (re:4450) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793963	4232	26388	936	311

Description

GTC ORF with score 400 to: (db:genpept) (de:aureobasidium pullulans multidrug resistance protein 1 (mdr1) gene,promoter region and complete cds.) (nt:atp-binding cassette (abc) transporter protein) (le:542) (re:4450) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793968	4233	26389	480	159

Description

GTC ORF with score 181 to: (db:genpept) (de:aureobasidium pullulans multidrug resistance protein 1 (mdr1) gene,promoter region and complete cds.) (nt:atp-binding cassette (abc) transporter protein) (le:542) (re:4450) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793985	4234	26390	870	289

Description

6500726975 ylpd:plsx hypothetical protein:involved in fatty acid/phospholipid synthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) plsX plsX Bacillus subtilis 1423 -11530833 7000694114 plsx involved in fatty acid/phospholipid synthesis plsx (cl:phospholipid synthesis protein) (db:pir2.dat) H69679 H69679 Bacillus subtilis 1423 -11530833 5500687810 plsx (fn:involved in fatty acid/phospholipid synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylpd) (le:63526) (re:64527) (di:direct) BSUB0009 Z99112 g2633961 Bacillus subtilis 1423 -11530833 7500964869 ylpd putative plsx protein (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis genomic dna from the spovm region.) (le:25298) (re:26299) (di:direct) BSY13937 Y13937 g2337818 Bacillus subtilis 1423 -11530833

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501793999	4235	26391	234	77

Description

6500726976 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylqB ylqB Bacillus subtilis 1423 -11530834 7000693474 ylqb hypothetical protein ylqb (db:pir2.dat) B69880 B69880 Bacillus subtilis 1423 -11530834 7500964429 ylqb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:72145) (re:72630) (di:complement) BSUB0009 Z99112 g2633968 Bacillus subtilis 1423 -11530834

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794002	4236	26392	450	149

Description

5000689585 hypothetical protein:hypothetical 13.2 kd protein in ffh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxM ylxM Bacillus subtilis 1423 -11530835 114485 ylxm (de:hypothetical 13.2 kd protein in ffh 5'region) (db:swissprot) YLXM_BACSU P37104 BACILLUS SUBTILIS 1423 -11530835 7000688144 ylxm conserved hypothetical protein ylxm (db:pir2.dat) A47154 A47154 Bacillus subtilis 1423 -11530835 7500951012 ylxm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:72807) (re:73139) (di:direct) BSUB0009 Z99112 g2633969 Bacillus subtilis 1423 -11530835 5500684817 orf1 orf1 (sr:bacillus subtilis (strain:168) dna) (db:genpept-bct1) (de:bacillus subtilis orf1, ffh, rpsp genes for orf1, ffh and 30sribosomal protein s16, complete cds.) (le:365) (re:697) (di:direct) D14356 D14356 g2424968 Bacillus subtilis 1423 -11530835 170389 ylxm conserved hypothetical protein ylxm (db:pir) A47154 A47154 Bacillus subtilis 1423 -11530835 6500726977 hypothetical protein:hypothetical 13.2 kd protein in ffh 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxM ylxM Bacillus subtilis 1423 -11530835

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794016	4237	26393	1002	333

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794026	4238	26394	408	135

Description

6500726978 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylqC ylqC Bacillus subtilis 1423 -11530836 7000692630 ylqc conserved hypothetical protein ylqc (db:pir2.dat) C69880 C69880 Bacillus subtilis 1423 -11530836 7500963743 ylqc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:74871) (re:75116) (di:direct) BSUB0009 Z99112 g2633972 Bacillus subtilis 1423 -11530836

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794028	4239	26395	798	265

Description

6500726979 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylqD ylqD Bacillus subtilis 1423 -11530837 7000693475 ylqd hypothetical protein ylqd (db:pir2.dat) D69880 D69880 Bacillus subtilis 1423 -11530837 7500964430 ylqd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:75238) (re:75624) (di:direct) BSUB0009 Z99112 g2633973 Bacillus subtilis 1423 -11530837

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794044	4240	26396	348	116

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794057	4241	26397	417	139

Description

6500726980 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylqE ylqE Bacillus subtilis 1423 -11530838 7502851688 rimm (de:probable 16s rrna processing protein rimm) (db:swissprot) RIMM_BACSU O31740 BACILLUS SUBTILIS 1423 -11530838 7000692631 ylqe conserved hypothetical protein ylqe (db:pir2.dat) E69880 E69880 Bacillus subtilis 1423 -11530838 7500963744 ylqe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:75629) (re:76153) (di:direct) BSUB0009 Z99112 g2633974 Bacillus subtilis 1423 -11530838

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794060	4242	26398	498	165

Description

6500726981 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylqF ylqF Bacillus subtilis 1423 -11530839 7000692632 ylqf conserved hypothetical protein ylqf (cl:conserved hypothetical protein mg442) (db:pir2.dat) F69880 F69880 Bacillus subtilis 1423 -11530839 7500963745 ylqf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:77511) (re:78359) (di:direct) BSUB0009 Z99112 g2633977 Bacillus subtilis 1423 -11530839

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794068	4243	26399	315	105

Description

6500726982 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylqG ylqG Bacillus subtilis 1423 -11530840 7000693476 ylqg hypothetical protein ylqg (db:pir2.dat) G69880 G69880 Bacillus subtilis 1423 -11530840 7500964431 ylqg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:79229) (re:80959) (di:direct) BSUB0009 Z99112 g2633979 Bacillus subtilis 1423 -11530840

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794072	4244	26400	240	79

Description

6500726983 hypothetical protein:similar to flagellar biosynthetic protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylqH ylqH Bacillus subtilis 1423 -11530841 7000692991 ylqh helicobacter pylori flhb protein homolog ylqh (cl:helicobacter pylori flhb protein) (db:pir2.dat) H69880 H69880 Bacillus subtilis 1423 -11530841 5500687814 ylqh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to flagellar biosynthetic protein) (le:80956) (re:81237) (di:direct) BSUB0009 Z99112 g2633980 Bacillus subtilis 1423 -11530841 7500963986 ylqh ylqh protein (db:genpept-bct1) (de:bacillus subtilis ylqg to codv gene region.) (le:124) (re:405) (di:direct) BSYLQGCOD AJ000975 g2462966 Bacillus subtilis 1423 -11530841

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794077	4245	26401	243	80

Description

5000689578 hypothetical protein:flaa locus 22.9 kd protein:orf 6 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxF ylxF Bacillus subtilis 1423 -11530842 215599 ylxf (de:flaa locus 22.9 kd protein (orf 6)) (db:swissprot) YLXF_BACSU P23454 BACILLUS SUBTILIS 1423 -11530842 7000688139 ylxf hypothetical protein ylxf:frzcd protein homolog:hypothetical protein 6 flaa operon (db:pir2.dat) F42365 F42365 Bacillus subtilis 1423 -11530842 7500951009 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 6) (le:4091) (re:4732) (di:direct) BACFLAAOA M72718 g142902 Bacillus subtilis 1423 -11530842 6500726984 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 6) (le:4091) (re:4732) (di:direct) BSFLAAO X56049 g39909 Bacillus subtilis 1423 -11530842 219200 ylxf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:98625) (re:99266) (di:direct) BSUB0009 Z99112 g2633998 Bacillus subtilis 1423 -11530842 7502851689 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 6) (le:4091) (re:4732) (di:direct) BSFLAAO X56049 g39909 Bacillus subtilis 1423 -11530842 114477 ylxf (de:flaa locus 22.9 kd protein (orf 6)) (db:swissprot) YLXF_BACSU P23454 BACILLUS SUBTILIS 1423 -11530842 170221 ylxf hypothetical protein ylxf:frzcd protein homolog:hypothetical protein 6 flaa operon (db:pir) F42365 F42365 Bacillus subtilis 1423 -11530842

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794078	4246	26402	774	257

Description

5000689579 hypothetical protein:flaa locus hypothetical 15.6 kd protein:orf 8 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxG ylxG Bacillus subtilis 1423 -11530843 215601 ylxg (de:flaa locus hypothetical 15.6 kd protein (orf 8)) (db:swissprot) YLXG_BACSU P23455 BACILLUS SUBTILIS 1423 -11530843 7000688140 ylxg flagellar hook assembly protein homolog ylxg:hypothetical protein 8 flaa operon (db:pir2.dat) H42365 H42365 Bacillus subtilis 1423 -11530843 7500951010 (sr:bacillus subtilis dna) (db:genpept-bct1) (de:b.subtilis flaa locus operon.) (nt:orf 8) (le:6179) (re:6601) (di:direct) BACFLAAOA M72718 g142904 Bacillus subtilis 1423 -11530843 6500726985 (db:genpept-bct1) (de:b. subtilis flaa locus operon.) (nt:orf 8) (le:6179) (re:6601) (di:direct) BSFLAAO X56049 g39911 Bacillus subtilis 1423 -11530843 219202 ylxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to flagellar hook assembly protein) (le:100713) (re:101135) (di:direct) BSUB0009 Z99112 g2634000 Bacillus subtilis 1423 -11530843 7502851690 (db:genpept) (de:b. subtilis flaa locus operon.) (nt:orf 8) (le:6179) (re:6601) (di:direct) BSFLAAO X56049 g39911 Bacillus subtilis 1423 -11530843 114478 ylxg (de:flaa locus hypothetical 15.6 kd protein (orf 8)) (db:swissprot) YLXG_BACSU P23455 BACILLUS SUBTILIS 1423 -11530843 170227 ylxg flagellar hook assembly protein homolog ylxg:hypothetical protein 8 flaa operon (db:pir) H42365 H42365 Bacillus subtilis 1423 -11530843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794079	4247	26403	285	95

Description

5000689580 hypothetical protein:hypothetical 33.2 kd protein in flhf-cheb intergenic region:orf298 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxH ylxH Bacillus subtilis 1423 -11530844 7500951011 ylxh (de:hypothetical 33.2 kd protein in flhf-cheb intergenic region (orf298)) (db:swissprot) YLXH_BACSU P40742 BACILLUS SUBTILIS 1423 -11530844 7000688141 ylxh flagellar biosynthesis switch protein homolog ylxh (cl:bacillus subtilis flagellar probable biosynthesis switch protein ylxh) (db:pir2.dat) I40434 I40434 Bacillus subtilis 1423 -11530844 6500726986 (db:genpept-bct1) (de:b.subtilis orf298.) (nt:orf298) (le:40) (re:936) (di:direct) BSORF298A X73682 g580903 Bacillus subtilis 1423 -11530844 219448 ylxh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to flagellar biosynthesis switch protein) (le:111813) (re:112709) (di:direct) BSUB0009 Z99112 g2634013 Bacillus subtilis 1423 -11530844 114480 ylxh (de:hypothetical 33.2 kd protein in flhf-cheb intergenic region (orf298)) (db:swissprot) YLXH_BACSU P40742 BACILLUS SUBTILIS 1423 -11530844 170201 ylxh flagellar biosynthesis switch protein homolog ylxh (db:pir) I40434 I40434 Bacillus subtilis 1423 -11530844

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794093	4248	26404	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794100	4249	26405	1434	478

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794108	4250	26406	360	119

Description

5000689582 ylxj:chec hypothetical protein:hypothetical 23.0 kd protein in sigd 5region:orfa (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cheC cheC Bacillus subtilis 1423 -11530845 114482 chec (de:chemotaxis protein chec) (db:swissprot) CHEC_BACSU P40403 BACILLUS SUBTILIS 1423 -11530845 7000688142 chec chemotactic methyltransferase inhibitor protein (db:pir2.dat) A55216 A55216 Bacillus subtilis 1423 -11530845 216742 (sr:b.subtilis (strain w168) dna, clones pjh(1-1,6-2)) (db:genpept-bct1) (de:b.subtilis distal fla/che region; complete orfa, orfb and sigma-28factor (sigd) gene; orfc, 5' end.) (nt:orfa) (le:27) (re:656) (di:direct) BACSIGD M20144 g289302 Bacillus subtilis 1423 -11530845 7500878639 chec (fn:inhibition of cher-mediated methylation of) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylxj) (le:116316) (re:116945) (di:direct) BSUB0009 Z99112 g2634017 Bacillus subtilis 1423 -11530845 170528 chec inhibition of cher-mediated methylation of mcps chec (db:pir) G69598 G69598 Bacillus subtilis 1423 -11530845 6500726987 ylxj hypothetical protein:hypothetical 23.0 kd protein in sigd 5region:orfa (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cheC cheC Bacillus subtilis 1423 -11530845

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794123	4251	26407	597	198

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794125	4252	26408	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794126	4253	26409	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794128	4254	26410	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794134	4255	26411	1281	426

Description

5000689583 ylxk:ched hypothetical protein:hypothetical 18.0 kd protein in sigd 5region:orfb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cheD cheD Bacillus subtilis 1423 -11530846 114483 ched (de:chemotaxis protein ched) (db:swissprot) CHED_BACSU P40404 BACILLUS SUBTILIS 1423 -11530846 7000688143 ched chemotaxis methylation system protein ched:sigd 5-region protein b (cl:chemotaxis methylation system protein ched) (db:pir2.dat) B55216 B55216 Bacillus subtilis 1423 -11530846 7500878640 (sr:b.subtilis (strain w168) dna, clones pjh(1-1,6-2)) (db:genpept-bct1) (de:b.subtilis distal fla/che region; complete orfa, orfb and sigma-28factor (sigd) gene; orfc, 5' end.) (nt:orfb) (le:653) (re:1153) (di:direct) BACSIGD M20144 g289303 Bacillus subtilis 1423 -11530846 216743 ched (fn:required for methylation of methyl-accepting) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylxk) (le:116942) (re:117442) (di:direct) BSUB0009 Z99112 g2634018 Bacillus subtilis 1423 -11530846 170529 ched chemotaxis methylation system protein ched:sigd 5-region protein b (db:pir) B55216 B55216 Bacillus subtilis 1423 -11530846 6500726988 ylxk hypothetical protein:hypothetical 18.0 kd protein in sigd 5region:orfb (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cheD cheD Bacillus subtilis 1423 -11530846

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794135	4256	26412	1416	471

Description

6500726989 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxL ylxL Bacillus subtilis 1423 -11530847 7000693477 ylxl hypothetical protein ylxl:sigd 3-region hypothetical protein c (db:pir2.dat) H69881 H69881 Bacillus subtilis 1423 -11530847 7500964432 ylxl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:118258) (re:118761) (di:direct) BSUB0009 Z99112 g2634020 Bacillus subtilis 1423 -11530847

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794158	4257	26413	1101	366

Description

6500726990 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yluA yluA Bacillus subtilis 1423 -11530848 7500951005 ylua (de:hypothetical 29.8 kd protein in frr-cdsa intergenic region) (db:swissprot) YLUA_BACSU O31751 BACILLUS SUBTILIS 1423 -11530848 7000692633 ylua conserved hypothetical protein ylua (cl:conserved hypothetical protein ybr002c) (db:pir2.dat) A69881 A69881 Bacillus subtilis 1423 -11530848 7500951007 ylua (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:122186) (re:122968) (di:direct) BSUB0009 Z99112 g2634025 Bacillus subtilis 1423 -11530848

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794162	4258	26414	465	154

Description

6500726991 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yluB yluB Bacillus subtilis 1423 -11530849 7502851691 dxr (ec:1.1.1.-) (de:reductoisomerase)) (db:swissprot) DXR_BACSU O31753 BACILLUS SUBTILIS 1423 -11530849 7000692634 ylub conserved hypothetical protein ylub (cl:conserved hypothetical protein hi0807) (db:pir2.dat) B69881 B69881 Bacillus subtilis 1423 -11530849 7500963746 ylub (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:123843) (re:125009) (di:direct) BSUB0009 Z99112 g2634027 Bacillus subtilis 1423 -11530849

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794194	4259	26415	1449	483

Description

6500726992 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yluC yluC Bacillus subtilis 1423 -11530850 7000692635 yluc conserved hypothetical protein yluc (db:pir2.dat) C69881 C69881 Bacillus subtilis 1423 -11530850 7500963747 yluc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:125000) (re:126268) (di:direct) BSUB0009 Z99112 g2634028 Bacillus subtilis 1423 -11530850

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794199	4260	26416	798	265

Description

6500726993 ymxa:ylxs hypothetical protein:hypothetical 17.6 kd protein in nusa 5region:p15a:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxS ylxS Bacillus subtilis 1423 -11530851 7500951017 ylxs (de:hypothetical 17.6 kd protein in nusa 5'region (p15a) (orf1)) (db:swissprot) YLXS_BACSU P32726 BACILLUS SUBTILIS 1423 -11530851 7000688148 ylxs conserved hypothetical protein ylxs (cl:nus operon 15k protein) (db:pir2.dat) B36905 B36905 Bacillus subtilis 1423 -11530851 5000689589 orf1 (db:genpept-bct1) (de:b.subtilis infb-nusa operon.) (le:456) (re:926) (di:direct) BSORF1T7A Z18631 g49315 Bacillus subtilis 1423 -11530851 219440 ylxs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymxa; similar to hypothetical) (le:132747) (re:133217) (di:direct) BSUB0009 Z99112 g2634031 Bacillus subtilis 1423 -11530851 114490 ylxs (de:hypothetical 17.6 kd protein in nusa 5'region (p15a) (orf1)) (db:swissprot) YLXS_BACSU P32726 BACILLUS SUBTILIS 1423 -11530851 157284 ylxs conserved hypothetical protein ylxs (cl:nus operon 15k protein) (db:pir) B36905 B36905 Bacillus subtilis 1423 -11530851

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794205	4261	26417	762	253

Description

6500726994 ymxb:ylxr hypothetical protein:hypothetical 10.4 kd protein in nusa-infb intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxR ylxR Bacillus subtilis 1423 -11530852 7500951016 ylxr (de:hypothetical 10.4 kd protein in nusa-infb intergenic region (orf3)) (db:swissprot) YLXR_BACSU P32728 BACILLUS SUBTILIS 1423 -11530852 7000688147 ylxr conserved hypothetical protein ylxr:hypothetical protein 1 nusa 3 region (db:pir2.dat) D36905 D36905 Bacillus subtilis 1423 -11530852 5000689588 orf3 (db:genpept-bct1) (de:b.subtilis infb-nusa operon.) (le:2090) (re:2365) (di:direct) BSORF1T7A Z18631 g580900 Bacillus subtilis 1423 -11530852 219442 ylxr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymxb; similar to hypothetical) (le:134381) (re:134656) (di:direct) BSUB0009 Z99112 g2634033 Bacillus subtilis 1423 -11530852 114489 ylxr (de:hypothetical 10.4 kd protein in nusa-infb intergenic region (orf3)) (db:swissprot) YLXR_BACSU P32728 BACILLUS SUBTILIS 1423 -11530852 170181 ylxr conserved hypothetical protein ylxr:hypothetical protein 1 nusa 3 region (db:pir) D36905 D36905 Bacillus subtilis 1423 -11530852

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794221	4262	26418	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794226	4263	26419	339	112

Description

6500726995 ymxc:ylxq hypothetical protein:probable ribosomal protein in nusa-infb intergenic region:orf4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxQ ylxQ Bacillus subtilis 1423 -11530853 7500951015 ylxq (de:probable ribosomal protein in nusa-infb intergenic region (orf4)) (db:swissprot) YLXQ_BACSU P32729 BACILLUS SUBTILIS 1423 -11530853 7000688146 ylxq ribosomal protein l7ae family homolog ylxq:hypothetical protein 2 infb 5 region (db:pir2.dat) E36905 E36905 Bacillus subtilis 1423 -11530853 5000688621 orf4 (db:genpept-bct1) (de:b.subtilis infb-nusa operon.) (le:2367) (re:2669) (di:direct) BSORF1T7A Z18631 g49318 Bacillus subtilis 1423 -11530853 219443 ylxq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymxc; similar to ribosomal) (le:134658) (re:134960) (di:direct) BSUB0009 Z99112 g2634034 Bacillus subtilis 1423 -11530853 114488 ylxq (de:probable ribosomal protein in nusa-infb intergenic region (orf4)) (db:swissprot) YLXQ_BACSU P32729 BACILLUS SUBTILIS 1423 -11530853 170195 ylxq ribosomal protein l7ae family homolog ylxq:hypothetical protein 2 infb 5 region (db:pir) E36905 E36905 Bacillus subtilis 1423 -11530853

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794241	4264	26420	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794246	4265	26421	1146	381

Description

6500726996 ymxd:ylxp hypothetical protein:hypothetical 10.7 kd protein in infb-rpso intergenic region:orf5 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxP ylxP Bacillus subtilis 1423 -11530854 7500951014 ylxp (de:hypothetical 10.7 kd protein in infb-rpso intergenic region (orf5)) (db:swissprot) YLXP_BACSU P32730 BACILLUS SUBTILIS 1423 -11530854 7000688145 ylxp conserved hypothetical protein ylxp:hypothetical protein 3 infb 3 region (db:pir2.dat) F36905 F36905 Bacillus subtilis 1423 -11530854 5000689587 orf5 (db:genpept-bct1) (de:b.subtilis infb-nusa operon.) (le:4836) (re:5114) (di:direct) BSORF1T7A Z18631 g580901 Bacillus subtilis 1423 -11530854 219445 ylxp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymxd; similar to hypothetical) (le:137127) (re:137405) (di:direct) BSUB0009 Z99112 g2634036 Bacillus subtilis 1423 -11530854 114487 ylxp (de:hypothetical 10.7 kd protein in infb-rpso intergenic region (orf5)) (db:swissprot) YLXP_BACSU P32730 BACILLUS SUBTILIS 1423 -11530854 170206 ylxp conserved hypothetical protein ylxp:hypothetical protein 3 infb 3 region (db:pir) F36905 F36905 Bacillus subtilis 1423 -11530854

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794251	4266	26422	228	75

Description

6500726997 ymxi:ylxy hypothetical protein:similar to deacetylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ylxY ylxY Bacillus subtilis 1423 -11530855 7000692908 ylxy deacetylase homolog ylxy (cl:nodb homology) (db:pir2.dat) H69882 H69882 Bacillus subtilis 1423 -11530855 7500963928 ylxy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ymxi; similar to deacetylase) (le:142589) (re:143548) (di:direct) BSUB0009 Z99112 g2634042 Bacillus subtilis 1423 -11530855

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794258	4267	26423	249	82

Description

6500726998 hypothetical protein:hypothetical processing protease:orfp (gtcfc:10.11) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymxG ymxG Bacillus subtilis 1423 -11530856 114747 ymxg (ec:3.4.-.-) (de:hypothetical processing protease, (orfp)) (db:swissprot) YMXG_BACSU Q04805 BACILLUS SUBTILIS 1423 -11530856 7000688155 ymxg processing proteinase homolog ymxg (db:pir2.dat) E69886 E69886 Bacillus subtilis 1423 -11530856 219900 orfp (db:genpept-bct1) (de:bacillus subtilis mpp-like orfp gene, complete cds.) (nt:orfp; similar to mitochondrial processing) (le:33) (re:1262) (di:direct) BSU27560 U27560 g881434 Bacillus subtilis 1423 -11530856 7500951510 ymxg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to processing protease) (le:143588) (re:144817) (di:direct) BSUB0009 Z99112 g2634043 Bacillus subtilis 1423 -11530856

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794260	4268	26424	312	103

Description

5000689592 hypothetical protein:hypothetical 9.8 kd protein in spovfa 5region:orfz (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymxH ymxH Bacillus subtilis 1423 -11530857 114748 ymxh (de:hypothetical 9.8 kd protein in spovfa 5'region (orfz)) (db:swissprot) YMXH_BACSU Q04811 BACILLUS SUBTILIS 1423 -11530857 7000688156 ymxh conserved hypothetical protein ymxh:hypothetical protein spovfa 5 region (cl:conserved hypothetical protein ymxh) (db:pir2.dat) A46665 A46665 Bacillus subtilis 1423 -11530857 7500951511 (sr:bacillus subtilis (strain w168) dna) (db:genpept-bct1) (de:bacillus subtilis protease, 3' end, dipicolinate synthase subunitsa and b (spovfa and spovfb), aspartate semialdehyde dehydrogenase(asd), aspartokinase i (dapg), dihydrodipicolinate synthas... BACDAP L08471 g142825 Bacillus subtilis 1423 -11530857 215476 ymxh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:144895) (re:145152) (di:direct) BSUB0009 Z99112 g2634044 Bacillus subtilis 1423 -11530857 170090 ymxh conserved hypothetical protein ymxh:hypothetical protein spovfa 5 region (db:pir) A46665 A46665 Bacillus subtilis 1423 -11530857 6500726999 hypothetical protein:hypothetical 9.8 kd protein in spovfa 5region:orfz (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymxH ymxH Bacillus subtilis 1423 -11530857

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794266	4269	26425	375	124

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794280	4270	26426	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794297	4271	26427	1020	340

Description

6500727000 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfA ymfA Bacillus subtilis 1423 -11530858 7000692645 ymfa conserved hypothetical protein ymfa (cl:conserved hypothetical protein mg139) (db:pir2.dat) H69884 H69884 Bacillus subtilis 1423 -11530858 7500963754 ymfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:150509) (re:152056) (di:direct) BSUB0009 Z99112 g2634050 Bacillus subtilis 1423 -11530858

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794311	4272	26428	741	246

Description

6500727001 ylxi:ymfb hypothetical protein:hypothetical protein in spoiiiea 5region:fragment (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfB ymfB Bacillus subtilis 1423 -11530859 7500951313 ymfb (de:hypothetical 26.4 kd protein in dapa-spoiiiea intergenic region) (db:swissprot) YMFB_BACSU Q99171 BACILLUS SUBTILIS 1423 -11530859 7000693481 ymfb hypothetical protein ymfb (db:pir2.dat) A69885 A69885 Bacillus subtilis 1423 -11530859 7500951315 ymfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:alternate gene name: ylxi) (le:152184) (re:152909) (di:direct) BSUB0009 Z99112 g2634051 Bacillus subtilis 1423 -11530859

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794316	4273	26429	597	198

Description

6500727002 hypothetical protein:similar to transcriptional regulator:gntr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfC ymfC Bacillus subtilis 1423 -11530860 7502851692 ymfc (de:region) (db:swissprot) YMFC_BACSU O31761 BACILLUS SUBTILIS 1423 -11530860 7000694738 ymfc transcription regulator gntr family homolog ymfc (db:pir2.dat) B69885 B69885 Bacillus subtilis 1423 -11530860 7500965311 ymfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to transcriptional regulator (gntr family)) (le:155754) (re:156479) (di:direct) BSUB0009 Z99112 g2634053 Bacillus subtilis 1423 -11530860

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794318	4274	26430	645	215

Description

6500727003 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfD ymfD Bacillus subtilis 1423 -11530861 7000694376 ymfd phage-related protein homolog ymfd (db:pir2.dat) C69885 C69885 Bacillus subtilis 1423 -11530861 7500965055 ymfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to phage-related protein) (le:156618) (re:156992) (di:direct) BSUB0009 Z99112 g2634054 Bacillus subtilis 1423 -11530861

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794330	4275	26431	606	201

Description

6500727004 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfE ymfE Bacillus subtilis 1423 -11530862 7000694377 ymfe phage-related protein homolog ymfe (db:pir2.dat) D69885 D69885 Bacillus subtilis 1423 -11530862 7500965056 ymfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to phage-related protein) (le:157244) (re:157828) (di:direct) BSUB0009 Z99112 g2634055 Bacillus subtilis 1423 -11530862

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794335	4276	26432	618	205

Description

GTC ORF with score 184 to: (sr:information) (db:genpept-pri2) (de:homo sapiens pac clone dj1159o04 from 7p21-p22, complete sequence.) (nt:similar to yeast hypothetical protein ybk4; similar) (le:96426:98942:101804) (re:96678:99111:101869) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794769	4277	26433	321	107

Description

6500727005 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfF ymfF Bacillus subtilis 1423 -11530863 7000693482 ymff hypothetical protein ymff (db:pir2.dat) E69885 E69885 Bacillus subtilis 1423 -11530863 7500964436 ymff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:158103) (re:158435) (di:direct) BSUB0009 Z99112 g2634056 Bacillus subtilis 1423 -11530863

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794770	4278	26434	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794773	4279	26435	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794777	4280	26436	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794781	4281	26437	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794783	4282	26438	456	151

Description

GTC ORF with score 212 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9954.) (nt:similar to s. cerevisiae hypothetical proteins) (le:28434) (re:29678) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794784	4283	26439	360	119

Description

6500727006 hypothetical protein:similar to processing protease (gtcfc:10.11) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfG ymfG Bacillus subtilis 1423 -11530864 7000694443 ymfg processing proteinase homolog ymfg (db:pir2.dat) F69885 F69885 Bacillus subtilis 1423 -11530864 7500965099 ymfg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to processing protease) (le:158500) (re:159222) (di:direct) BSUB0009 Z99112 g2634057 Bacillus subtilis 1423 -11530864

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794786	4284	26440	630	209

Description

GTC ORF with score 142 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9954.) (nt:similar to s. cerevisiae hypothetical proteins) (le:28434) (re:29678) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794788	4285	26441	501	167

Description

6500727007 hypothetical protein:similar to processing protease (gtcfc:10.11) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfH ymfH Bacillus subtilis 1423 -11530865 7000694444 ymfh processing proteinase homolog ymfh (db:pir2.dat) G69885 G69885 Bacillus subtilis 1423 -11530865 7500965100 ymfh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to processing protease) (le:159305) (re:160552) (di:direct) BSUB0009 Z99112 g2634058 Bacillus subtilis 1423 -11530865

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794794	4286	26442	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794797	4287	26443	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794798	4288	26444	429	143

Description

6500727008 hypothetical protein:similar to 3-oxoacyl-acyl-carrier protein reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfI ymfI Bacillus subtilis 1423 -11530866 7000692053 ymfi 3-oxoacyl-acyl-carrier protein reductase homolog ymfi (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) H69885 H69885 Bacillus subtilis 1423 -11530866 7500963298 ymfi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to 3-oxoacyl- acyl-carrier protein) (le:160607) (re:161335) (di:direct) BSUB0009 Z99112 g2634059 Bacillus subtilis 1423 -11530866

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794823	4289	26445	255	84

Description

GTC ORF with score 129 to: (db:genpept-pln1) (de:cochliobolus heterostrophus gtpase activating protein homolog(gap1), hmg dna binding protein (mat-2), and beta glucosidasehomolog (bgl1) genes, complete cds.) (le:633:794:1153:1965) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794826	4290	26446	600	199

Description

GTC ORF with score 456 to: (db:genpept-pln1) (de:cochliobolus heterostrophus gtpase activating protein homolog(gap1), hmg dna binding protein (mat-2), and beta glucosidasehomolog (bgl1) genes, complete cds.) (le:633:794:1153:1965) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794827	4291	26447	675	224

Description

GTC ORF with score 316 to: (db:genpept-pln1) (de:cochliobolus heterostrophus gtpase activating protein homolog(gap1), dna binding protein with alpha box domain (mat-1), and betaglucosidase homolog (bgl1) genes, complete cds.) (le:633:794:1153:1965) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794828	4292	26448	210	69

Description

GTC ORF with score 154 to: (db:genpept-pln1) (de:cochliobolus heterostrophus gtpase activating protein homolog(gap1), hmg dna binding protein (mat-2), and beta glucosidasehomolog (bgl1) genes, complete cds.) (le:633:794:1153:1965) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794829	4293	26449	207	68

Description

GTC ORF with score 119 to: (db:genpept-pln1) (de:cochliobolus heterostrophus gtpase activating protein homolog(gap1), hmg dna binding protein (mat-2), and beta glucosidasehomolog (bgl1) genes, complete cds.) (le:633:794:1153:1965) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794837	4294	26450	459	152

Description

6500727009 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfJ ymfJ Bacillus subtilis 1423 -11530867 7000692646 ymfj conserved hypothetical protein ymfj (cl:hypothetical protein yflh) (db:pir2.dat) A69886 A69886 Bacillus subtilis 1423 -11530867 7500955913 ymfj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins from b. subtilis) (le:161416) (re:161673) (di:direct) BSUB0009 Z99112 g2634060 Bacillus subtilis 1423 -11530867

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794839	4295	26451	288	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794840	4296	26452	663	221

Description

6500727010 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfK ymfK Bacillus subtilis 1423 -11530868 7000692647 ymfk conserved hypothetical protein ymfk (db:pir2.dat) B69886 B69886 Bacillus subtilis 1423 -11530868 7500963755 ymfk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins from b. subtilis) (le:161817) (re:162317) (di:direct) BSUB0009 Z99112 g2634061 Bacillus subtilis 1423 -11530868

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794841	4297	26453	816	272

Description

6500727011 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfL ymfL Bacillus subtilis 1423 -11530869 7000693483 ymfl hypothetical protein ymfl (db:pir2.dat) C69886 C69886 Bacillus subtilis 1423 -11530869 7500964437 ymfl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:162314) (re:162592) (di:direct) BSUB0009 Z99112 g2634062 Bacillus subtilis 1423 -11530869

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794844	4298	26454	300	99

Description

6500727012 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymfM ymfM Bacillus subtilis 1423 -11530870 7000692648 ymfm conserved hypothetical protein ymfm (db:pir2.dat) D69886 D69886 Bacillus subtilis 1423 -11530870 7500963756 ymfm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins from b. subtilis) (le:162659) (re:163228) (di:direct) BSUB0009 Z99112 g2634063 Bacillus subtilis 1423 -11530870

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794845	4299	26455	246	81

Description

6500727013 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymdA ymdA Bacillus subtilis 1423 -11530871 7000692643 ymda conserved hypothetical protein ymda (cl:hypothetical protein ymda) (db:pir2.dat) F69884 F69884 Bacillus subtilis 1423 -11530871 7500955923 ymda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:168258) (re:169820) (di:direct) BSUB0009 Z99112 g2634068 Bacillus subtilis 1423 -11530871

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794867	4300	26456	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794874	4301	26457	597	198

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794885	4302	26458	1623	541

Description

6500727014 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymdB ymdB Bacillus subtilis 1423 -11530872 7000692644 ymdb conserved hypothetical protein ymdb (cl:hypothetical protein ymdb) (db:pir2.dat) G69884 G69884 Bacillus subtilis 1423 -11530872 7500955952 ymdb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:169889) (re:170683) (di:direct) BSUB0009 Z99112 g2634069 Bacillus subtilis 1423 -11530872

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794893	4303	26459	936	312

Description

6500727015 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymcB ymcB Bacillus subtilis 1423 -11530873 7000692642 ymcb conserved hypothetical protein ymcb (cl:conserved hypothetical protein hi0019) (db:pir2.dat) D69884 D69884 Bacillus subtilis 1423 -11530873 7500963753 ymcb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:173791) (re:175320) (di:direct) BSUB0009 Z99112 g2634073 Bacillus subtilis 1423 -11530873

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794928	4304	26460	900	299

Description

6500727016 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymcA ymcA Bacillus subtilis 1423 -11530874 7000692641 ymca conserved hypothetical protein ymca (db:pir2.dat) C69884 C69884 Bacillus subtilis 1423 -11530874 7500963752 ymca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (nt:similar to hypothetical proteins) (le:175322) (re:175753) (di:direct) BSUB0009 Z99112 g2634074 Bacillus subtilis 1423 -11530874

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794930	4305	26461	711	236

Description

6500727017 hypothetical protein:dna mismatch repair recognition (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) mutS mutS Bacillus subtilis 1423 -11530875 7000692933 muts dna mismatch repair recognition muts (cl:dna mismatch repair protein muts) (db:pir2.dat) C69663 C69663 Bacillus subtilis 1423 -11530875 7500963949 muts (fn:dna mismatch repair recognition) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:176693) (re:179269) (di:direct) BSUB0009 Z99112 g2634076 Bacillus subtilis 1423 -11530875

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794937	4306	26462	297	98

Description

5000689093 hypothetical protein:dna mismatch repair protein mutl (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) mutL mutL Bacillus subtilis 1423 -11530876 84738 mutl (de:dna mismatch repair protein mutl) (db:swissprot) MUTL_BACSU P49850 BACILLUS SUBTILIS 1423 -11530876 7000685896 mutl dna mismatch repair mutl (cl:mismatch repair protein hexb) (db:pir2.dat) A69663 A69663 Bacillus subtilis 1423 -11530876 219898 mutl mutl (fn:mismatch-repair recognition) (db:genpept-bct1) (de:bacillus subtilis spore coat protein (cote) gene, partial cds, andmismatch repair recognition proteins (muts) and (mutl) genes,complete cds.) (le:2782) (re:4665) (di:direct) BSU27343 U27343 g1002521 Bacillus subtilis 1423 -11530876 7500886158 mutl (fn:dna mismatch repair) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:179285) (re:181168) (di:direct) BSUB0009 Z99112 g2634077 Bacillus subtilis 1423 -11530876 6500727018 hypothetical protein:dna mismatch repair protein mutl (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) mutL mutL Bacillus subtilis 1423 -11530876

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794942	4307	26463	1179	393

Description

6500727019 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymcC ymcC Bacillus subtilis 1423 -11530877 7000693480 ymcc hypothetical protein ymcc (db:pir2.dat) E69884 E69884 Bacillus subtilis 1423 -11530877 7500964435 ymcc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:182177) (re:182734) (di:complement) BSUB0009 Z99112 g2634078 Bacillus subtilis 1423 -11530877

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794948	4308	26464	414	138

Description

6500727020 hypothetical protein:involved in polyketide synthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) pksB pksB Bacillus subtilis 1423 -11530878 7000694115 pksb involved in polyketide synthesis pksb (db:pir2.dat) H69677 H69677 Bacillus subtilis 1423 -11530878 6000690886 pksb (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:183662) (re:184339) (di:direct) BSUB0009 Z99112 g2634080 Bacillus subtilis 1423 -11530878 7500964870 pksb (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:882) (re:1559) (di:direct) BSUB0010 Z99113 g2634092 Bacillus subtilis 1423 -11530878

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794952	4309	26465	249	82

Description

6500727021 hypothetical protein:involved in polyketide synthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) pksC pksC Bacillus subtilis 1423 -11530879 7000694116 pksc involved in polyketide synthesis pksc (cl:(acyl-carrier-protein) s-malonyltransferase:(acyl-carrier-protein) s-malonyltransferase homology) (db:pir2.dat) A69678 A69678 Bacillus subtilis 1423 -11530879 6000690888 pksc (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:184712) (re:185578) (di:direct) BSUB0009 Z99112 g2634081 Bacillus subtilis 1423 -11530879 7500964871 pksc (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:1932) (re:2798) (di:direct) BSUB0010 Z99113 g2634093 Bacillus subtilis 1423 -11530879

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794964	4310	26466	312	103

Description

6500727022 hypothetical protein:involved in polyketide synthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) pksD pksD Bacillus subtilis 1423 -11530880 7000694117 pksd involved in polyketide synthesis pksd (cl:(acyl-carrier-protein) s-malonyltransferase homology) (db:pir2.dat) B69678 B69678 Bacillus subtilis 1423 -11530880 6000690890 pksd (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:186082) (re:186972) (di:direct) BSUB0009 Z99112 g2634082 Bacillus subtilis 1423 -11530880 7500964872 pksd (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:3302) (re:4192) (di:direct) BSUB0010 Z99113 g2634094 Bacillus subtilis 1423 -11530880

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794965	4311	26467	726	242

Description

6500727023 hypothetical protein:involved in polyketide synthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) pksE pksE Bacillus subtilis 1423 -11530881 7000694118 pkse involved in polyketide synthesis pkse (cl:(acyl-carrier-protein) s-malonyltransferase homology) (db:pir2.dat) C69678 C69678 Bacillus subtilis 1423 -11530881 6000690892 pkse (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.) (le:186969) (re:188921) (di:direct) BSUB0009 Z99112 g2634083 Bacillus subtilis 1423 -11530881 7500964873 pkse (fn:involved in polyketide synthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:4189) (re:6141) (di:direct) BSUB0010 Z99113 g2634095 Bacillus subtilis 1423 -11530881

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794967	4312	26468	441	146

Description

6500727024 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymzB ymzB Bacillus subtilis 1423 -11530882 7000693485 ymzb hypothetical protein ymzb (db:pir2.dat) H69886 H69886 Bacillus subtilis 1423 -11530882 7500964439 ymzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:78142) (re:78414) (di:complement) BSUB0010 Z99113 g2634108 Bacillus subtilis 1423 -11530882

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501794983	4313	26469	888	295

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795001	4314	26470	798	265

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795011	4315	26471	420	139

Description

6500727025 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaE ymaE Bacillus subtilis 1423 -11530883 7000693478 ymae hypothetical protein ymae (db:pir2.dat) G69883 G69883 Bacillus subtilis 1423 -11530883 7500964433 ymae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:78490) (re:79188) (di:complement) BSUB0010 Z99113 g2634109 Bacillus subtilis 1423 -11530883

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795014	4316	26472	576	191

Description

GTC ORF with score 91 to: (sr:schistosoma mansoni (clone: psmf 61-46) blood fluke cdna to mrna) (db:genpept-inv) (de:schistosoma mansoni female-specific developmentally regulated mrna,complete cds.) (nt:orf-rf2; putative) (le:125) (re:685) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795021	4317	26473	396	131

Description

6500727026 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaC ymaC Bacillus subtilis 1423 -11530884 7000694375 ymac phage-related replication protein homolog ymac (cl:phage-related replication protein) (db:pir2.dat) E69883 E69883 Bacillus subtilis 1423 -11530884 7500955718 ymac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to phage-related protein) (le:81490) (re:82197) (di:direct) BSUB0010 Z99113 g2634111 Bacillus subtilis 1423 -11530884

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795023	4318	26474	1095	364

Description

6500727027 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaD ymaD Bacillus subtilis 1423 -11530885 7000692640 ymad conserved hypothetical protein ymad (db:pir2.dat) F69883 F69883 Bacillus subtilis 1423 -11530885 7500963751 ymad (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins) (le:82267) (re:82719) (di:direct) BSUB0010 Z99113 g2634112 Bacillus subtilis 1423 -11530885

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795027	4319	26475	738	245

Description

6500727028 hypothetical protein:similar to cell wall protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaG ymaG Bacillus subtilis 1423 -11530886 7000692335 ymag cell wall protein homolog ymag (db:pir2.dat) A69884 A69884 Bacillus subtilis 1423 -11530886 7500963502 ymag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to cell wall protein) (le:83554) (re:83925) (di:complement) BSUB0010 Z99113 g2634115 Bacillus subtilis 1423 -11530886

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795028	4320	26476	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795034	4321	26477	1119	372

Description

6500727029 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaF ymaF Bacillus subtilis 1423 -11530887 7000693479 ymaf hypothetical protein ymaf (db:pir2.dat) H69883 H69883 Bacillus subtilis 1423 -11530887 7500964434 ymaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:83918) (re:84331) (di:direct) BSUB0010 Z99113 g2634116 Bacillus subtilis 1423 -11530887

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795039	4322	26478	441	146

Description

GTC ORF with score 128 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid r04e5.) (nt:proline rich; coded for by c. elegans cdna) (le:8839:9150:9494) (re:8875:9435:10157) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795057	4323	26479	420	140

Description

6500727030 hypothetical protein:similar to host factor-1 protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaH ymaH Bacillus subtilis 1423 -11530888 7000693111 ymah host factor-1 protein homolog ymah (cl:host factor i) (db:pir2.dat) B69884 B69884 Bacillus subtilis 1423 -11530888 7500964058 ymah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to host factor-1 protein) (le:85414) (re:85635) (di:direct) BSUB0010 Z99113 g2634118 Bacillus subtilis 1423 -11530888

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795069	4324	26480	789	263

Description

6500727031 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymzC ymzC Bacillus subtilis 1423 -11530889 7000693486 ymzc hypothetical protein ymzc (db:pir2.dat) A69887 A69887 Bacillus subtilis 1423 -11530889 7500964440 ymzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:85831) (re:86103) (di:direct) BSUB0010 Z99113 g2634119 Bacillus subtilis 1423 -11530889

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795075	4325	26481	450	149

Description

6500727032 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymzA ymzA Bacillus subtilis 1423 -11530890 7000693484 ymza hypothetical protein ymza (db:pir2.dat) G69886 G69886 Bacillus subtilis 1423 -11530890 7500964438 ymza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:86185) (re:86415) (di:direct) BSUB0010 Z99113 g2634120 Bacillus subtilis 1423 -11530890

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795082	4326	26482	234	77

Description

6500727033 nrdi:ymaa hypothetical protein:nrdi protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaA ymaA Bacillus subtilis 1423 -11530891 219426 nrdi (de:nrdi protein) (db:swissprot) NRDI_BACSU P50618 BACILLUS SUBTILIS 1423 -11530891 7000685983 ymaa ribonucleoprotein homolog ymaa (db:pir2.dat) C69883 C69883 Bacillus subtilis 1423 -11530891 5000689199 ymaa ymaa (fn:unknown) (db:genpept-bct1) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (le:939) (re:1331) (di:direct) BSNRDYMA Z68500 g1262335 Bacillus subtilis 1423 -11530891 7500886578 ymaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to ribonucleoprotein) (le:86658) (re:87050) (di:direct) BSUB0010 Z99113 g2634121 Bacillus subtilis 1423 -11530891 7502851693 ymaa ymaa (fn:unknown) (db:genpept) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (le:939) (re:1331) (di:direct) BSNRDYMA Z68500 g1262335 Bacillus subtilis 1423 -11530891 114608 nrdi (de:nrdi protein) (db:swissprot) NRDI_BACSU P50618 BACILLUS SUBTILIS 1423 -11530891

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795083	4327	26483	522	174

Description

5000689200 hypothetical protein:hypothetical 23.4 kd protein in nrdf-cwlc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaB ymaB Bacillus subtilis 1423 -11530892 219429 ymab (de:hypothetical 23.4 kd protein in nrdf-cwlc intergenic region) (db:swissprot) YMAB_BACSU P50619 BACILLUS SUBTILIS 1423 -11530892 7000688149 ymab hypothetical protein ymab (db:pir2.dat) D69883 D69883 Bacillus subtilis 1423 -11530892 7500951249 ymab ymab (fn:unknown) (db:genpept-bct1) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (nt:no similarities, cannot be inactivated) (le:4450) (re:5070) (di:direct) BSNRDYMA Z68500 g1154634 Bacillus subtilis 1423 -11530892 7502851694 ymab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:90169) (re:90789) (di:direct) BSUB0010 Z99113 g2634124 Bacillus subtilis 1423 -11530892 7502851695 ymab ymab (fn:unknown) (db:genpept) (de:b.subtilis cwlc, nrde, nrdf, ymaa and ymab genes.) (nt:no similarities, cannot be inactivated) (le:4450) (re:5070) (di:direct) BSNRDYMA Z68500 g1154634 Bacillus subtilis 1423 -11530892 114609 ymab (de:hypothetical 23.4 kd protein in nrdf-cwlc intergenic region) (db:swissprot) YMAB_BACSU P50619 BACILLUS SUBTILIS 1423 -11530892 6500727034 hypothetical protein:hypothetical 23.4 kd protein in nrdf-cwlc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ymaB ymaB Bacillus subtilis 1423 -11530892

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795099	4328	26484	1074	358

Description

6500727035 hypothetical protein:similar to gtp-binding protein protease modulator (gtcfc:12.13:10.11) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynbA ynbA Bacillus subtilis 1423 -11530893 7000693077 ynba gtp-binding protein proteinase modulator homolog ynba (cl:gtp-binding protein hflx) (db:pir2.dat) B69888 B69888 Bacillus subtilis 1423 -11530893 220162 ynba ynba (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750108 Bacillus subtilis 1423 -11530893 7500964041 ynba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to gtp-binding protein protease modulator) (le:93433) (re:94437) (di:direct) BSUB0010 Z99113 g2634127 Bacillus subtilis 1423 -11530893

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795114	4329	26485	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795122	4330	26486	561	187

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795123	4331	26487	306	101

Description

6500727036 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynbB ynbB Bacillus subtilis 1423 -11530894 7000692650 ynbb conserved hypothetical protein ynbb (cl:hypothetical protein ynbb) (db:pir2.dat) C69888 C69888 Bacillus subtilis 1423 -11530894 220163 ynbb ynbb (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750109 Bacillus subtilis 1423 -11530894 7500955876 ynbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins) (le:94625) (re:95890) (di:direct) BSUB0010 Z99113 g2634128 Bacillus subtilis 1423 -11530894

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795146	4332	26488	867	289

Description

6500727037 ynaa:ynxb hypothetical protein:hypothetical 10.2 kd protein in glna 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynxB ynxB Bacillus subtilis 1423 -11530895 115118 ynaa (de:hypothetical 10.2 kd protein in glna 3'region) (db:swissprot) YNAA_BACSU P31844 BACILLUS SUBTILIS 1423 -11530895 7000688157 ynxb hypothetical protein ynxb (db:pir2.dat) JT0394 JT0394 Bacillus subtilis 1423 -11530895 7500951706 unknown protein (sr:bacillus subtilis (sub_strain jh642/168, strain marburg) dna) (db:genpept-bct1) (de:bacillus subtilis glutamine synthetase (glna) gene, complete cds.) (nt:orf2; putative) (le:2292) (re:2582) (di:direct) BACGLNAZ M22811 g1119205 Bacillus subtilis 1423 -11530895 215677 ynaa ynaa (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750112 Bacillus subtilis 1423 -11530895 220166 ynxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: ynaa) (le:98131) (re:98421) (di:direct) BSUB0010 Z99113 g2634131 Bacillus subtilis 1423 -11530895 170074 ynxb hypothetical protein ynxb (db:pir) JT0394 JT0394 Bacillus subtilis 1423 -11530895 5000689593 (de:(ynxb) (pn:hypothetical 10) (gtcfc:13.07) (ec:) (ynxb_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ynxB ynxB Bacillus subtilis 1423 10056843

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795174	4333	26489	336	111

Description

6500727038 hypothetical protein:similar to delta-endotoxin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzF ynzF Bacillus subtilis 1423 -11530896 7000692909 ynzf delta-endotoxin homolog ynzf (db:pir2.dat) H69894 H69894 Bacillus subtilis 1423 -11530896 7500963930 ynzf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to delta-endotoxin) (le:98667) (re:99011) (di:direct) BSUB0010 Z99113 g2634132 Bacillus subtilis 1423 -11530896

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795177	4334	26490	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795178	4335	26491	645	214

Description

6500727039 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzG ynzG Bacillus subtilis 1423 -11530897 7000693513 ynzg hypothetical protein ynzg (cl:hypothetical protein yolf) (db:pir2.dat) A69895 A69895 Bacillus subtilis 1423 -11530897 7500955900 ynzg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:99142) (re:99393) (di:direct) BSUB0010 Z99113 g2634133 Bacillus subtilis 1423 -11530897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795179	4336	26492	465	154

Description

6500727040 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaB ynaB Bacillus subtilis 1423 -11530898 7000693487 ynab hypothetical protein ynab (db:pir2.dat) B69887 B69887 Bacillus subtilis 1423 -11530898 220167 ynab ynab (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750113 Bacillus subtilis 1423 -11530898 7500964441 ynab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:99713) (re:100024) (di:direct) BSUB0010 Z99113 g2634134 Bacillus subtilis 1423 -11530898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795705	4337	26493	1425	474

Description

6500727041 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaC ynaC Bacillus subtilis 1423 -11530899 7000693488 ynac hypothetical protein ynac (db:pir2.dat) C69887 C69887 Bacillus subtilis 1423 -11530899 220168 ynac ynac (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750114 Bacillus subtilis 1423 -11530899 7500964442 ynac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:100094) (re:100885) (di:direct) BSUB0010 Z99113 g2634135 Bacillus subtilis 1423 -11530899

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795709	4338	26494	906	301

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795716	4339	26495	237	78

Description

6500727042 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaE ynaE Bacillus subtilis 1423 -11530900 7000693489 ynae hypothetical protein ynae (db:pir2.dat) E69887 E69887 Bacillus subtilis 1423 -11530900 220170 ynae ynae (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750116 Bacillus subtilis 1423 -11530900 7500964443 ynae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:102292) (re:102933) (di:direct) BSUB0010 Z99113 g2634137 Bacillus subtilis 1423 -11530900

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795717	4340	26496	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795737	4341	26497	582	193

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795751	4342	26498	417	138

Description

6500727043 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaF ynaF Bacillus subtilis 1423 -11530901 7000693490 ynaf hypothetical protein ynaf (db:pir2.dat) F69887 F69887 Bacillus subtilis 1423 -11530901 220171 ynaf ynaf (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750117 Bacillus subtilis 1423 -11530901 7500964444 ynaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:103022) (re:103375) (di:direct) BSUB0010 Z99113 g2634138 Bacillus subtilis 1423 -11530901

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795754	4343	26499	867	288

Description

6500727044 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaG ynaG Bacillus subtilis 1423 -11530902 7000693491 ynag hypothetical protein ynag (db:pir2.dat) G69887 G69887 Bacillus subtilis 1423 -11530902 220172 ynag ynag (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750118 Bacillus subtilis 1423 -11530902 7500964445 ynag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:103419) (re:103694) (di:direct) BSUB0010 Z99113 g2634139 Bacillus subtilis 1423 -11530902

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795770	4344	26500	408	135

Description

6500727045 hypothetical protein:similar to phosphoribosylanthranilate isomerase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaI ynaI Bacillus subtilis 1423 -11530903 7000694419 ynai phosphoribosylanthranilate isomerase homolog ynai (db:pir2.dat) H69887 H69887 Bacillus subtilis 1423 -11530903 220174 ynai ynai (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750119 Bacillus subtilis 1423 -11530903 7500965075 ynai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to phosphoribosylanthranilate isomerase) (le:104297) (re:104581) (di:direct) BSUB0010 Z99113 g2634140 Bacillus subtilis 1423 -11530903

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795771	4345	26501	549	182

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795788	4346	26502	225	74

Description

6500727046 hypothetical protein:similar to h+-symporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynaJ ynaJ Bacillus subtilis 1423 -11530904 7502851696 ynaj (de:hypothetical symporter in glna-xynb intergenic region) (db:swissprot) YNAJ_BACSU P94488 BACILLUS SUBTILIS 1423 -11530904 7000693080 ynaj h+-symporter homolog ynaj (cl:melibiose carrier protein) (db:pir2.dat) A69888 A69888 Bacillus subtilis 1423 -11530904 220175 ynaj ynaj (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750121 Bacillus subtilis 1423 -11530904 7500964044 ynaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to h+-symporter) (le:105406) (re:106797) (di:direct) BSUB0010 Z99113 g2634141 Bacillus subtilis 1423 -11530904

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795803	4347	26503	609	202

Description

GTC ORF with score 630 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c3e7.) (nt:spbc3e7.10, putative methionine aminopeptidase 1,) (le:23540:23709:23779:23885) (re:23656:23729:23824:24840) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795808	4348	26504	378	125

Description

GTC ORF with score 188 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c3e7.) (nt:spbc3e7.10, putative methionine aminopeptidase 1,) (le:23540:23709:23779:23885) (re:23656:23729:23824:24840) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795823	4349	26505	798	265

Description

6500727047 hypothetical protein:similar to micrococcal nuclease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yncB yncB Bacillus subtilis 1423 -11530905 7000694220 yncb micrococcal nuclease homolog yncb (cl:micrococcal nuclease) (db:pir2.dat) D69888 D69888 Bacillus subtilis 1423 -11530905 220180 yncb yncb (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750126 Bacillus subtilis 1423 -11530905 7500964945 yncb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to micrococcal nuclease) (le:113432) (re:114067) (di:complement) BSUB0010 Z99113 g2634146 Bacillus subtilis 1423 -11530905

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795833	4350	26506	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795838	4351	26507	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795840	4352	26508	474	157

Description

6500727048 hypothetical protein:similar to metabolite transport protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yncC yncC Bacillus subtilis 1423 -11530906 7000694205 yncc metabolite transport protein homolog yncc (cl:glucose transport protein) (db:pir2.dat) E69888 E69888 Bacillus subtilis 1423 -11530906 220181 yncc yncc (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750127 Bacillus subtilis 1423 -11530906 7500964932 yncc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to metabolite transport protein) (le:114478) (re:115737) (di:direct) BSUB0010 Z99113 g2634147 Bacillus subtilis 1423 -11530906

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795846	4353	26509	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795854	4354	26510	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795861	4355	26511	402	134

Description

6500727049 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yncE yncE Bacillus subtilis 1423 -11530907 7000693492 ynce hypothetical protein ynce (db:pir2.dat) G69888 G69888 Bacillus subtilis 1423 -11530907 220183 ynce ynce (db:genpept-bct1) (de:bacillus subtilis spovk (spovk), ynba (ynba), ynbb (ynbb), glnr(glnr), glutamine synthetase (glna), ynaa (ynaa), ynab (ynab), ynac(ynac), ynad (ynad), ynae (ynae), ynaf (ynaf), ynag (ynag), ynah(ynah), ynai (ynai), ynaj (ynaj), xy... BSU66480 U66480 g1750129 Bacillus subtilis 1423 -11530907 7500964446 ynce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:117643) (re:118104) (di:direct) BSUB0010 Z99113 g2634149 Bacillus subtilis 1423 -11530907

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795869	4356	26512	339	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795870	4357	26513	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795887	4358	26514	417	138

Description

6500727050 hypothetical protein:similar to spore coat protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzH ynzH Bacillus subtilis 1423 -11530908 7000694611 ynzh spore coat protein homolog ynzh (db:pir2.dat) B69895 B69895 Bacillus subtilis 1423 -11530908 7500965206 ynzh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to spore coat protein) (le:119172) (re:119432) (di:complement) BSUB0010 Z99113 g2634151 Bacillus subtilis 1423 -11530908

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795888	4359	26515	372	123

Description

6500727051 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yncM yncM Bacillus subtilis 1423 -11530909 7502851697 yncm (de:hypothetical 26.6 kd protein in thya-cotc intergenic region) (db:swissprot) YNCM_BACSU O31803 BACILLUS SUBTILIS 1423 -11530909 7000693493 yncm hypothetical protein yncm (db:pir2.dat) A69889 A69889 Bacillus subtilis 1423 -11530909 7500964447 yncm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:121566) (re:122318) (di:complement) BSUB0010 Z99113 g2634153 Bacillus subtilis 1423 -11530909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795892	4360	26516	438	145

Description

6500727052 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzA ynzA Bacillus subtilis 1423 -11530910 7000692656 ynza conserved hypothetical protein ynza (cl:conserved hypothetical secreted protein hp0320) (db:pir2.dat) C69894 C69894 Bacillus subtilis 1423 -11530910 7500963761 ynza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins) (le:123425) (re:123613) (di:complement) BSUB0010 Z99113 g2634155 Bacillus subtilis 1423 -11530910

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795899	4361	26517	231	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795910	4362	26518	603	200

Description

GTC ORF with score 437 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome ii cosmid c6b1.) (nt:spbc6b1.10, unknown; (n terminal region may need) (le:27086:27238:28042:28701) (re:27196:28002:28657:28748) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795917	4363	26519	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795936	4364	26520	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795942	4365	26521	1797	598

Description

6500727053 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndA yndA Bacillus subtilis 1423 -11530911 7000693494 ynda hypothetical protein ynda (db:pir2.dat) B69889 B69889 Bacillus subtilis 1423 -11530911 7500964448 ynda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:123864) (re:124262) (di:direct) BSUB0010 Z99113 g2634156 Bacillus subtilis 1423 -11530911

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795967	4366	26522	510	169

Description

6500727054 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndB yndB Bacillus subtilis 1423 -11530912 7000693495 yndb hypothetical protein yndb (db:pir2.dat) C69889 C69889 Bacillus subtilis 1423 -11530912 7500964449 yndb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:124327) (re:124761) (di:complement) BSUB0010 Z99113 g2634157 Bacillus subtilis 1423 -11530912

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795968	4367	26523	237	78

Description

6500727055 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzB ynzB Bacillus subtilis 1423 -11530913 7000693509 ynzb hypothetical protein ynzb (db:pir2.dat) D69894 D69894 Bacillus subtilis 1423 -11530913 7500964461 ynzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:125068) (re:125256) (di:direct) BSUB0010 Z99113 g2634158 Bacillus subtilis 1423 -11530913

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795971	4368	26524	240	79

Description

6500727056 hypothetical protein:similar to spore germination protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndD yndD Bacillus subtilis 1423 -11530914 7000694627 yndd spore germination protein homolog yndd (cl:spore germination protein gerba) (db:pir2.dat) D69889 D69889 Bacillus subtilis 1423 -11530914 7500965222 yndd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to spore germination protein) (le:125549) (re:127111) (di:direct) BSUB0010 Z99113 g2634159 Bacillus subtilis 1423 -11530914

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795980	4369	26525	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795982	4370	26526	267	88

Description

6500727057 hypothetical protein:similar to spore germination protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndE yndE Bacillus subtilis 1423 -11530915 7000694628 ynde spore germination protein homolog ynde (cl:spore germination protein) (db:pir2.dat) E69889 E69889 Bacillus subtilis 1423 -11530915 7500955382 ynde (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to spore germination protein) (le:127141) (re:128232) (di:direct) BSUB0010 Z99113 g2634160 Bacillus subtilis 1423 -11530915

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795984	4371	26527	231	77

Description

6500727058 hypothetical protein:similar to spore germination protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndF yndF Bacillus subtilis 1423 -11530916 7000694629 yndf spore germination protein homolog yndf (cl:spore germination protein iii) (db:pir2.dat) F69889 F69889 Bacillus subtilis 1423 -11530916 7500955384 yndf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to spore germination protein) (le:128222) (re:129436) (di:direct) BSUB0010 Z99113 g2634161 Bacillus subtilis 1423 -11530916

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795988	4372	26528	654	217

Description

6500727059 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndG yndG Bacillus subtilis 1423 -11530917 7000693496 yndg hypothetical protein yndg (db:pir2.dat) G69889 G69889 Bacillus subtilis 1423 -11530917 7500964450 yndg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:129583) (re:130389) (di:direct) BSUB0010 Z99113 g2634162 Bacillus subtilis 1423 -11530917

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501795996	4373	26529	219	72

Description

6500727060 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndH yndH Bacillus subtilis 1423 -11530918 7000693497 yndh hypothetical protein yndh (db:pir2.dat) H69889 H69889 Bacillus subtilis 1423 -11530918 7500964451 yndh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:130394) (re:131011) (di:direct) BSUB0010 Z99113 g2634163 Bacillus subtilis 1423 -11530918

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796004	4374	26530	219	72

Description

6500727061 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndJ yndJ Bacillus subtilis 1423 -11530919 7000693498 yndj hypothetical protein yndj (db:pir2.dat) A69890 A69890 Bacillus subtilis 1423 -11530919 7500964452 yndj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:131008) (re:132648) (di:direct) BSUB0010 Z99113 g2634164 Bacillus subtilis 1423 -11530919

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796005	4375	26531	696	231

Description

6500727062 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndK yndK Bacillus subtilis 1423 -11530920 7000693499 yndk hypothetical protein yndk (db:pir2.dat) B69890 B69890 Bacillus subtilis 1423 -11530920 7500964453 yndk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:132685) (re:133050) (di:direct) BSUB0010 Z99113 g2634165 Bacillus subtilis 1423 -11530920

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796006	4376	26532	381	126

Description

6500727063 hypothetical protein:similar to phage-related replication protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndL yndL Bacillus subtilis 1423 -11530921 7000694389 yndl phage-related replication protein homolog yndl (cl:phage-related replication protein) (db:pir2.dat) C69890 C69890 Bacillus subtilis 1423 -11530921 7500955717 yndl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to phage-related replication protein) (le:133276) (re:134034) (di:direct) BSUB0010 Z99113 g2634166 Bacillus subtilis 1423 -11530921

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796010	4377	26533	603	200

Description

GTC ORF with score 281 to: (or:Homo sapiens) (sr:homo sapiens male myeloblast cell_line:kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0210 gene, complete cds.) (nt:similar to a putative protein coded in) (le:1665) (re:4052) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796029	4378	26534	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796049	4379	26535	1818	606

Description

6500727064 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndM yndM Bacillus subtilis 1423 -11530922 7000692651 yndm conserved hypothetical protein yndm (cl:hypothetical protein ycbp) (db:pir2.dat) D69890 D69890 Bacillus subtilis 1423 -11530922 7500963758 yndm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins from b. subtilis) (le:134061) (re:134600) (di:complement) BSUB0010 Z99113 g2634167 Bacillus subtilis 1423 -11530922

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796082	4380	26536	591	196

Description

6500727065 hypothetical protein:similar to fosfomycin resistance protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yndN yndN Bacillus subtilis 1423 -11530923 7000693006 yndn fosfomycin resistance protein homolog yndn (cl:fosfomycin resistance protein) (db:pir2.dat) E69890 E69890 Bacillus subtilis 1423 -11530923 7500954046 yndn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to fosfomycin resistance protein) (le:134718) (re:135152) (di:direct) BSUB0010 Z99113 g2634168 Bacillus subtilis 1423 -11530923

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796084	4381	26537	903	300

Description

6500727066 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneA yneA Bacillus subtilis 1423 -11530924 7000693500 ynea hypothetical protein ynea (db:pir2.dat) F69890 F69890 Bacillus subtilis 1423 -11530924 7500964454 ynea ynea (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:82) (re:399) (di:direct) BC170DEGR Z73234 g1405444 Bacillus subtilis 1423 -11530924 217875 ynea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:136461) (re:136778) (di:direct) BSUB0010 Z99113 g2634170 Bacillus subtilis 1423 -11530924

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796113	4382	26538	1128	375

Description

6500727067 hypothetical protein:similar to resolvase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneB yneB Bacillus subtilis 1423 -11530925 7000694494 yneb resolvase homolog yneb (db:pir2.dat) G69890 G69890 Bacillus subtilis 1423 -11530925 7500965133 yneb yneb (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:similar to gamma-delta resolvase) (le:418) (re:1071) (di:direct) BC170DEGR Z73234 g1405445 Bacillus subtilis 1423 -11530925 217876 yneb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to resolvase) (le:136797) (re:137450) (di:direct) BSUB0010 Z99113 g2634171 Bacillus subtilis 1423 -11530925

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796131	4383	26539	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796140	4384	26540	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796141	4385	26541	819	272

Description

6500727068 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzC ynzC Bacillus subtilis 1423 -11530926 7000693510 ynzc hypothetical protein ynzc (db:pir2.dat) E69894 E69894 Bacillus subtilis 1423 -11530926 7500964462 ynzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:137514) (re:137747) (di:direct) BSUB0010 Z99113 g2634172 Bacillus subtilis 1423 -11530926

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796163	4386	26542	549	182

Description

5000689598 yoxf:ynee hypothetical protein:hypothetical 18.1 kd protein in ttk-ccda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneE yneE Bacillus subtilis 1423 -11530927 219725 ynee (de:hypothetical 18.1 kd protein in ttk-ccda intergenic region) (db:swissprot) YNEE_BACSU P45707 BACILLUS SUBTILIS 1423 -11530927 7000688161 ynee hypothetical protein ynee (db:pir2.dat) S57402 S57402 Bacillus subtilis 1423 -11530927 6500727069 ynee ynee (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:identical to yoxf (from acc. no. x87845)) (le:3693) (re:4139) (di:direct) BC170DEGR Z73234 g1405447 Bacillus subtilis 1423 -11530927 308410 orf (db:genpept-bct1) (de:b.subtilis orf120, orf160, tkt and ccda genes.) (le:479) (re:925) (di:direct) BSTKTCCDA X87845 g870923 Bacillus subtilis 1423 -11530927 217878 ynee (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: yoxf) (le:140072) (re:140518) (di:direct) BSUB0010 Z99113 g2634174 Bacillus subtilis 1423 -11530927 115414 ynee (de:hypothetical 18.1 kd protein in ttk-ccda intergenic region) (db:swissprot) YNEE_BACSU P45707 BACILLUS SUBTILIS 1423 -11530927 170175 ynee hypothetical protein ynee (db:pir) S57402 S57402 Bacillus subtilis 1423 -11530927

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796165	4387	26543	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796167	4388	26544	648	215

Description

5000689599 yoxg:ynef hypothetical protein:hypothetical 8.3 kd protein in ttk-ccda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneF yneF Bacillus subtilis 1423 -11530928 219726 ynef (de:hypothetical 8.3 kd protein in ttk-ccda intergenic region) (db:swissprot) YNEF_BACSU P45708 BACILLUS SUBTILIS 1423 -11530928 7000688162 ynef hypothetical protein ynef (cl:conserved hypothetical protein ynef) (db:pir2.dat) S57403 S57403 Bacillus subtilis 1423 -11530928 6500727070 ynef ynef (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:identical to yoxg (from acc. no. x87845)) (le:4225) (re:4443) (di:direct) BC170DEGR Z73234 g1405448 Bacillus subtilis 1423 -11530928 308411 orf (db:genpept-bct1) (de:b.subtilis orf120, orf160, tkt and ccda genes.) (le:1011) (re:1229) (di:direct) BSTKTCCDA X87845 g870924 Bacillus subtilis 1423 -11530928 217879 ynef (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: yoxg) (le:140604) (re:140822) (di:direct) BSUB0010 Z99113 g2634175 Bacillus subtilis 1423 -11530928 115415 ynef (de:hypothetical 8.3 kd protein in ttk-ccda intergenic region) (db:swissprot) YNEF_BACSU P45708 BACILLUS SUBTILIS 1423 -11530928 170176 ynef hypothetical protein ynef (db:pir) S57403 S57403 Bacillus subtilis 1423 -11530928

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796687	4389	26545	519	172

Description

6500727071 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzD ynzD Bacillus subtilis 1423 -11530929 7000693511 ynzd hypothetical protein ynzd (db:pir2.dat) F69894 F69894 Bacillus subtilis 1423 -11530929 7500964463 ynzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:140896) (re:141069) (di:complement) BSUB0010 Z99113 g2634176 Bacillus subtilis 1423 -11530929

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796690	4390	26546	228	76

Description

5000689600 yoxh:ccdb:ynei hypothetical protein:ccdb protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneI yneI Bacillus subtilis 1423 -11530930 219728 ccdb (de:ccdb protein) (db:swissprot) CCDB_BACSU P45709 BACILLUS SUBTILIS 1423 -11530930 7000684766 ynei response regulator homolog ynei (cl:chemotaxis chey protein:response regulator homology) (db:pir2.dat) S57405 S57405 Bacillus subtilis 1423 -11530930 6500727072 ynei ynei (fn:response regulator) (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:identical to yoxh (from acc. no. x87845)) (le:5706) (re:6068) (di:direct) BC170DEGR Z73234 g1405450 Bacillus subtilis 1423 -11530930 308413 orf120 response regulator (db:genpept-bct1) (de:b.subtilis orf120, orf160, tkt and ccda genes.) (le:2492) (re:2854) (di:direct) BSTKTCCDA X87845 g870926 Bacillus subtilis 1423 -11530930 217881 ynei (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: yoxh; similar to two-component) (le:142085) (re:142447) (di:direct) BSUB0010 Z99113 g2634178 Bacillus subtilis 1423 -11530930 115416 ccdb (de:ccdb protein) (db:swissprot) CCDB_BACSU P45709 BACILLUS SUBTILIS 1423 -11530930 170506 ynei response regulator homolog ynei (cl:response regulator homology) (db:pir) S57405 S57405 Bacillus subtilis 1423 -11530930

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796691	4391	26547	663	220

Description

6500727073 yoxi:ccdc:ynej hypothetical protein:ccdc protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneJ yneJ Bacillus subtilis 1423 -11530931 7000693501 ynej ynej protein:protein 160 (db:pir2.dat) C69891 C69891 Bacillus subtilis 1423 -11530931 7500965439 ynej ynej (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:identical to yoxi (from acc. no. x87845)) (le:6147) (re:6638) (di:direct) BC170DEGR Z73234 g1405451 Bacillus subtilis 1423 -11530931 217882 ynej (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: yoxi) (le:142526) (re:143017) (di:direct) BSUB0010 Z99113 g2634179 Bacillus subtilis 1423 -11530931

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796697	4392	26548	555	184

Description

6500727074 yoxj:ynek hypothetical protein:hypothetical 17.0 kd protein in ccdc-citb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneK yneK Bacillus subtilis 1423 -11530932 7500951789 ynek (de:hypothetical 17.0 kd protein in ccdc-citb intergenic region) (db:swissprot) YNEK_BACSU P45711 BACILLUS SUBTILIS 1423 -11530932 7000688165 ynek ynek protein (db:pir2.dat) D69891 D69891 Bacillus subtilis 1423 -11530932 217883 ynek ynek (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:identical to yoxj (from acc. no. x87845)) (le:6669) (re:7097) (di:complement) BC170DEGR Z73234 g1405452 Bacillus subtilis 1423 -11530932 7502851698 ynek (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: yoxj) (le:143048) (re:143476) (di:complement) BSUB0010 Z99113 g2634180 Bacillus subtilis 1423 -11530932 115418 ynek (de:hypothetical 17.0 kd protein in ccdc-citb intergenic region) (db:swissprot) YNEK_BACSU P45711 BACILLUS SUBTILIS 1423 -11530932

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796710	4393	26549	603	200

Description

6500727075 hypothetical protein:similar to thiol:disulfide interchange protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneN yneN Bacillus subtilis 1423 -11530933 7000694678 ynen thiol:disulfide interchange protein homolog ynen (cl:bacillus subtilis thioredoxin related protein ykvv) (db:pir2.dat) E69891 E69891 Bacillus subtilis 1423 -11530933 7500965263 ynen (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to thiol:disulfide interchange protein) (le:147536) (re:148048) (di:direct) BSUB0010 Z99113 g2634185 Bacillus subtilis 1423 -11530933

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796712	4394	26550	498	165

Description

6500727076 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneP yneP Bacillus subtilis 1423 -11530934 7000692652 ynep conserved hypothetical protein ynep (db:pir2.dat) F69891 F69891 Bacillus subtilis 1423 -11530934 7500963759 ynep ynep (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:12510) (re:12875) (di:direct) BC170DEGR Z73234 g1405456 Bacillus subtilis 1423 -11530934 217887 ynep (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins) (le:148889) (re:149254) (di:direct) BSUB0010 Z99113 g2634187 Bacillus subtilis 1423 -11530934

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796721	4395	26551	480	159

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796727	4396	26552	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796742	4397	26553	801	266

Description

6500727077 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneQ yneQ Bacillus subtilis 1423 -11530935 7000693502 yneq hypothetical protein yneq (db:pir2.dat) G69891 G69891 Bacillus subtilis 1423 -11530935 7500964455 yneq yneq (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:12891) (re:13190) (di:direct) BC170DEGR Z73234 g1405457 Bacillus subtilis 1423 -11530935 217888 yneq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:149270) (re:149569) (di:direct) BSUB0010 Z99113 g2634188 Bacillus subtilis 1423 -11530935

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796744	4398	26554	279	92

Description

6500727078 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneR yneR Bacillus subtilis 1423 -11530936 7000693503 yner hypothetical protein yner (db:pir2.dat) H69891 H69891 Bacillus subtilis 1423 -11530936 7500964456 yner yner (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:13221) (re:13508) (di:complement) BC170DEGR Z73234 g1405458 Bacillus subtilis 1423 -11530936 217889 yner (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:149600) (re:149887) (di:complement) BSUB0010 Z99113 g2634189 Bacillus subtilis 1423 -11530936

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796752	4399	26555	495	164

Description

6500727079 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneS yneS Bacillus subtilis 1423 -11530937 7000692653 ynes conserved hypothetical protein ynes (cl:escherichia coli ygih protein) (db:pir2.dat) A69892 A69892 Bacillus subtilis 1423 -11530937 7500955828 ynes ynes (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (nt:similar to hypothetical protein mg247 from) (le:13596) (re:14177) (di:complement) BC170DEGR Z73234 g1405459 Bacillus subtilis 1423 -11530937 217890 ynes (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins) (le:149975) (re:150556) (di:complement) BSUB0010 Z99113 g2634190 Bacillus subtilis 1423 -11530937

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796765	4400	26556	336	111

Description

GTC ORF with score 143 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796768	4401	26557	507	168

Description

GTC ORF with score 94 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796771	4402	26558	432	143

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796772	4403	26559	996	331

Description

6500727080 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yneT yneT Bacillus subtilis 1423 -11530938 7000692654 ynet conserved hypothetical protein ynet (cl:hypothetical protein ynet) (db:pir2.dat) B69892 B69892 Bacillus subtilis 1423 -11530938 7500955839 ynet ynet (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:14347) (re:14754) (di:direct) BC170DEGR Z73234 g1405460 Bacillus subtilis 1423 -11530938 217891 ynet (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins) (le:150726) (re:151133) (di:direct) BSUB0010 Z99113 g2634191 Bacillus subtilis 1423 -11530938

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796810	4404	26560	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796815	4405	26561	345	114

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796832	4406	26562	573	191

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796835	4407	26563	420	139

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796836	4408	26564	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796850	4409	26565	1812	604

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796865	4410	26566	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796882	4411	26567	1002	333

Description

6500727081 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynfC ynfC Bacillus subtilis 1423 -11530939 7000693504 ynfc hypothetical protein ynfc (db:pir2.dat) C69892 C69892 Bacillus subtilis 1423 -11530939 7500964457 ynfc ynfc (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:19742) (re:20152) (di:complement) BC170DEGR Z73234 g1405463 Bacillus subtilis 1423 -11530939 217894 ynfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:156121) (re:156531) (di:complement) BSUB0010 Z99113 g2634194 Bacillus subtilis 1423 -11530939

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796883	4412	26568	615	205

Description

6500727082 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynfE ynfE Bacillus subtilis 1423 -11530940 7000693505 ynfe hypothetical protein ynfe (db:pir2.dat) D69892 D69892 Bacillus subtilis 1423 -11530940 7500964458 ynfe ynfe (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:23868) (re:24131) (di:direct) BC170DEGR Z73234 g1405466 Bacillus subtilis 1423 -11530940 217897 ynfe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:160247) (re:160510) (di:direct) BSUB0010 Z99113 g2634197 Bacillus subtilis 1423 -11530940

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796887	4413	26569	657	218

Description

6500727083 hypothetical protein:similar to endo-xylanase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynfF ynfF Bacillus subtilis 1423 -11530941 7000692964 ynff endo-xylanase homolog ynff (db:pir2.dat) E69892 E69892 Bacillus subtilis 1423 -11530941 7500963970 ynff ynff (db:genpept-bct1) (de:b.subtilis dna (26.2 kb fragment; 170 degree region).) (le:24390) (re:25658) (di:complement) BC170DEGR Z73234 g1405467 Bacillus subtilis 1423 -11530941 217898 ynff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to endo-xylanase) (le:160769) (re:162037) (di:complement) BSUB0010 Z99113 g2634198 Bacillus subtilis 1423 -11530941

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796888	4414	26570	564	187

Description

6500727084 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngA yngA Bacillus subtilis 1423 -11530942 7000693506 ynga hypothetical protein ynga (db:pir2.dat) F69892 F69892 Bacillus subtilis 1423 -11530942 7500964459 ynga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:164304) (re:164750) (di:direct) BSUB0010 Z99113 g2634200 Bacillus subtilis 1423 -11530942

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796915	4415	26571	1242	414

Description

6500727085 hypothetical protein:similar to alkaline phosphatase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngC yngC Bacillus subtilis 1423 -11530943 7000692174 yngc alkaline phosphatase homolog yngc (cl:probable alkaline phosphatase yngc) (db:pir2.dat) H69892 H69892 Bacillus subtilis 1423 -11530943 7500963393 yngc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to alkaline phosphatase) (le:165723) (re:166319) (di:direct) BSUB0010 Z99113 g2634202 Bacillus subtilis 1423 -11530943

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796923	4416	26572	951	317

Description

6500727086 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngD yngD Bacillus subtilis 1423 -11530944 7000693507 yngd hypothetical protein yngd (db:pir2.dat) A69893 A69893 Bacillus subtilis 1423 -11530944 7500964460 yngd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:166368) (re:167567) (di:complement) BSUB0010 Z99113 g2634203 Bacillus subtilis 1423 -11530944

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796925	4417	26573	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796926	4418	26574	633	210

Description

6500727087 hypothetical protein:similar to propionyl-coa carboxylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngE yngE Bacillus subtilis 1423 -11530945 7000694455 ynge propionyl-coa carboxylase homolog ynge (cl:propionyl-coa carboxylase beta chain) (db:pir2.dat) B69893 B69893 Bacillus subtilis 1423 -11530945 7500954519 ynge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to propionyl-coa carboxylase) (le:167737) (re:169524) (di:complement) BSUB0010 Z99113 g2634204 Bacillus subtilis 1423 -11530945

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796928	4419	26575	243	80

Description

6500727088 hypothetical protein:similar to 3-hydroxbutyryl-coa dehydratase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngF yngF Bacillus subtilis 1423 -11530946 7000692042 yngf 3-hydroxbutyryl-coa dehydratase homolog yngf (cl:naphthoate synthase:enoyl-coa hydratase homology) (db:pir2.dat) C69893 C69893 Bacillus subtilis 1423 -11530946 4000714536 yngf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to 3-hydroxbutyryl-coa dehydratase) (le:169283) (re:170065) (di:complement) BSUB0010 Z99113 g2634205 Bacillus subtilis 1423 -11530946 7500963294 yngf (db:genpept-bct1) (de:bacillus subtilis ppse, yngl, yngk, yotb, yngj, yngi, yngh, ynggand yngf genes, ppsd and ynge partial genes.) (le:13638) (re:14420) (di:direct) BSY13917 Y13917 g2266427 Bacillus subtilis 1423 -11530946

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796939	4420	26576	252	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796943	4421	26577	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796951	4422	26578	1233	410

Description

6500727089 hypothetical protein:similar to hydroxymethylglutaryl-coa lyase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngG yngG Bacillus subtilis 1423 -11530947 7000693118 yngg hydroxymethylglutaryl-coa lyase homolog yngg (cl:hydroxymethylglutaryl-coa lyase) (db:pir2.dat) D69893 D69893 Bacillus subtilis 1423 -11530947 4000714535 yngg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hydroxymethylglutaryl-coa lyase) (le:170086) (re:170985) (di:complement) BSUB0010 Z99113 g2634206 Bacillus subtilis 1423 -11530947 7500954398 yngg (db:genpept-bct1) (de:bacillus subtilis ppse, yngl, yngk, yotb, yngj, yngi, yngh, ynggand yngf genes, ppsd and ynge partial genes.) (le:12718) (re:13617) (di:direct) BSY13917 Y13917 g2266426 Bacillus subtilis 1423 -11530947

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796956	4423	26579	756	251

Description

6500727090 hypothetical protein:similar to biotin carboxylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngH yngH Bacillus subtilis 1423 -11530948 7000692287 yngh biotin carboxylase homolog yngh (cl:biotin carboxylase:biotin carboxylase homology) (db:pir2.dat) E69893 E69893 Bacillus subtilis 1423 -11530948 4000714534 yngh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to biotin carboxylase) (le:171236) (re:172570) (di:complement) BSUB0010 Z99113 g2634207 Bacillus subtilis 1423 -11530948 7500954524 yngh (db:genpept-bct1) (de:bacillus subtilis ppse, yngl, yngk, yotb, yngj, yngi, yngh, ynggand yngf genes, ppsd and ynge partial genes.) (le:11133) (re:12467) (di:direct) BSY13917 Y13917 g2266425 Bacillus subtilis 1423 -11530948

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796960	4424	26580	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796977	4425	26581	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501796979	4426	26582	420	139

Description

6500727091 hypothetical protein:similar to long-chain acyl-coa synthetase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngI yngI Bacillus subtilis 1423 -11530949 7000694171 yngi long-chain acyl-coa synthetase homolog yngi (cl:acetate--coa ligase homology) (db:pir2.dat) F69893 F69893 Bacillus subtilis 1423 -11530949 7500964901 yngi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to long-chain acyl-coa synthetase) (le:172580) (re:174229) (di:complement) BSUB0010 Z99113 g2634208 Bacillus subtilis 1423 -11530949

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797006	4427	26583	1062	353

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797015	4428	26584	189	63

Description

6500727092 hypothetical protein:similar to butyryl-coa dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngJ yngJ Bacillus subtilis 1423 -11530950 7000692297 yngj butyryl-coa dehydrogenase homolog yngj (cl:acyl-coa dehydrogenase) (db:pir2.dat) G69893 G69893 Bacillus subtilis 1423 -11530950 4000714532 yngj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to butyryl-coa dehydrogenase) (le:174273) (re:175415) (di:complement) BSUB0010 Z99113 g2634209 Bacillus subtilis 1423 -11530950 7500953847 yngj (db:genpept-bct1) (de:bacillus subtilis ppse, yngl, yngk, yotb, yngj, yngi, yngh, ynggand yngf genes, ppsd and ynge partial genes.) (le:8289) (re:9431) (di:direct) BSY13917 Y13917 g2266423 Bacillus subtilis 1423 -11530950

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797017	4429	26585	300	99

Description

6500727093 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ynzE ynzE Bacillus subtilis 1423 -11530951 7000693512 ynze hypothetical protein ynze (db:pir2.dat) G69894 G69894 Bacillus subtilis 1423 -11530951 4000714531 ynze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:175506) (re:175811) (di:complement) BSUB0010 Z99113 g2634210 Bacillus subtilis 1423 -11530951 7500964464 yotb (db:genpept-bct1) (de:bacillus subtilis ppse, yngl, yngk, yotb, yngj, yngi, yngh, ynggand yngf genes, ppsd and ynge partial genes.) (le:7893) (re:8198) (di:direct) BSY13917 Y13917 g2266422 Bacillus subtilis 1423 -11530951

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797026	4430	26586	975	325

Description

6500727094 yota:yngk hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngK yngK Bacillus subtilis 1423 -11530952 7000692655 yngk conserved hypothetical protein yngk (db:pir2.dat) H69893 H69893 Bacillus subtilis 1423 -11530952 4000714530 yngk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:alternate gene name: yota; similar to hypothetical) (le:176082) (re:177614) (di:complement) BSUB0010 Z99113 g2634211 Bacillus subtilis 1423 -11530952 7500963760 yngk (db:genpept-bct1) (de:bacillus subtilis ppse, yngl, yngk, yotb, yngj, yngi, yngh, ynggand yngf genes, ppsd and ynge partial genes.) (le:6090) (re:7622) (di:direct) BSY13917 Y13917 g2266421 Bacillus subtilis 1423 -11530952

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797039	4431	26587	957	319

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797042	4432	26588	237	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797058	4433	26589	225	74

Description

6500727095 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yngL yngL Bacillus subtilis 1423 -11530953 7000693508 yngl hypothetical protein yngl (cl:hypothetical protein yngl) (db:pir2.dat) A69894 A69894 Bacillus subtilis 1423 -11530953 4000714529 yngl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:177750) (re:178142) (di:complement) BSUB0010 Z99113 g2634212 Bacillus subtilis 1423 -11530953 7500955831 yngl (db:genpept-bct1) (de:bacillus subtilis ppse, yngl, yngk, yotb, yngj, yngi, yngh, ynggand yngf genes, ppsd and ynge partial genes.) (le:5562) (re:5954) (di:direct) BSY13917 Y13917 g2266420 Bacillus subtilis 1423 -11530953

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797059	4434	26590	1122	374

Description

6500727096 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoxA yoxA Bacillus subtilis 1423 -11530954 7502851699 yoxa (de:hypothetical 37.2 kd protein in pbp-ggt intergenic region) (db:swissprot) YOXA_BACSU P39840 BACILLUS SUBTILIS 1423 -11530954 7000692710 yoxa conserved hypothetical protein yoxa:hypothetical protein peptide synthetase operon (db:pir2.dat) A69930 A69930 Bacillus subtilis 1423 -11530954 7500963795 yoxa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins from b. subtilis) (le:217904) (re:218881) (di:complement) BSUB0010 Z99113 g2634219 Bacillus subtilis 1423 -11530954

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797063	4435	26591	480	159

Description

GTC ORF with score 95 to: (sr:herpes simplex virus type 2 (isolate:hg52) dna, clone:f, p and g) (db:genpept-vrl) (de:herpes simplex virus type 2 genomic dna for 0.74-0.84 region,complete cds.) (nt:rl2 orf) (le:8251:10156:<11242) (re:9974:10834:11316) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797073	4436	26592	693	230

Description

6500727097 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoeA yoeA Bacillus subtilis 1423 -11530955 7000692674 yoea conserved hypothetical protein yoea (db:pir2.dat) A69905 A69905 Bacillus subtilis 1423 -11530955 6000690952 yoea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to hypothetical proteins from b. subtilis) (le:219015) (re:220406) (di:complement) BSUB0010 Z99113 g2634220 Bacillus subtilis 1423 -11530955 7500963777 yoea (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:45) (re:1436) (di:complement) BSUB0011 Z99114 g2634231 Bacillus subtilis 1423 -11530955

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797076	4437	26593	1269	422

Description

6500727098 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoeB yoeB Bacillus subtilis 1423 -11530956 7000693543 yoeb hypothetical protein yoeb (db:pir2.dat) B69905 B69905 Bacillus subtilis 1423 -11530956 6000690954 yoeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:220692) (re:221237) (di:direct) BSUB0010 Z99113 g2634221 Bacillus subtilis 1423 -11530956 7500964494 yoeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:1722) (re:2267) (di:direct) BSUB0011 Z99114 g2634232 Bacillus subtilis 1423 -11530956

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797094	4438	26594	1065	354

Description

6500727099 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoeC yoeC Bacillus subtilis 1423 -11530957 7000693544 yoec hypothetical protein yoec (db:pir2.dat) C69905 C69905 Bacillus subtilis 1423 -11530957 6000690956 yoec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:221715) (re:222002) (di:complement) BSUB0010 Z99113 g2634222 Bacillus subtilis 1423 -11530957 7500964495 yoec (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:2745) (re:3032) (di:complement) BSUB0011 Z99114 g2634233 Bacillus subtilis 1423 -11530957

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797098	4439	26595	231	76

Description

6500727100 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoeD yoeD Bacillus subtilis 1423 -11530958 7000693545 yoed hypothetical protein yoed (db:pir2.dat) D69905 D69905 Bacillus subtilis 1423 -11530958 6000690958 yoed (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (le:222318) (re:222548) (di:complement) BSUB0010 Z99113 g2634223 Bacillus subtilis 1423 -11530958 7500964496 yoed (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:3348) (re:3578) (di:complement) BSUB0011 Z99114 g2634234 Bacillus subtilis 1423 -11530958

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797107	4440	26596	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797109	4441	26597	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797118	4442	26598	621	206

Description

6500727101 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yofA yofA Bacillus subtilis 1423 -11530959 7000694756 yofa transcription regulator lysr family homolog yofa (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) E69905 E69905 Bacillus subtilis 1423 -11530959 6000690960 yofa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to transcriptional regulator (lysr family)) (le:224597) (re:225454) (di:complement) BSUB0010 Z99113 g2634225 Bacillus subtilis 1423 -11530959 7500965326 yofa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to transcriptional regulator (lysr family)) (le:5627) (re:6484) (di:complement) BSUB0011 Z99114 g2634236 Bacillus subtilis 1423 -11530959

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797121	4443	26599	636	211

Description

6500727102 hypothetical protein:similar to alcohol dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yogA yogA Bacillus subtilis 1423 -11530960 7000692168 yoga alcohol dehydrogenase homolog yoga (cl:long-chain alcohol dehydrogenase homology) (db:pir2.dat) F69905 F69905 Bacillus subtilis 1423 -11530960 6000690962 yoga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.) (nt:similar to alcohol dehydrogenase) (le:225582) (re:226571) (di:direct) BSUB0010 Z99113 g2634226 Bacillus subtilis 1423 -11530960 7500963389 yoga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to alcohol dehydrogenase) (le:6612) (re:7601) (di:direct) BSUB0011 Z99114 g2634237 Bacillus subtilis 1423 -11530960

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797125	4444	26600	468	155

Description

6500727103 yoxe:proh hypothetical protein:involved in proline biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) proH proH Bacillus subtilis 1423 -11530961 7500888554 yoxe:proc (de:pyrroline-5-carboxylate reductase homolog 1) (db:swissprot) PROH_BACSU P14383 BACILLUS SUBTILIS 1423 -11530961 7000694119 proh pyrroline-5-carboxylate reductase::proline biosynthesis protein proh (cl:pyrroline-5-carboxylate reductase) (ec:1.5.1.2) (db:pir2.dat) E69682 E69682 Bacillus subtilis 1423 -11530961 7500888556 proh (fn:involved in proline biosynthesis) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yoxe) (le:16011) (re:16823) (di:complement) BSUB0011 Z99114 g2634242 Bacillus subtilis 1423 -11530961

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797126	4445	26601	1074	357

Description

GTC ORF with score 1411 to: (sr:aspergillus oryzae (strain a1560) (library: lambda gem11) dna) (db:genpept-pln1) (de:aspergillus oryzae regulatory protein (amdr) gene, complete cds.) (le:348:486:1724) (re:390:1659:2813) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797138	4446	26602	513	170

Description

6500727104 hypothetical protein:hypothetical oxidoreductase in rtp 5region:orf238 (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoxD yoxD Bacillus subtilis 1423 -11530962 115413 yoxd (ec:1.-.-.-) (de:(orf238)) (db:swissprot) YOXD_BACSU P14802 BACILLUS SUBTILIS 1423 -11530962 7000688192 yoxd 3-oxoacyl-acyl-carrier protein reductase homolog yoxd (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D69930 D69930 Bacillus subtilis 1423 -11530962 7500952134 yoxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to 3-oxoacyl- acyl-carrier protein) (le:17638) (re:18354) (di:complement) BSUB0011 Z99114 g2634244 Bacillus subtilis 1423 -11530962 5000689597 (de:(yoxd) (pn:hypothetical oxidoreductase in rtp 5"region:orf238:hypothetical 25) (gtcfc:13.07) (ec:1.-.-.-) (yoxd_bacsu) (keggfc:11.1) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yoxD yoxD Bacillus subtilis 1423 10057139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797143	4447	26603	1110	370

Description

GTC ORF with score 122 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.).) (nt:orf_id:o267#4; similar to (swissprot accession) (le:9391) (re:11949) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797704	4448	26604	1449	482

Description

5000689596 hypothetical protein:hypothetical 11.4 kd protein in rtp 5region:orf101 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoxC yoxC Bacillus subtilis 1423 -11530963 115412 yoxc (de:hypothetical 11.4 kd protein in rtp 5'region (orf101)) (db:swissprot) YOXC_BACSU P28670 BACILLUS SUBTILIS 1423 -11530963 7000688191 yoxc hypothetical protein yoxc (db:pir2.dat) C69930 C69930 Bacillus subtilis 1423 -11530963 7500952133 yoxc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:18505) (re:18810) (di:direct) BSUB0011 Z99114 g2634245 Bacillus subtilis 1423 -11530963 6500727105 hypothetical protein:hypothetical 11.4 kd protein in rtp 5region:orf101 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoxC yoxC Bacillus subtilis 1423 -11530963

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797720	4449	26605	237	78

Description

6500727106 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoxB yoxB Bacillus subtilis 1423 -11530964 7000693829 yoxb hypothetical protein yoxb (db:pir2.dat) B69930 B69930 Bacillus subtilis 1423 -11530964 7500964643 yoxb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:18881) (re:19651) (di:direct) BSUB0011 Z99114 g2634246 Bacillus subtilis 1423 -11530964

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797722	4450	26606	255	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797723	4451	26607	387	128

Description

6500727107 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaA yoaA Bacillus subtilis 1423 -11530965 7000692657 yoaa conserved hypothetical protein yoaa (cl:hypothetical protein yoaa) (db:pir2.dat) C69895 C69895 Bacillus subtilis 1423 -11530965 5500701865 yoaa putative alanine acetyl transferase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis p20 protein and e.coli) (le:604) (re:1101) (di:direct) AF027868 AF027868 g2618995 Bacillus subtilis 1423 -11530965 7500955878 yoaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:19695) (re:20192) (di:direct) BSUB0011 Z99114 g2634247 Bacillus subtilis 1423 -11530965

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797736	4452	26608	654	218

Description

6500727108 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaB yoaB Bacillus subtilis 1423 -11530966 7000692658 yoab conserved hypothetical protein yoab (db:pir2.dat) D69895 D69895 Bacillus subtilis 1423 -11530966 5500701866 yoab putative transporter (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis multidrug resistance protein) (le:1217) (re:2461) (di:complement) AF027868 AF027868 g2619020 Bacillus subtilis 1423 -11530966 7500963762 yoab (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:20308) (re:21552) (di:complement) BSUB0011 Z99114 g2634248 Bacillus subtilis 1423 -11530966

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797737	4453	26609	501	166

Description

6500727109 hypothetical protein:similar to xylulokinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaC yoaC Bacillus subtilis 1423 -11530967 7000694906 yoac xylulokinase homolog yoac (db:pir2.dat) E69895 E69895 Bacillus subtilis 1423 -11530967 5500701867 yoac xylulose kinase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to lactobacillus xylulose kinase (501 aa)) (le:2555) (re:4018) (di:complement) AF027868 AF027868 g2619021 Bacillus subtilis 1423 -11530967 7500965438 yoac (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to xylulokinase) (le:21646) (re:23109) (di:complement) BSUB0011 Z99114 g2634249 Bacillus subtilis 1423 -11530967

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797738	4454	26610	744	247

Description

6500727110 hypothetical protein:similar to formate dehydrogenase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaE yoaE Bacillus subtilis 1423 -11530968 7000693001 yoae formate dehydrogenase homolog yoae (db:pir2.dat) G69895 G69895 Bacillus subtilis 1423 -11530968 5500701869 yoae putative formate dehydrogenase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis yyae protein (667 aa) and) (le:5394) (re:7427) (di:direct) AF027868 AF027868 g2618996 Bacillus subtilis 1423 -11530968 7500963992 yoae (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to formate dehydrogenase) (le:24485) (re:26518) (di:direct) BSUB0011 Z99114 g2634251 Bacillus subtilis 1423 -11530968

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797741	4455	26611	660	219

Description

GTC ORF with score 143 to: (or:Mus musculus) (sr:mouse (strain cd-1) dna, library of o.smithies, clone pump-3 hb) (db:genpept-rod) (de:mouse prp gene encoding proline-rich protein mp-3, exon 2.) (nt:proline-rich protein mp-3) (le:<1) (re:893) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797745	4456	26612	447	148

Description

6500727111 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaF yoaF Bacillus subtilis 1423 -11530969 7000693514 yoaf hypothetical protein yoaf (db:pir2.dat) H69895 H69895 Bacillus subtilis 1423 -11530969 7500964465 yoaf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:26595) (re:26888) (di:direct) BSUB0011 Z99114 g2634252 Bacillus subtilis 1423 -11530969

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797750	4457	26613	810	269

Description

GTC ORF with score 352 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome 1 bac f12f1 sequence, completesequence.) (nt:very strong similarity to aminomethyltransferase) (le:111379:112049) (re:111925:112167) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797755	4458	26614	321	106

Description

6500727112 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaG yoaG Bacillus subtilis 1423 -11530970 7000692659 yoag conserved hypothetical protein yoag (cl:conserved hypothetical protein ynef) (db:pir2.dat) A69896 A69896 Bacillus subtilis 1423 -11530970 7500963763 yoag (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:27261) (re:27665) (di:complement) BSUB0011 Z99114 g2634253 Bacillus subtilis 1423 -11530970

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797756	4459	26615	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797757	4460	26616	216	71

Description

6500727113 hypothetical protein:similar to methyl-accepting chemotaxis protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaH yoaH Bacillus subtilis 1423 -11530971 7000694215 yoah methyl-accepting chemotaxis protein homolog yoah (db:pir2.dat) B69896 B69896 Bacillus subtilis 1423 -11530971 5500701870 yoah yoah (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis methyl-accepting chemotaxis) (le:9423) (re:11027) (di:complement) AF027868 AF027868 g2619023 Bacillus subtilis 1423 -11530971 7500964940 yoah (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to methyl-accepting chemotaxis protein) (le:28514) (re:30118) (di:complement) BSUB0011 Z99114 g2634254 Bacillus subtilis 1423 -11530971

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797768	4461	26617	342	113

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797784	4462	26618	1620	539

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797822	4463	26619	1281	426

Description

6500727114 hypothetical protein:similar to 4-hydroxyphenylacetate-3-hydroxylase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaI yoaI Bacillus subtilis 1423 -11530972 7000692066 yoai 4-hydroxyphenylacetate-3-hydroxylase homolog yoai (db:pir2.dat) C69896 C69896 Bacillus subtilis 1423 -11530972 5500701871 yoai transcription antiterminator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to h.influenzae hi0035 protein (551 aa)) (le:11755) (re:12882) (di:direct) AF027868 AF027868 g2618997 Bacillus subtilis 1423 -11530972 7500963310 yoai (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to 4-hydroxyphenylacetate-3-hydroxylase) (le:30846) (re:31973) (di:direct) BSUB0011 Z99114 g2634255 Bacillus subtilis 1423 -11530972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797835	4464	26620	1131	376

Description

GTC ORF with score 172 to: (fn:potential guanine nucleotide exchange factor) (sr:human) (db:genpept) (de:homo sapiens herc2 (herc2) mrna, complete cds.) (nt:contains three rcc1 like domains, a zz zinc finger) (le:62) (re:14566) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797864	4465	26621	705	234

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797871	4466	26622	798	265

Description

6500727115 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaJ yoaJ Bacillus subtilis 1423 -11530973 7000693515 yoaj hypothetical protein yoaj (db:pir2.dat) D69896 D69896 Bacillus subtilis 1423 -11530973 5500701872 yoaj yoaj (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli outer membrane usher protein papc) (le:12919) (re:13617) (di:complement) AF027868 AF027868 g2619024 Bacillus subtilis 1423 -11530973 7500964466 yoaj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:32010) (re:32708) (di:complement) BSUB0011 Z99114 g2634256 Bacillus subtilis 1423 -11530973

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797885	4467	26623	351	117

Description

6500727116 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaK yoaK Bacillus subtilis 1423 -11530974 7000693516 yoak hypothetical protein yoak (db:pir2.dat) E69896 E69896 Bacillus subtilis 1423 -11530974 5500701873 yoak putative permease (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to s.typhimurium oligopeptide synthase) (le:13887) (re:14564) (di:complement) AF027868 AF027868 g2619025 Bacillus subtilis 1423 -11530974 7500964467 yoak (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:32978) (re:33655) (di:complement) BSUB0011 Z99114 g2634257 Bacillus subtilis 1423 -11530974

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797900	4468	26624	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797915	4469	26625	534	177

Description

6500727117 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaM yoaM Bacillus subtilis 1423 -11530975 7000692660 yoam conserved hypothetical protein yoam (db:pir2.dat) F69896 F69896 Bacillus subtilis 1423 -11530975 5500701875 yoam yoam (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli putative general secretion) (le:16031) (re:16714) (di:direct) AF027868 AF027868 g2618999 Bacillus subtilis 1423 -11530975 7500963764 yoam (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:35122) (re:35805) (di:direct) BSUB0011 Z99114 g2634259 Bacillus subtilis 1423 -11530975

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797919	4470	26626	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797924	4471	26627	690	229

Description

6500727118 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaN yoaN Bacillus subtilis 1423 -11530976 7000692661 yoan conserved hypothetical protein yoan (cl:conserved hypothetical protein yoan) (db:pir2.dat) G69896 G69896 Bacillus subtilis 1423 -11530976 5500701876 yoan yoan (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to vicia faba legumin type b (335 aa)) (le:17593) (re:18771) (di:complement) AF027868 AF027868 g2619026 Bacillus subtilis 1423 -11530976 7500955954 yoan (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:36684) (re:37862) (di:complement) BSUB0011 Z99114 g2634260 Bacillus subtilis 1423 -11530976

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797925	4472	26628	336	111

Description

6500727119 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaO yoaO Bacillus subtilis 1423 -11530977 7000692662 yoao conserved hypothetical protein yoao (db:pir2.dat) H69896 H69896 Bacillus subtilis 1423 -11530977 5500701877 yoao yoao (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to african clawed frog enkephalin precursor) (le:18894) (re:19382) (di:complement) AF027868 AF027868 g2619027 Bacillus subtilis 1423 -11530977 7500963765 yoao (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:37985) (re:38473) (di:complement) BSUB0011 Z99114 g2634261 Bacillus subtilis 1423 -11530977

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797927	4473	26629	645	214

Description

6500727120 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaP yoaP Bacillus subtilis 1423 -11530978 7000693517 yoap hypothetical protein yoap (db:pir2.dat) A69897 A69897 Bacillus subtilis 1423 -11530978 5500701878 yoap ras-like protein homolog (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to d.melanogaster ras-like protein 1 (189) (le:19602) (re:20357) (di:complement) AF027868 AF027868 g2619028 Bacillus subtilis 1423 -11530978 7500964468 yoap (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:38693) (re:39448) (di:complement) BSUB0011 Z99114 g2634262 Bacillus subtilis 1423 -11530978

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797949	4474	26630	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797962	4475	26631	501	166

Description

6500727121 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaQ yoaQ Bacillus subtilis 1423 -11530979 7000693518 yoaq hypothetical protein yoaq (db:pir2.dat) B69897 B69897 Bacillus subtilis 1423 -11530979 7500964469 yoaq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:39756) (re:40112) (di:direct) BSUB0011 Z99114 g2634263 Bacillus subtilis 1423 -11530979

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501797986	4476	26632	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798003	4477	26633	1518	506

Description

6500727122 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozF yozF Bacillus subtilis 1423 -11530980 7000693833 yozf hypothetical protein yozf (db:pir2.dat) B69931 B69931 Bacillus subtilis 1423 -11530980 7500964647 yozf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:40660) (re:40911) (di:complement) BSUB0011 Z99114 g2634264 Bacillus subtilis 1423 -11530980

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798013	4478	26634	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798020	4479	26635	660	219

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798029	4480	26636	474	157

Description

6500727123 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaR yoaR Bacillus subtilis 1423 -11530981 7000693519 yoar hypothetical protein yoar (db:pir2.dat) C69897 C69897 Bacillus subtilis 1423 -11530981 5500701879 yoar yoar (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to s.aureus capi protein (334 aa)) (le:21921) (re:22832) (di:complement) AF027868 AF027868 g2619029 Bacillus subtilis 1423 -11530981 7500964470 yoar (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:41012) (re:41923) (di:complement) BSUB0011 Z99114 g2634265 Bacillus subtilis 1423 -11530981

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798032	4481	26637	363	120

Description

GTC ORF with score 225 to: (sr:sinapis alba (library: lambda gt10) cdna to mrna) (db:genpept-pln1) (de:sinapis alba rna-binding protein homologue (grp1a) mrna, completecds.) (nt:homology with rna-binding proteins in meristematic) (le:19) (re:519) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798039	4482	26638	759	253

Description

GTC ORF with score 244 to: (or:Arabidopsis thaliana) (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana bac t12h20.) (nt:similar to schizosaccharomyces pombe isp4 protein) (le:11336:11441:11976:12205) (re:11366:11839:12130:12302) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798047	4483	26639	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798052	4484	26640	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798057	4485	26641	561	186

Description

6500727124 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaS yoaS Bacillus subtilis 1423 -11530982 7000693520 yoas hypothetical protein yoas (db:pir2.dat) D69897 D69897 Bacillus subtilis 1423 -11530982 7500964471 yoas (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:42270) (re:42752) (di:direct) BSUB0011 Z99114 g2634266 Bacillus subtilis 1423 -11530982

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798064	4486	26642	579	192

Description

GTC ORF with score 587 to: (sr:gibberella zeae (sub_species:graminearum, strain:f15) dna) (db:genpept-pln2) (de:gibberella zeae genes for trichothecene 3-o-acetyltransferase,utp-ammonia ligase and phosphate permease, complete cds.) (le:6588:7075:7622) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798078	4487	26643	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798079	4488	26644	330	109

Description

6500727125 hypothetical protein:similar to transcriptional regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozG yozG Bacillus subtilis 1423 -11530983 7000694789 yozg transcription regulator homolog yozg (db:pir2.dat) C69931 C69931 Bacillus subtilis 1423 -11530983 7500965350 yozg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to transcriptional regulator) (le:42762) (re:43016) (di:direct) BSUB0011 Z99114 g2634267 Bacillus subtilis 1423 -11530983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798085	4489	26645	510	169

Description

6500727126 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaT yoaT Bacillus subtilis 1423 -11530984 7000693521 yoat hypothetical protein yoat (db:pir2.dat) E69897 E69897 Bacillus subtilis 1423 -11530984 5500701880 yoat yoat (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to h.influezae protein hi1620 (167 aa)) (le:24031) (re:24825) (di:direct) AF027868 AF027868 g2619000 Bacillus subtilis 1423 -11530984 7500964472 yoat (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:43122) (re:43916) (di:direct) BSUB0011 Z99114 g2634268 Bacillus subtilis 1423 -11530984

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798089	4490	26646	354	117

Description

6500727127 hypothetical protein:similar to transcriptional regulator:lysr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaU yoaU Bacillus subtilis 1423 -11530985 7000694755 yoau transcription regulator lysr family homolog yoau (db:pir2.dat) F69897 F69897 Bacillus subtilis 1423 -11530985 5500701881 yoau transcription regulator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis gltc regulatory protein (300) (le:24949) (re:25821) (di:complement) AF027868 AF027868 g2619030 Bacillus subtilis 1423 -11530985 7500965325 yoau (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to transcriptional regulator (lysr family)) (le:44040) (re:44912) (di:complement) BSUB0011 Z99114 g2634269 Bacillus subtilis 1423 -11530985

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798091	4491	26647	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798093	4492	26648	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798104	4493	26649	333	110

Description

6500727128 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaV yoaV Bacillus subtilis 1423 -11530986 7000692663 yoav conserved hypothetical protein yoav (db:pir2.dat) G69897 G69897 Bacillus subtilis 1423 -11530986 5500701882 yoav yoav (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli yije hypothetical protein (312) (le:25922) (re:26800) (di:direct) AF027868 AF027868 g2619001 Bacillus subtilis 1423 -11530986 7500963766 yoav (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:45013) (re:45891) (di:direct) BSUB0011 Z99114 g2634270 Bacillus subtilis 1423 -11530986

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798106	4494	26650	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798107	4495	26651	690	229

Description

6500727129 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaW yoaW Bacillus subtilis 1423 -11530987 7000693522 yoaw hypothetical protein yoaw (db:pir2.dat) H69897 H69897 Bacillus subtilis 1423 -11530987 5500701883 yoaw putative regulator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to h.influenzae ferric uptake regulatory) (le:26973) (re:27404) (di:complement) AF027868 AF027868 g2619031 Bacillus subtilis 1423 -11530987 7500964473 yoaw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:46064) (re:46495) (di:complement) BSUB0011 Z99114 g2634271 Bacillus subtilis 1423 -11530987

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798114	4496	26652	486	161

Description

6500727130 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoaZ yoaZ Bacillus subtilis 1423 -11530988 7000692664 yoaz conserved hypothetical protein yoaz (db:pir2.dat) A69898 A69898 Bacillus subtilis 1423 -11530988 5500701884 yoaz yoaz (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to glyceraldehyde 3-phosphate dehydrogenase) (le:27668) (re:28300) (di:complement) AF027868 AF027868 g2619032 Bacillus subtilis 1423 -11530988 7500963767 yoaz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:46759) (re:47391) (di:complement) BSUB0011 Z99114 g2634272 Bacillus subtilis 1423 -11530988

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798115	4497	26653	474	157

Description

6500727131 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobA yobA Bacillus subtilis 1423 -11530989 7000693523 yoba hypothetical protein yoba (db:pir2.dat) B69898 B69898 Bacillus subtilis 1423 -11530989 7500964474 yoba (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:49034) (re:49396) (di:complement) BSUB0011 Z99114 g2634274 Bacillus subtilis 1423 -11530989

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798116	4498	26654	249	82

Description

6500727132 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobB yobB Bacillus subtilis 1423 -11530990 7000693524 yobb hypothetical protein yobb (db:pir2.dat) C69898 C69898 Bacillus subtilis 1423 -11530990 7500964475 yobb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:49773) (re:50036) (di:direct) BSUB0011 Z99114 g2634275 Bacillus subtilis 1423 -11530990

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798120	4499	26655	207	68

Description

6500727133 hypothetical protein:similar to transcriptional regulator:phage-related:xre family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobD yobD Bacillus subtilis 1423 -11530991 7000694779 yobd transcription regulator phage-related homolog yobd (cl:probable transcription repressor yowr) (db:pir2.dat) D69898 D69898 Bacillus subtilis 1423 -11530991 5500701887 yobd transcription regulator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis yqae putative transcriptional) (le:36271) (re:36609) (di:direct) AF027868 AF027868 g2619003 Bacillus subtilis 1423 -11530991 7500965342 yobd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to transcriptional regulator) (le:55362) (re:55700) (di:direct) BSUB0011 Z99114 g2634278 Bacillus subtilis 1423 -11530991

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798129	4500	26656	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798136	4501	26657	231	76

Description

6500727134 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozH yozH Bacillus subtilis 1423 -11530992 7000693834 yozh hypothetical protein yozh (db:pir2.dat) D69931 D69931 Bacillus subtilis 1423 -11530992 7500964648 yozh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:55734) (re:56054) (di:complement) BSUB0011 Z99114 g2634279 Bacillus subtilis 1423 -11530992

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798137	4502	26658	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798139	4503	26659	825	275

Description

6500727135 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozI yozI Bacillus subtilis 1423 -11530993 7000693835 yozi hypothetical protein yozi (db:pir2.dat) E69931 E69931 Bacillus subtilis 1423 -11530993 7500964649 yozi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:56299) (re:56664) (di:direct) BSUB0011 Z99114 g2634280 Bacillus subtilis 1423 -11530993

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798145	4504	26660	684	227

Description

6500727136 hypothetical protein:similar to general secretion pathway protein (gtcfc:12.10) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobE yobE Bacillus subtilis 1423 -11530994 7000693018 yobe general secretion pathway protein homolog yobe (db:pir2.dat) E69898 E69898 Bacillus subtilis 1423 -11530994 5500701888 yobe yobe (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to n-terminal part of b.thuringiensis 130) (le:37795) (re:38454) (di:direct) AF027868 AF027868 g2619004 Bacillus subtilis 1423 -11530994 7500964003 yobe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to general secretion pathway protein) (le:56886) (re:57545) (di:direct) BSUB0011 Z99114 g2634281 Bacillus subtilis 1423 -11530994

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798155	4505	26661	1392	464

Description

6500727137 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobF yobF Bacillus subtilis 1423 -11530995 7000693525 yobf hypothetical protein yobf (db:pir2.dat) F69898 F69898 Bacillus subtilis 1423 -11530995 5500701889 yobf radc homolog (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis radc dna repair protein) (le:38709) (re:39632) (di:complement) AF027868 AF027868 g2619035 Bacillus subtilis 1423 -11530995 7500964476 yobf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:57800) (re:58723) (di:complement) BSUB0011 Z99114 g2634282 Bacillus subtilis 1423 -11530995

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798163	4506	26662	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798170	4507	26663	216	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798186	4508	26664	261	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798193	4509	26665	468	156

Description

6500727138 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozJ yozJ Bacillus subtilis 1423 -11530996 7000693836 yozj hypothetical protein yozj (db:pir2.dat) F69931 F69931 Bacillus subtilis 1423 -11530996 7500964650 yozj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:59322) (re:59777) (di:complement) BSUB0011 Z99114 g2634283 Bacillus subtilis 1423 -11530996

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798197	4510	26666	264	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798208	4511	26667	690	229

Description

6500727139 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobH yobH Bacillus subtilis 1423 -11530997 7000692665 yobh conserved hypothetical protein yobh (db:pir2.dat) G69898 G69898 Bacillus subtilis 1423 -11530997 5500701891 yobh umuc homolog (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis yqjw protein (412 aa) and) (le:43504) (re:44115) (di:complement) AF027868 AF027868 g2619036 Bacillus subtilis 1423 -11530997 7500963768 yobh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:62595) (re:63206) (di:complement) BSUB0011 Z99114 g2634286 Bacillus subtilis 1423 -11530997

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798848	4512	26668	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798866	4513	26669	291	96

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798868	4514	26670	1500	500

Description

6500727140 hypothetical protein:similar to dna repair protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozK yozK Bacillus subtilis 1423 -11530998 7000692944 yozk dna repair protein homolog yozk (db:pir2.dat) G69931 G69931 Bacillus subtilis 1423 -11530998 7500963955 yozk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to dna repair protein) (le:63285) (re:63632) (di:complement) BSUB0011 Z99114 g2634287 Bacillus subtilis 1423 -11530998

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798888	4515	26671	186	61

Description

6500727141 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozL yozL Bacillus subtilis 1423 -11530999 7000693837 yozl hypothetical protein yozl (db:pir2.dat) H69931 H69931 Bacillus subtilis 1423 -11530999 7500964651 yozl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:63625) (re:63918) (di:complement) BSUB0011 Z99114 g2634288 Bacillus subtilis 1423 -11530999

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798889	4516	26672	747	248

Description

6500727142 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozM yozM Bacillus subtilis 1423 -11531000 7000693838 yozm hypothetical protein yozm (db:pir2.dat) A69932 A69932 Bacillus subtilis 1423 -11531000 7500964652 yozm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:64127) (re:64462) (di:direct) BSUB0011 Z99114 g2634289 Bacillus subtilis 1423 -11531000

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798904	4517	26673	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798905	4518	26674	246	81

Description

GTC ORF with score 99 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798907	4519	26675	594	197

Description

GTC ORF with score 289 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798922	4520	26676	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798923	4521	26677	1134	378

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798930	4522	26678	699	232

Description

GTC ORF with score 176 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c28h8.) (nt:similar to yeast antiviral protein ski2 and) (le:26085:26897:27388:28779) (re:26850:27339:28734:29002) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798931	4523	26679	606	202

Description

GTC ORF with score 278 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c28h8.) (nt:similar to yeast antiviral protein ski2 and) (le:26085:26897:27388:28779) (re:26850:27339:28734:29002) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798935	4524	26680	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798943	4525	26681	855	284

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798945	4526	26682	468	155

Description

6500727143 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobI yobI Bacillus subtilis 1423 -11531001 7000693526 yobi hypothetical protein yobi (db:pir2.dat) H69898 H69898 Bacillus subtilis 1423 -11531001 5500701892 yobi dna-binding protein (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to human centromeric protein e (2663 aa)) (le:45418) (re:49023) (di:complement) AF027868 AF027868 g2619037 Bacillus subtilis 1423 -11531001 7500964477 yobi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:64509) (re:68114) (di:complement) BSUB0011 Z99114 g2634290 Bacillus subtilis 1423 -11531001

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798955	4527	26683	510	169

Description

6500727144 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobJ yobJ Bacillus subtilis 1423 -11531002 7000693527 yobj hypothetical protein yobj (db:pir2.dat) A69899 A69899 Bacillus subtilis 1423 -11531002 5500701893 yobj yobj (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (le:50238) (re:51080) (di:complement) AF027868 AF027868 g2619038 Bacillus subtilis 1423 -11531002 7500964478 yobj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:69329) (re:70171) (di:complement) BSUB0011 Z99114 g2634291 Bacillus subtilis 1423 -11531002

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798961	4528	26684	696	231

Description

6500727145 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobK yobK Bacillus subtilis 1423 -11531003 7000693528 yobk hypothetical protein yobk (db:pir2.dat) B69899 B69899 Bacillus subtilis 1423 -11531003 5500701894 yobk spore coat protein (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis spore coat protein e (181) (le:51280) (re:51738) (di:complement) AF027868 AF027868 g2619039 Bacillus subtilis 1423 -11531003 7500964479 yobk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:70371) (re:70829) (di:complement) BSUB0011 Z99114 g2634292 Bacillus subtilis 1423 -11531003

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501798987	4529	26685	405	134

Description

6500727146 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobL yobL Bacillus subtilis 1423 -11531004 7000692666 yobl conserved hypothetical protein yobl (db:pir2.dat) C69899 C69899 Bacillus subtilis 1423 -11531004 5500701895 yobl topi homolog (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis hypothetical protein yqcg) (le:51748) (re:53550) (di:complement) AF027868 AF027868 g2619040 Bacillus subtilis 1423 -11531004 7500963769 yobl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:70839) (re:72641) (di:complement) BSUB0011 Z99114 g2634293 Bacillus subtilis 1423 -11531004

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799001	4530	26686	543	180

Description

6500727147 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobM yobM Bacillus subtilis 1423 -11531005 7000692667 yobm conserved hypothetical protein yobm (db:pir2.dat) D69899 D69899 Bacillus subtilis 1423 -11531005 5500701896 yobm spore coat protein (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis hypothetical protein yrkn) (le:53652) (re:54140) (di:complement) AF027868 AF027868 g2619041 Bacillus subtilis 1423 -11531005 7500963770 yobm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:72743) (re:73231) (di:complement) BSUB0011 Z99114 g2634294 Bacillus subtilis 1423 -11531005

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799024	4531	26687	1230	409

Description

6500727148 hypothetical protein:similar to l-amino acid oxidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobN yobN Bacillus subtilis 1423 -11531006 7000694140 yobn l-amino acid oxidase homolog yobn (db:pir2.dat) E69899 E69899 Bacillus subtilis 1423 -11531006 5500701897 yobn putative l-amino acid oxidase precursor (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to human amine oxidase (527 aa)) (le:54433) (re:55773) (di:direct) AF027868 AF027868 g2619006 Bacillus subtilis 1423 -11531006 7500964880 yobn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to l-amino acid oxidase) (le:73524) (re:74864) (di:direct) BSUB0011 Z99114 g2634295 Bacillus subtilis 1423 -11531006

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799053	4532	26688	435	144

Description

6500727149 hypothetical protein:similar to phage-related pre-neck appendage protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobO yobO Bacillus subtilis 1423 -11531007 7000694374 yobo phage-related pre-neck appendage protein homolog yobo (db:pir2.dat) F69899 F69899 Bacillus subtilis 1423 -11531007 5500701898 yobo yobo (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to phage phi-29 gene 12 protein (854 aa)) (le:56200) (re:58620) (di:direct) AF027868 AF027868 g2619007 Bacillus subtilis 1423 -11531007 7500965054 yobo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to phage-related pre-neck appendage) (le:75291) (re:77711) (di:direct) BSUB0011 Z99114 g2634296 Bacillus subtilis 1423 -11531007

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799063	4533	26689	2103	701

Description

6500727150 hypothetical protein:similar to transcriptional regulator:arac/xyls family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobQ yobQ Bacillus subtilis 1423 -11531008 7000694718 yobq transcription regulator arac/xyls family homolog yobq (db:pir2.dat) G69899 G69899 Bacillus subtilis 1423 -11531008 5500701899 yobq transcription regulator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to s.typhimurium arac regulatory protein) (le:59605) (re:60330) (di:complement) AF027868 AF027868 g2619043 Bacillus subtilis 1423 -11531008 7500965293 yobq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to transcriptional regulator (arac/xyls) (le:78696) (re:79421) (di:complement) BSUB0011 Z99114 g2634298 Bacillus subtilis 1423 -11531008

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799067	4534	26690	231	76

Description

6500727151 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobR yobR Bacillus subtilis 1423 -11531009 7000693529 yobr hypothetical protein yobr (db:pir2.dat) H69899 H69899 Bacillus subtilis 1423 -11531009 5500701900 yobr putative acetyl transferase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to different acetyltrasferases) (le:60345) (re:61088) (di:complement) AF027868 AF027868 g2619044 Bacillus subtilis 1423 -11531009 7500964480 yobr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:79436) (re:80179) (di:complement) BSUB0011 Z99114 g2634299 Bacillus subtilis 1423 -11531009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799068	4535	26691	192	64

Description

6500727152 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobS yobS Bacillus subtilis 1423 -11531010 7000693530 yobs hypothetical protein yobs (db:pir2.dat) A69900 A69900 Bacillus subtilis 1423 -11531010 5500701901 yobs transcription regulator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli tetracycline repressor protein) (le:61166) (re:61741) (di:complement) AF027868 AF027868 g2619045 Bacillus subtilis 1423 -11531010 7500964481 yobs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:80257) (re:80832) (di:complement) BSUB0011 Z99114 g2634300 Bacillus subtilis 1423 -11531010

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799075	4536	26692	786	261

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799089	4537	26693	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799092	4538	26694	627	208

Description

6500727153 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobT yobT Bacillus subtilis 1423 -11531011 7000692668 yobt conserved hypothetical protein yobt (db:pir2.dat) B69900 B69900 Bacillus subtilis 1423 -11531011 5500701902 yobt yobt (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar toh xanthomonas l1 metallo-beta-lactamase) (le:61747) (re:62448) (di:complement) AF027868 AF027868 g2619046 Bacillus subtilis 1423 -11531011 7500963771 yobt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:80838) (re:81539) (di:complement) BSUB0011 Z99114 g2634301 Bacillus subtilis 1423 -11531011

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799119	4539	26695	243	80

Description

6500727154 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobU yobU Bacillus subtilis 1423 -11531012 7000693531 yobu hypothetical protein yobu (db:pir2.dat) C69900 C69900 Bacillus subtilis 1423 -11531012 5500701903 yobu dna-binding protein yobu (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to mouse growth arrest and dna damage) (le:62525) (re:63007) (di:complement) AF027868 AF027868 g2619047 Bacillus subtilis 1423 -11531012 7500964482 yobu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:81616) (re:82098) (di:complement) BSUB0011 Z99114 g2634302 Bacillus subtilis 1423 -11531012

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799127	4540	26696	987	328

Description

6500727155 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobV yobV Bacillus subtilis 1423 -11531013 7000692669 yobv conserved hypothetical protein yobv (db:pir2.dat) D69900 D69900 Bacillus subtilis 1423 -11531013 5500701904 yobv transcription regulator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to mycobacterium tuberculosis hypothetical) (le:63061) (re:64002) (di:complement) AF027868 AF027868 g2619048 Bacillus subtilis 1423 -11531013 7500963772 yobv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:82152) (re:83093) (di:complement) BSUB0011 Z99114 g2634303 Bacillus subtilis 1423 -11531013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799132	4541	26697	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799135	4542	26698	516	171

Description

6500727156 csk22:yobw hypothetical protein:similar to sporulation membrane protein sigma-k-controlled (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yobW yobW Bacillus subtilis 1423 -11531014 7000693532 yobw hypothetical protein yobw (db:pir2.dat) E69900 E69900 Bacillus subtilis 1423 -11531014 220189 yobw channel protein (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to h.influenzae rod-shape-determining) (le:64208) (re:64753) (di:direct) AF027868 AF027868 g2619008 Bacillus subtilis 1423 -11531014 5500687786 csk22 membrane protein csk22 (db:genpept-bct1) (de:bacillus subtilis membrane protein csk22 (csk22) gene, completecds.) (le:291) (re:836) (di:direct) BSU70042 U70042 g1710303 Bacillus subtilis 1423 -11531014 7500964483 yobw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: csk22; similar to sporulation) (le:83299) (re:83844) (di:direct) BSUB0011 Z99114 g2634304 Bacillus subtilis 1423 -11531014

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799138	4543	26699	1332	444

Description

6500727157 hypothetical protein:similar to transcriptional regulator:arsr family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozA yozA Bacillus subtilis 1423 -11531015 7000694723 yoza transcription regulator arsr family homolog yoza (db:pir2.dat) E69930 E69930 Bacillus subtilis 1423 -11531015 7500965298 yoza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to transcriptional regulator (arsr family)) (le:83871) (re:84194) (di:complement) BSUB0011 Z99114 g2634305 Bacillus subtilis 1423 -11531015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799153	4544	26700	393	130

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799157	4545	26701	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799165	4546	26702	537	179

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799168	4547	26703	273	90

Description

6500727158 hypothetical protein:similar to transposon-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocA yocA Bacillus subtilis 1423 -11531016 7000694827 yoca transposon-related protein homolog yoca (db:pir2.dat) F69900 F69900 Bacillus subtilis 1423 -11531016 5500701905 yoca ras-related protein (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to human ras-related protein rab-27 (221) (le:65297) (re:65974) (di:direct) AF027868 AF027868 g2619009 Bacillus subtilis 1423 -11531016 7500965380 yoca (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to transposon-related protein) (le:84388) (re:85065) (di:direct) BSUB0011 Z99114 g2634306 Bacillus subtilis 1423 -11531016

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799173	4548	26704	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799184	4549	26705	678	225

Description

6500727159 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozB yozB Bacillus subtilis 1423 -11531017 7000692711 yozb conserved hypothetical protein yozb (db:pir2.dat) F69930 F69930 Bacillus subtilis 1423 -11531017 7500963796 yozb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:85155) (re:85691) (di:complement) BSUB0011 Z99114 g2634307 Bacillus subtilis 1423 -11531017

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799185	4550	26706	864	287

Description

6500727160 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocB yocB Bacillus subtilis 1423 -11531018 7000693533 yocb hypothetical protein yocb (db:pir2.dat) G69900 G69900 Bacillus subtilis 1423 -11531018 5500701906 yocb putative replication factor (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to mouse dna replication licensing factor) (le:66737) (re:67519) (di:complement) AF027868 AF027868 g2619049 Bacillus subtilis 1423 -11531018 7500964484 yocb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:85828) (re:86610) (di:complement) BSUB0011 Z99114 g2634308 Bacillus subtilis 1423 -11531018

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799212	4551	26707	396	132

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799215	4552	26708	234	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799217	4553	26709	192	63

Description

6500727161 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocC yocC Bacillus subtilis 1423 -11531019 7000693534 yocc hypothetical protein yocc (db:pir2.dat) H69900 H69900 Bacillus subtilis 1423 -11531019 5500701907 yocc yocc (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (le:67690) (re:68187) (di:direct) AF027868 AF027868 g2619010 Bacillus subtilis 1423 -11531019 7500964485 yocc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:86781) (re:87278) (di:direct) BSUB0011 Z99114 g2634309 Bacillus subtilis 1423 -11531019

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799218	4554	26710	243	80

Description

6500727162 hypothetical protein:similar to immunity to bacteriotoxins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocD yocD Bacillus subtilis 1423 -11531020 7000694103 yocd immunity to bacteriotoxins homolog yocd (db:pir2.dat) A69901 A69901 Bacillus subtilis 1423 -11531020 5500701908 yocd yocd (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli cryptic l-xylulose kinase (418) (le:68251) (re:69228) (di:direct) AF027868 AF027868 g2619011 Bacillus subtilis 1423 -11531020 7500964864 yocd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to immunity to bacteriotoxins) (le:87342) (re:88319) (di:direct) BSUB0011 Z99114 g2634310 Bacillus subtilis 1423 -11531020

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799219	4555	26711	426	141

Description

6500727163 hypothetical protein:similar to fatty-acid desaturase (gtcfc:14.1) (ec:1.14.99.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocE yocE Bacillus subtilis 1423 -11531021 7000692977 yoce fatty-acid desaturase homolog yoce (db:pir2.dat) B69901 B69901 Bacillus subtilis 1423 -11531021 5500701909 yoce fatty acid desaturase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to synechocystis fatty acid desaturase (351) (le:69390) (re:70448) (di:direct) AF027868 AF027868 g2619012 Bacillus subtilis 1423 -11531021 7500963977 yoce (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to fatty-acid desaturase) (le:88481) (re:89539) (di:direct) BSUB0011 Z99114 g2634311 Bacillus subtilis 1423 -11531021 7500963978 membrane bound delta 5 acyl lipid desaturase (db:genpept-bct2) (de:bacillus subtilis membrane bound delta 5 acyl lipid desaturasegene, complete cds.) (le:1) (re:1059) (di:direct) AF037430 AF037430 g3064243 Bacillus subtilis 1423 -11531021

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799220	4556	26712	405	134

Description

6500727164 hypothetical protein:similar to two-component sensor histidine kinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocF yocF Bacillus subtilis 1423 -11531022 7000694876 yocf two-component sensor histidine kinase homolog yocf (db:pir2.dat) C69901 C69901 Bacillus subtilis 1423 -11531022 5500701910 yocf sensor kinase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis degs sensor kinase (385 aa)) (le:70568) (re:71680) (di:direct) AF027868 AF027868 g2619013 Bacillus subtilis 1423 -11531022 7500965415 yocf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to two-component sensor histidine kinase) (le:89659) (re:90771) (di:direct) BSUB0011 Z99114 g2634312 Bacillus subtilis 1423 -11531022

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799221	4557	26713	267	89

Description

6500727165 hypothetical protein:similar to two-component response regulator (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocG yocG Bacillus subtilis 1423 -11531023 7000694847 yocg two-component response regulator yocf homolog yocg) (cl:regulatory protein coma:response regulator homology) (db:pir2.dat) D69901 D69901 Bacillus subtilis 1423 -11531023 5500701911 yocg sensor regulator (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis spo0a protein (267 aa)) (le:71699) (re:72298) (di:direct) AF027868 AF027868 g2619014 Bacillus subtilis 1423 -11531023 7500965396 yocg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to two-component response regulator (yocf)) (le:90790) (re:91389) (di:direct) BSUB0011 Z99114 g2634313 Bacillus subtilis 1423 -11531023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799222	4558	26714	237	78

Description

6500727166 hypothetical protein:similar to cell wall-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocH yocH Bacillus subtilis 1423 -11531024 7000692338 yoch cell wall-binding protein homolog yoch (db:pir2.dat) E69901 E69901 Bacillus subtilis 1423 -11531024 5500701912 yoch yoch (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis phosphatase-associated) (le:72893) (re:73756) (di:complement) AF027868 AF027868 g2619050 Bacillus subtilis 1423 -11531024 7500963505 yoch (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to cell wall-binding protein) (le:91984) (re:92847) (di:complement) BSUB0011 Z99114 g2634314 Bacillus subtilis 1423 -11531024

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799223	4559	26715	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799228	4560	26716	417	138

Description

GTC ORF with score 95 to: (sr:synechococcus sp. strain=wh8102) (db:genpept-bct2) (de:synechococcus sp. strain wh8102 cell-surface-associated polypeptide(swma) gene, complete cds.) (nt:swma; contains calcium-binding motifs, including an) (le:503) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799234	4561	26717	609	202

Description

6500727167 hypothetical protein:similar to atp-dependent dna helicase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocI yocI Bacillus subtilis 1423 -11531025 7000692251 yoci dna helicase recq:atp-dependent dna helicase homolog yoci (cl:recq protein:dead/h box helicase homology:recq helicase homology) (db:pir2.dat) F69901 F69901 Bacillus subtilis 1423 -11531025 5500701913 yoci recq homolog (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli recq protein (607 aa)) (le:74004) (re:75779) (di:complement) AF027868 AF027868 g2619051 Bacillus subtilis 1423 -11531025 7500963947 yoci (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to atp-dependent dna helicase) (le:93095) (re:94870) (di:complement) BSUB0011 Z99114 g2634315 Bacillus subtilis 1423 -11531025

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799236	4562	26718	855	284

Description

GTC ORF with score 549 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799255	4563	26719	318	105

Description

6500727168 hypothetical protein:similar to acyl-carrier protein phosphodiesterase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocJ yocJ Bacillus subtilis 1423 -11531026 7000692149 yocj acyl-carrier protein phosphodiesterase homolog yocj (cl:acyl carrier protein phosphodiesterase) (db:pir2.dat) G69901 G69901 Bacillus subtilis 1423 -11531026 5500701914 yocj acyl carrier protein phosphodiesterase (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli acyl-carrier protein) (le:76344) (re:76970) (di:complement) AF027868 AF027868 g2619052 Bacillus subtilis 1423 -11531026 7500963377 yocj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to acyl-carrier protein phosphodiesterase) (le:95435) (re:96061) (di:complement) BSUB0011 Z99114 g2634316 Bacillus subtilis 1423 -11531026

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799258	4564	26720	276	91

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799265	4565	26721	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799280	4566	26722	291	96

Description

6500727169 hypothetical protein:similar to general stress protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocK yocK Bacillus subtilis 1423 -11531027 7000693020 yock general stress protein homolog yock (db:pir2.dat) H69901 H69901 Bacillus subtilis 1423 -11531027 5500701915 yock dnak suppressor homolog (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis hypothetical protein yzwb) (le:77121) (re:77750) (di:complement) AF027868 AF027868 g2619053 Bacillus subtilis 1423 -11531027 7500964005 yock (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to general stress protein) (le:96212) (re:96841) (di:complement) BSUB0011 Z99114 g2634317 Bacillus subtilis 1423 -11531027

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799293	4567	26723	1122	373

Description

6500727170 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocL yocL Bacillus subtilis 1423 -11531028 7000693535 yocl hypothetical protein yocl (db:pir2.dat) A69902 A69902 Bacillus subtilis 1423 -11531028 5500701916 yocl yocl (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to phage spp2 hypothetical 16.2k protein) (le:77687) (re:78019) (di:complement) AF027868 AF027868 g2619054 Bacillus subtilis 1423 -11531028 7500964486 yocl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:96778) (re:97110) (di:complement) BSUB0011 Z99114 g2634318 Bacillus subtilis 1423 -11531028

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799294	4568	26724	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799298	4569	26725	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799303	4570	26726	987	328

Description

6500727171 hypothetical protein:similar to small heat-shock protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocM yocM Bacillus subtilis 1423 -11531029 7000694591 yocm small heat-shock protein homolog yocm (db:pir2.dat) B69902 B69902 Bacillus subtilis 1423 -11531029 5500701917 yocm spore protein (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to stigmatella aurantiaca spore protein) (le:78311) (re:78787) (di:complement) AF027868 AF027868 g2619055 Bacillus subtilis 1423 -11531029 7500965190 yocm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to small heat-shock protein) (le:97402) (re:97878) (di:complement) BSUB0011 Z99114 g2634319 Bacillus subtilis 1423 -11531029

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799314	4571	26727	345	114

Description

6500727172 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozN yozN Bacillus subtilis 1423 -11531030 7000693839 yozn hypothetical protein yozn (db:pir2.dat) B69932 B69932 Bacillus subtilis 1423 -11531030 7500964653 yozn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:97945) (re:98208) (di:direct) BSUB0011 Z99114 g2634320 Bacillus subtilis 1423 -11531030

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799315	4572	26728	381	126

Description

6500727173 hypothetical protein:similar to permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocN yocN Bacillus subtilis 1423 -11531031 7000694362 yocn permease homolog yocn (db:pir2.dat) C69902 C69902 Bacillus subtilis 1423 -11531031 5500701918 yocn yocn (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to e.coli high-affinity gluconate) (le:79122) (re:79355) (di:direct) AF027868 AF027868 g2619015 Bacillus subtilis 1423 -11531031 7500965048 yocn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to permease) (le:98213) (re:98446) (di:direct) BSUB0011 Z99114 g2634321 Bacillus subtilis 1423 -11531031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799317	4573	26729	456	151

Description

6500727174 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozO yozO Bacillus subtilis 1423 -11531032 7000693840 yozo hypothetical protein yozo (cl:hypothetical protein yozo) (db:pir2.dat) C69932 C69932 Bacillus subtilis 1423 -11531032 7500955882 yozo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:98532) (re:98876) (di:complement) BSUB0011 Z99114 g2634322 Bacillus subtilis 1423 -11531032

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799319	4574	26730	246	82

Description

6500727175 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozC yozC Bacillus subtilis 1423 -11531033 7000693830 yozc hypothetical protein yozc (db:pir2.dat) G69930 G69930 Bacillus subtilis 1423 -11531033 7500964644 yozc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:99233) (re:99436) (di:complement) BSUB0011 Z99114 g2634323 Bacillus subtilis 1423 -11531033

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799326	4575	26731	348	115

Description

6500727176 hypothetical protein:similar to sodium-dependent transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocR yocR Bacillus subtilis 1423 -11531034 7000694594 yocr sodium-dependent transporter homolog yocr (cl:gamma-aminobutyric acid transporter) (db:pir2.dat) D69902 D69902 Bacillus subtilis 1423 -11531034 5500701922 yocr putative transporter (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to h.influenzae hypothetical) (le:84928) (re:86265) (di:complement) AF027868 AF027868 g2619056 Bacillus subtilis 1423 -11531034 7500965193 yocr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to sodium-dependent transporter) (le:104019) (re:105356) (di:complement) BSUB0011 Z99114 g2634327 Bacillus subtilis 1423 -11531034

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799332	4576	26732	504	167

Description

6500727177 hypothetical protein:similar to sodium-dependent transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yocS yocS Bacillus subtilis 1423 -11531035 7000694595 yocs sodium-dependent transporter homolog yocs (db:pir2.dat) E69902 E69902 Bacillus subtilis 1423 -11531035 5500701923 yocs putative transporter (db:genpept-bct1) (de:bacillus subtilis chromosome region between terc and odhab.) (nt:similar to b.subtilis 2-keto-3-deoxygluconate) (le:86484) (re:87449) (di:direct) AF027868 AF027868 g2619019 Bacillus subtilis 1423 -11531035 7500965194 yocs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to sodium-dependent transporter) (le:105575) (re:106540) (di:direct) BSUB0011 Z99114 g2634328 Bacillus subtilis 1423 -11531035

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799339	4577	26733	1125	374

Description

6500727178 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojO yojO Bacillus subtilis 1423 -11531036 7000693550 yojo hypothetical protein yojo (db:pir2.dat) D69907 D69907 Bacillus subtilis 1423 -11531036 7500964504 yojo yojo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169331 Bacillus subtilis 1423 -11531036 7500964505 yojo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:110914) (re:112899) (di:complement) BSUB0011 Z99114 g2634331 Bacillus subtilis 1423 -11531036

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799341	4578	26734	624	207

Description

6500727179 hypothetical protein:similar to nitric-oxide reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojN yojN Bacillus subtilis 1423 -11531037 7000694324 yojn nitric-oxide reductase homolog yojn (db:pir2.dat) C69907 C69907 Bacillus subtilis 1423 -11531037 7500965021 yojn yojn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169330 Bacillus subtilis 1423 -11531037 7500965022 yojn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to nitric-oxide reductase) (le:112841) (re:113755) (di:complement) BSUB0011 Z99114 g2634332 Bacillus subtilis 1423 -11531037

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799342	4579	26735	240	79

Description

6500727180 hypothetical protein:similar to superoxide dismutase (gtcfc:14.1) (ec:1.15.1.1) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojM yojM Bacillus subtilis 1423 -11531038 7000694659 yojm superoxide dismutase homolog yojm (cl:superoxide dismutase (cu-zn)) (db:pir2.dat) B69907 B69907 Bacillus subtilis 1423 -11531038 7500965241 yojm yojm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169329 Bacillus subtilis 1423 -11531038 7500965242 yojm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to superoxide dismutase) (le:113819) (re:114409) (di:complement) BSUB0011 Z99114 g2634333 Bacillus subtilis 1423 -11531038

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799344	4580	26736	684	227

Description

6500727181 hypothetical protein:similar to cell wall-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojL yojL Bacillus subtilis 1423 -11531039 7000692339 yojl cell wall-binding protein homolog yojl (db:pir2.dat) A69907 A69907 Bacillus subtilis 1423 -11531039 7500963506 yojl yojl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169328 Bacillus subtilis 1423 -11531039 7500963507 yojl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to cell wall-binding protein) (le:114502) (re:115746) (di:complement) BSUB0011 Z99114 g2634334 Bacillus subtilis 1423 -11531039

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799359	4581	26737	441	146

Description

6500727182 hypothetical protein:similar to macrolide glycosyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojK yojK Bacillus subtilis 1423 -11531040 7000694179 yojk macrolide glycosyltransferase homolog yojk (cl:glycosyltransferase) (db:pir2.dat) H69906 H69906 Bacillus subtilis 1423 -11531040 7500954262 yojk yojk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169327 Bacillus subtilis 1423 -11531040 7500954263 yojk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to macrolide glycosyltransferase) (le:116128) (re:116991) (di:complement) BSUB0011 Z99114 g2634335 Bacillus subtilis 1423 -11531040

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799360	4582	26738	198	65

Description

6500727183 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojJ yojJ Bacillus subtilis 1423 -11531041 7000692678 yojj conserved hypothetical protein yojj (db:pir2.dat) G69906 G69906 Bacillus subtilis 1423 -11531041 7500963782 yojj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:117597) (re:118202) (di:complement) BSUB0011 Z99114 g2634336 Bacillus subtilis 1423 -11531041

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799366	4583	26739	672	224

Description

6500727184 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojI yojI Bacillus subtilis 1423 -11531042 7000692677 yoji conserved hypothetical protein yoji (cl:conserved hypothetical protein hi1612) (db:pir2.dat) F69906 F69906 Bacillus subtilis 1423 -11531042 7500963780 yoji yoji (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169325 Bacillus subtilis 1423 -11531042 7500963781 yoji (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:118467) (re:119825) (di:direct) BSUB0011 Z99114 g2634337 Bacillus subtilis 1423 -11531042

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799369	4584	26740	468	155

Description

6500727185 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojH yojH Bacillus subtilis 1423 -11531043 7000692676 yojh conserved hypothetical protein yojh (cl:sigma-h activator ispu) (db:pir2.dat) E69906 E69906 Bacillus subtilis 1423 -11531043 7500963778 yojh yojh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169324 Bacillus subtilis 1423 -11531043 7500963779 yojh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:119841) (re:120689) (di:direct) BSUB0011 Z99114 g2634338 Bacillus subtilis 1423 -11531043

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799379	4585	26741	288	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799407	4586	26742	603	200

Description

6500727186 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojG yojG Bacillus subtilis 1423 -11531044 7000693549 yojg hypothetical protein yojg (db:pir2.dat) D69906 D69906 Bacillus subtilis 1423 -11531044 7500964502 yojg yojg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169323 Bacillus subtilis 1423 -11531044 7500964503 yojg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:120715) (re:121143) (di:complement) BSUB0011 Z99114 g2634339 Bacillus subtilis 1423 -11531044

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799413	4587	26743	417	138

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799417	4588	26744	423	140

Description

6500727187 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojF yojF Bacillus subtilis 1423 -11531045 7000693548 yojf hypothetical protein yojf (db:pir2.dat) C69906 C69906 Bacillus subtilis 1423 -11531045 7500964500 yojf yojf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169322 Bacillus subtilis 1423 -11531045 7500964501 yojf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:121397) (re:121747) (di:complement) BSUB0011 Z99114 g2634340 Bacillus subtilis 1423 -11531045

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799423	4589	26745	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799425	4590	26746	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799433	4591	26747	1083	360

Description

6500727188 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojE yojE Bacillus subtilis 1423 -11531046 7000692675 yoje rard protein homolog yoje (cl:escherichia coli rard protein) (db:pir2.dat) B69906 B69906 Bacillus subtilis 1423 -11531046 7500955841 yojd yojd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169320 Bacillus subtilis 1423 -11531046 7500955842 yoje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:122204) (re:122995) (di:complement) BSUB0011 Z99114 g2634341 Bacillus subtilis 1423 -11531046

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799435	4592	26748	396	132

Description

6500727189 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojC yojC Bacillus subtilis 1423 -11531047 7000693547 yojc hypothetical protein yojc (db:pir2.dat) A69906 A69906 Bacillus subtilis 1423 -11531047 7500964499 yojc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:123461) (re:123694) (di:complement) BSUB0011 Z99114 g2634342 Bacillus subtilis 1423 -11531047

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799446	4593	26749	1068	356

Description

6500727190 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojB yojB Bacillus subtilis 1423 -11531048 7000693546 yojb hypothetical protein yojb (db:pir2.dat) H69905 H69905 Bacillus subtilis 1423 -11531048 7500964497 yojb yojb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) gene... AF026147 AF026147 g3169318 Bacillus subtilis 1423 -11531048 7500964498 yojb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:123603) (re:123839) (di:complement) BSUB0011 Z99114 g2634343 Bacillus subtilis 1423 -11531048

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799449	4594	26750	270	89

Description

6500727191 hypothetical protein:similar to gluconate permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yojA yojA Bacillus subtilis 1423 -11531049 7000693028 yoja gluconate permease homolog yoja (cl:d-serine permease) (db:pir2.dat) G69905 G69905 Bacillus subtilis 1423 -11531049 7500964009 yoja yoja (db:genpept-bct1) (de:bacillus subtilis yoja (yoja), yojb (yojb), yojc (yojc), yojd(yojd), yoje (yoje), yojf (yojf), yojg (yojg), yojh (yojh), yoji(yoji), yojj (yojj), yojk (yojk), yojl (yojl), yojm (yojm), yojn(yojn), and yojo (yojo) genes, complete c... AF026147 AF026147 g3169317 Bacillus subtilis 1423 -11531049 7500964010 yoja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to gluconate permease) (le:123924) (re:125258) (di:complement) BSUB0011 Z99114 g2634344 Bacillus subtilis 1423 -11531049

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501799451	4595	26751	387	128

Description

6500727192 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodA yodA Bacillus subtilis 1423 -11531050 7000692670 yoda conserved hypothetical protein yoda (cl:hypothetical protein yrdn) (db:pir2.dat) F69902 F69902 Bacillus subtilis 1423 -11531050 5500687359 yoli yoli (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:similar to the orf129 of b. subtilis; similar to) (le:29247) (re:29636) (di:complement) AF006665 AF006665 g2529483 Bacillus subtilis 1423 -11531050 5500687360 yoda yoda (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415384 Bacillus subtilis 1423 -11531050 7500963773 yoda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:125623) (re:126012) (di:direct) BSUB0011 Z99114 g2634345 Bacillus subtilis 1423 -11531050

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800291	4596	26752	1149	382

Description

6500727193 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodB yodB Bacillus subtilis 1423 -11531051 7000692671 yodb conserved hypothetical protein yodb (cl:conserved hypothetical protein mth1285) (db:pir2.dat) G69902 G69902 Bacillus subtilis 1423 -11531051 5500687361 yolh yolh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:similar to hypothetical protein 14.7 kda protein of) (le:28503) (re:28841) (di:direct) AF006665 AF006665 g2529482 Bacillus subtilis 1423 -11531051 5500687362 yodb yodb (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415392 Bacillus subtilis 1423 -11531051 7500963774 yodb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:126419) (re:126757) (di:complement) BSUB0011 Z99114 g2634346 Bacillus subtilis 1423 -11531051

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800300	4597	26753	501	166

Description

6500727194 hypothetical protein:similar to nitroreductase (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodC yodC Bacillus subtilis 1423 -11531052 7000694327 yodc nitroreductase homolog yodc (cl:nitroreductase) (db:pir2.dat) H69902 H69902 Bacillus subtilis 1423 -11531052 5500687363 yodc yodc (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415385 Bacillus subtilis 1423 -11531052 7500965024 yodc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to nitroreductase) (le:126887) (re:127495) (di:direct) BSUB0011 Z99114 g2634347 Bacillus subtilis 1423 -11531052

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800318	4598	26754	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800335	4599	26755	1206	402

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800339	4600	26756	1194	397

Description

6500727195 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodD yodD Bacillus subtilis 1423 -11531053 7000693536 yodd hypothetical protein yodd (db:pir2.dat) A69903 A69903 Bacillus subtilis 1423 -11531053 5500687364 yolf yolf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:27120) (re:27722) (di:direct) AF006665 AF006665 g2529480 Bacillus subtilis 1423 -11531053 5500687365 yodd yodd (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415393 Bacillus subtilis 1423 -11531053 7500964487 yodd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:127538) (re:128140) (di:complement) BSUB0011 Z99114 g2634348 Bacillus subtilis 1423 -11531053

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800358	4601	26757	1089	363

Description

6500727196 hypothetical protein:similar to aromatic metabolite transporter (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodE yodE Bacillus subtilis 1423 -11531054 7000692228 yode aromatic metabolite transporter homolog yode (cl:probable abc transporter protein ydfo) (db:pir2.dat) B69903 B69903 Bacillus subtilis 1423 -11531054 5500687366 yode abc-transporter (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415394 Bacillus subtilis 1423 -11531054 7500963429 yode (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to aromatic metabolite transporter) (le:128156) (re:129067) (di:complement) BSUB0011 Z99114 g2634349 Bacillus subtilis 1423 -11531054

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800370	4602	26758	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800376	4603	26759	279	92

Description

6500727197 hypothetical protein:similar to proline permease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodF yodF Bacillus subtilis 1423 -11531055 7000694448 yodf proline permease homolog yodf (cl:proline carrier protein) (db:pir2.dat) C69903 C69903 Bacillus subtilis 1423 -11531055 5500687367 yodf permease (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415386 Bacillus subtilis 1423 -11531055 7500965101 yodf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to proline permease) (le:129451) (re:130941) (di:direct) BSUB0011 Z99114 g2634350 Bacillus subtilis 1423 -11531055

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800398	4604	26760	771	256

Description

6500727198 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodH yodH Bacillus subtilis 1423 -11531056 7000693537 yodh hypothetical protein yodh (cl:bioc homology) (db:pir2.dat) D69903 D69903 Bacillus subtilis 1423 -11531056 5500687370 yolb yolb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:similar to the biotin synthesis protein bioc of) (le:22032) (re:22733) (di:complement) AF006665 AF006665 g2529475 Bacillus subtilis 1423 -11531056 5500687371 yodh yodh (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415387 Bacillus subtilis 1423 -11531056 7500964488 yodh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:132529) (re:133230) (di:direct) BSUB0011 Z99114 g2634352 Bacillus subtilis 1423 -11531056

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800402	4605	26761	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800409	4606	26762	525	174

Description

6500727199 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodI yodI Bacillus subtilis 1423 -11531057 7000693538 yodi hypothetical protein yodi (db:pir2.dat) E69903 E69903 Bacillus subtilis 1423 -11531057 5500687372 yola yola (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:21694) (re:21945) (di:complement) AF006665 AF006665 g2529474 Bacillus subtilis 1423 -11531057 5500687373 yodi yodi (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415388 Bacillus subtilis 1423 -11531057 7500964489 yodi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:133318) (re:133569) (di:direct) BSUB0011 Z99114 g2634353 Bacillus subtilis 1423 -11531057

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800413	4607	26763	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800423	4608	26764	807	268

Description

6500727200 hypothetical protein:similar to d-alanyl-d-alanine carboxypeptidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodJ yodJ Bacillus subtilis 1423 -11531058 7000692904 yodj d-alanyl-d-alanine carboxypeptidase homolog yodj (db:pir2.dat) F69903 F69903 Bacillus subtilis 1423 -11531058 5500687374 yodj carboxypeptidase (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415396 Bacillus subtilis 1423 -11531058 7500963926 yodj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to d-alanyl-d-alanine carboxypeptidase) (le:133640) (re:134461) (di:complement) BSUB0011 Z99114 g2634354 Bacillus subtilis 1423 -11531058

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800431	4609	26765	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800455	4610	26766	225	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800466	4611	26767	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800468	4612	26768	453	151

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800475	4613	26769	777	258

Description

6500727201 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodL yodL Bacillus subtilis 1423 -11531059 7000693539 yodl hypothetical protein yodl (db:pir2.dat) G69903 G69903 Bacillus subtilis 1423 -11531059 5500687377 yodl yodl (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415398 Bacillus subtilis 1423 -11531059 7500964490 yodl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:135612) (re:135929) (di:complement) BSUB0011 Z99114 g2634356 Bacillus subtilis 1423 -11531059

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800486	4614	26770	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800493	4615	26771	1446	482

Description

6500727202 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodM yodM Bacillus subtilis 1423 -11531060 7000692672 yodm conserved hypothetical protein yodm (db:pir2.dat) H69903 H69903 Bacillus subtilis 1423 -11531060 5500687378 yodm yodm (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415399 Bacillus subtilis 1423 -11531060 7500963775 yodm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:135987) (re:136598) (di:complement) BSUB0011 Z99114 g2634357 Bacillus subtilis 1423 -11531060

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800502	4616	26772	240	79

Description

GTC ORF with score 108 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone 1750.) (nt:similar to s.pombe swiss_prot hypothetical protein) (le:19195) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800503	4617	26773	1191	397

Description

6500727203 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozD yozD Bacillus subtilis 1423 -11531061 7000693831 yozd hypothetical protein yozd (db:pir2.dat) H69930 H69930 Bacillus subtilis 1423 -11531061 7500964645 yozd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:136676) (re:136852) (di:complement) BSUB0011 Z99114 g2634358 Bacillus subtilis 1423 -11531061

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800510	4618	26774	567	188

Description

6500727204 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodN yodN Bacillus subtilis 1423 -11531062 7000693540 yodn hypothetical protein yodn (db:pir2.dat) A69904 A69904 Bacillus subtilis 1423 -11531062 5500687379 yokv yokv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:17474) (re:18154) (di:direct) AF006665 AF006665 g2529469 Bacillus subtilis 1423 -11531062 5500687380 yodn yodn (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415400 Bacillus subtilis 1423 -11531062 7500964491 yodn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:137111) (re:137791) (di:complement) BSUB0011 Z99114 g2634359 Bacillus subtilis 1423 -11531062

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800516	4619	26775	561	186

Description

6500727205 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozE yozE Bacillus subtilis 1423 -11531063 7000693832 yoze hypothetical protein yoze (db:pir2.dat) A69931 A69931 Bacillus subtilis 1423 -11531063 7500964646 yoze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:137942) (re:138166) (di:complement) BSUB0011 Z99114 g2634360 Bacillus subtilis 1423 -11531063

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800520	4620	26776	432	143

Description

6500727206 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodO yodO Bacillus subtilis 1423 -11531064 7502851700 yodo:yoks (de:hypothetical 54.1 kd protein in deod-arge intergenic region) (db:swissprot) YODO_BACSU O34676 BACILLUS SUBTILIS 1423 -11531064 7000692673 yodo conserved hypothetical protein yodo (cl:conserved hypothetical protein yodo) (db:pir2.dat) B69904 B69904 Bacillus subtilis 1423 -11531064 5500687381 yodo yodo (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415401 Bacillus subtilis 1423 -11531064 7500963776 yodo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:138527) (re:139942) (di:complement) BSUB0011 Z99114 g2634361 Bacillus subtilis 1423 -11531064

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800529	4621	26777	1110	370

Description

6500727207 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodP yodP Bacillus subtilis 1423 -11531065 7000693541 yodp hypothetical protein yodp (db:pir2.dat) C69904 C69904 Bacillus subtilis 1423 -11531065 5500687382 yokr yokr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:14466) (re:15293) (di:direct) AF006665 AF006665 g2529466 Bacillus subtilis 1423 -11531065 5500687383 yodp yodp (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415402 Bacillus subtilis 1423 -11531065 7500964492 yodp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:139971) (re:140798) (di:complement) BSUB0011 Z99114 g2634362 Bacillus subtilis 1423 -11531065

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800556	4622	26778	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800557	4623	26779	480	159

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800560	4624	26780	234	77

Description

6500727208 hypothetical protein:similar to butyrate-acetoacetate coa-transferase (gtcfc:14.1) (ec:2.8.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodR yodR Bacillus subtilis 1423 -11531066 7000692295 yodr butyrate-acetoacetate coa-transferase homolog yodr (cl:3-oxoadipate coa-transferase beta chain:3-oxoadipate coa-transferase beta chain homology) (db:pir2.dat) D69904 D69904 Bacillus subtilis 1423 -11531066 5500687385 yoko yoko (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:similar to the probable 3-oxoadipate) (le:12516) (re:13169) (di:direct) AF006665 AF006665 g2529464 Bacillus subtilis 1423 -11531066 5500687386 yodr butirate-acetoacetate coa transferase (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415404 Bacillus subtilis 1423 -11531066 7500954176 yodr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to butyrate-acetoacetate coa-transferase) (le:142095) (re:142748) (di:complement) BSUB0011 Z99114 g2634364 Bacillus subtilis 1423 -11531066

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800567	4625	26781	393	130

Description

6500727209 hypothetical protein:similar to 3-oxoadipate coa-transferase (gtcfc:14.1) (ec:2.8.3.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodS yodS Bacillus subtilis 1423 -11531067 7000692061 yods 3-oxoadipate coa-transferase homolog yods (cl:3-oxoadipate coa-transferase alpha chain:3-oxoadipate coa-transferase alpha chain homology) (db:pir2.dat) E69904 E69904 Bacillus subtilis 1423 -11531067 5500687387 yokn yokn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:similar to acetyl-coa:acetoacetyl-coa transferase a) (le:11842) (re:12531) (di:direct) AF006665 AF006665 g2529463 Bacillus subtilis 1423 -11531067 5500687388 yods butyrate acetoacetate-coa transferase (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415405 Bacillus subtilis 1423 -11531067 7500963305 yods (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to 3-oxoadipate coa-transferase) (le:142733) (re:143422) (di:complement) BSUB0011 Z99114 g2634365 Bacillus subtilis 1423 -11531067

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800570	4626	26782	450	149

Description

6500727210 hypothetical protein:similar to adenosylmethionine-8-amino-7-oxononanoate aminotransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodT yodT Bacillus subtilis 1423 -11531068 7502851701 yodt:yokm (ec:2.6.-.-) (de:probable aminotransferase yodt,) (db:swissprot) YODT_BACSU O34662 BACILLUS SUBTILIS 1423 -11531068 7000692157 yodt adenosylmethionine-8-amino-7-oxononanoate homolog yodt (cl:beta-alanine--pyruvate transaminase) (db:pir2.dat) F69904 F69904 Bacillus subtilis 1423 -11531068 5500687389 yodt yodt (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415406 Bacillus subtilis 1423 -11531068 7500954058 yodt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to) (le:143429) (re:144763) (di:complement) BSUB0011 Z99114 g2634366 Bacillus subtilis 1423 -11531068

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800572	4627	26783	423	140

Description

6500727211 cgebc:cgee hypothetical protein:involved in maturation of the outermost layer of the spore (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeE cgeE Bacillus subtilis 1423 -11531069 7000694199 cgee maturation of the outermost layer of the spore cgee (db:pir2.dat) D69598 D69598 Bacillus subtilis 1423 -11531069 5500687390 cgee cgee (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415407 Bacillus subtilis 1423 -11531069 7500964926 cgee (fn:involved in maturation of the outermost layer) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: cgebc) (le:145086) (re:145865) (di:complement) BSUB0011 Z99114 g2634367 Bacillus subtilis 1423 -11531069

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800573	4628	26784	351	116

Description

5000689458 cgebb:cged hypothetical protein:cged protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeD cgeD Bacillus subtilis 1423 -11531070 63976 cged:cgebb (de:cged protein) (db:swissprot) CGED_BACSU P42092 BACILLUS SUBTILIS 1423 -11531070 7000684798 cged maturation of the outermost layer of the spore cged (db:pir2.dat) C69598 C69598 Bacillus subtilis 1423 -11531070 219848 cged cged (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:a protein in the cge cluster) (le:8090) (re:9370) (di:direct) AF006665 AF006665 g2529460 Bacillus subtilis 1423 -11531070 5500684507 cged cged (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415408 Bacillus subtilis 1423 -11531070 5500684508 cged cged (db:genpept-bct1) (de:bacillus subtilis gene cluster cgee (cgee) gene, partial cds, cgea(cgea), cgeb (cgeb), cged (cged), and cgec (cgec) genes, completecds, and orf181 gene, partial cds.) (le:341) (re:1621) (di:complement) BSU18421 U18421 g604485 Bacillus subtilis 1423 -11531070 7500878577 cged (fn:involved in maturation of the outermost layer) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: cgebb) (le:145894) (re:147174) (di:complement) BSUB0011 Z99114 g2634368 Bacillus subtilis 1423 -11531070 6500727212 cgebb hypothetical protein:cged protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeD cgeD Bacillus subtilis 1423 -11531070

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800587	4629	26785	1368	455

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800613	4630	26786	420	139

Description

5000689457 cgeba:cgec hypothetical protein:cgec protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeC cgeC Bacillus subtilis 1423 -11531071 63975 cgec:cgeba (de:cgec protein) (db:swissprot) CGEC_BACSU P42091 BACILLUS SUBTILIS 1423 -11531071 7000684797 cgec maturation of the outermost layer of the spore cgec (db:pir2.dat) B69598 B69598 Bacillus subtilis 1423 -11531071 219849 cgec cgec (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:a protein in the cge cluster) (le:7720) (re:8025) (di:direct) AF006665 AF006665 g2529459 Bacillus subtilis 1423 -11531071 5500684505 cgec cgec (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415409 Bacillus subtilis 1423 -11531071 5500684506 cgec cgec (db:genpept-bct1) (de:bacillus subtilis gene cluster cgee (cgee) gene, partial cds, cgea(cgea), cgeb (cgeb), cged (cged), and cgec (cgec) genes, completecds, and orf181 gene, partial cds.) (nt:ttg start codon) (le:1686) (re:1991) (di:complement) BSU18421 U18421 g604486 Bacillus subtilis 1423 -11531071 7500878576 cgec (fn:involved in maturation of the outermost layer) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: cgeba) (le:147239) (re:147544) (di:complement) BSUB0011 Z99114 g2634369 Bacillus subtilis 1423 -11531071 6500727213 cgeba hypothetical protein:cgec protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeC cgeC Bacillus subtilis 1423 -11531071

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800614	4631	26787	252	83

Description

5000689455 cgeaa:cgea hypothetical protein:cgea protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeA cgeA Bacillus subtilis 1423 -11531072 63960 cgea:cgeaa (de:cgea protein) (db:swissprot) CGEA_BACSU P42089 BACILLUS SUBTILIS 1423 -11531072 7000684795 cgea maturation of the outermost layer of the spore cgea (db:pir2.dat) H69597 H69597 Bacillus subtilis 1423 -11531072 219850 cgea cgea (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:a protein in the cge cluster) (le:7114) (re:7515) (di:complement) AF006665 AF006665 g2529458 Bacillus subtilis 1423 -11531072 5500684501 cgea cgea (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415389 Bacillus subtilis 1423 -11531072 5500684502 cgea cgea (db:genpept-bct1) (de:bacillus subtilis gene cluster cgee (cgee) gene, partial cds, cgea(cgea), cgeb (cgeb), cged (cged), and cgec (cgec) genes, completecds, and orf181 gene, partial cds.) (le:2196) (re:2597) (di:direct) BSU18421 U18421 g604481 Bacillus subtilis 1423 -11531072 7500878574 cgea (fn:involved in maturation of the outermost layer) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: cgeaa) (le:147749) (re:148150) (di:direct) BSUB0011 Z99114 g2634370 Bacillus subtilis 1423 -11531072 6500727214 cgeaa hypothetical protein:cgea protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeA cgeA Bacillus subtilis 1423 -11531072

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800622	4632	26788	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800626	4633	26789	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800629	4634	26790	345	114

Description

5000689456 cgeab:cgeb hypothetical protein:cgeb protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeB cgeB Bacillus subtilis 1423 -11531073 63961 cgeb:cgeab (de:cgeb protein) (db:swissprot) CGEB_BACSU P42090 BACILLUS SUBTILIS 1423 -11531073 7000684796 cgeb maturation of the outermost layer of the spore cgeb (db:pir2.dat) A69598 A69598 Bacillus subtilis 1423 -11531073 219851 cgeb cgeb (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:a protein in the cge cluster) (le:6154) (re:7107) (di:complement) AF006665 AF006665 g2529457 Bacillus subtilis 1423 -11531073 5500684503 cgeb cgeb (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415390 Bacillus subtilis 1423 -11531073 5500684504 cgeb cgeb (db:genpept-bct1) (de:bacillus subtilis gene cluster cgee (cgee) gene, partial cds, cgea(cgea), cgeb (cgeb), cged (cged), and cgec (cgec) genes, completecds, and orf181 gene, partial cds.) (le:2604) (re:3557) (di:direct) BSU18421 U18421 g604482 Bacillus subtilis 1423 -11531073 7500878575 cgeb (fn:involved in maturation of the outermost layer) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: cgeab) (le:148157) (re:149110) (di:direct) BSUB0011 Z99114 g2634371 Bacillus subtilis 1423 -11531073 6500727215 cgeab hypothetical protein:cgeb protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) cgeB cgeB Bacillus subtilis 1423 -11531073

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800631	4635	26791	582	193

Description

6500727216 yzxa:yodv hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodV yodV Bacillus subtilis 1423 -11531074 7502851702 phy (ec:3.1.3.8) (de:3-phytase precursor,) (db:swissprot) PHYT_BACSU P42094 BACILLUS SUBTILIS 1423 -11531074 7000693542 yodv hypothetical protein yodv (db:pir2.dat) H69904 H69904 Bacillus subtilis 1423 -11531074 5500687391 yokk yokk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (nt:orf181 at the 3' region of b. subtilis cgeab) (le:4935) (re:6083) (di:direct) AF006665 AF006665 g2529456 Bacillus subtilis 1423 -11531074 5500687392 yzxa yzxa (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415410 Bacillus subtilis 1423 -11531074 7500964493 yodv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yzxa) (le:149181) (re:150329) (di:complement) BSUB0011 Z99114 g2634372 Bacillus subtilis 1423 -11531074

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800666	4636	26792	702	233

Description

6500727217 hypothetical protein:similar to capsular polysaccharide biosynthesis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yodU yodU Bacillus subtilis 1423 -11531075 7000692307 yodu capsular polysaccharide biosynthesis protein homolog yodu:udp-glucose epimerase (db:pir2.dat) G69904 G69904 Bacillus subtilis 1423 -11531075 5500687393 yodu udp-glucose epimerase (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415391 Bacillus subtilis 1423 -11531075 7500963487 yodu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to capsular polysaccharide biosynthesis) (le:150699) (re:151124) (di:direct) BSUB0011 Z99114 g2634373 Bacillus subtilis 1423 -11531075

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800684	4637	26793	1173	390

Description

GTC ORF with score 887 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri3) (de:homo sapiens mrna for kiaa0017 protein, complete cds.) (nt:similar to human xeroderma pigmentosum groupe) (le:157) (re:3810) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800688	4638	26794	1005	335

Description

6500727218 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotN yotN Bacillus subtilis 1423 -11531076 7000693827 yotn hypothetical protein yotn (db:pir2.dat) H69929 H69929 Bacillus subtilis 1423 -11531076 5500697853 yokj yokj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:3929) (re:4105) (di:direct) AF006665 AF006665 g2529454 Bacillus subtilis 1423 -11531076 7000693828 yotn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:151159) (re:151335) (di:complement) BSUB0011 Z99114 g2634374 Bacillus subtilis 1423 -11531076 7500964642 yotn unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:134185) (re:134361) (di:direct) AF020713 AF020713 g3025663 Bacteriophage SPBc2 66797 -11531076

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800703	4639	26795	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800706	4640	26796	480	159

Description

6500727219 yodv:yotm hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotM yotM Bacillus subtilis 1423 -11531077 7000693825 yotm hypothetical protein yotm (db:pir2.dat) G69929 G69929 Bacillus subtilis 1423 -11531077 5500687394 yoki yoki (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:3339) (re:3926) (di:direct) AF006665 AF006665 g2529453 Bacillus subtilis 1423 -11531077 5500687395 yodv yodv (db:genpept-bct1) (de:bacillus subtilis yoda (yoda), yodb (yodb), yodc (yodc), yodd(yodd), abc-transporter (yode), permease (yodf), proteinase (ctpa),yodh (yodh), yodi (yodi), carboxypeptidase (yodj), purinenucleoside phosphorylase (deod), yodl (yodl),... AF015775 AF015775 g2415411 Bacillus subtilis 1423 -11531077 7000693826 yotm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yodv) (le:151338) (re:151925) (di:complement) BSUB0011 Z99114 g2634375 Bacillus subtilis 1423 -11531077 7500964641 yotm unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:133595) (re:134182) (di:direct) AF020713 AF020713 g3025662 Bacteriophage SPBc2 66797 -11531077

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800711	4641	26797	858	285

Description

6500727220 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotL yotL Bacillus subtilis 1423 -11531078 7000692708 yotl conserved hypothetical protein yotl (cl:hypothetical protein yotl) (db:pir2.dat) F69929 F69929 Bacillus subtilis 1423 -11531078 7000692709 yotl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:152000) (re:152242) (di:direct) BSUB0011 Z99114 g2634376 Bacillus subtilis 1423 -11531078 7500955945 yotl unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:133278) (re:133520) (di:complement) AF020713 AF020713 g3025661 Bacteriophage SPBc2 66797 -11531078

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800714	4642	26798	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800715	4643	26799	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800722	4644	26800	855	284

Description

6500727221 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotK yotK Bacillus subtilis 1423 -11531079 7000693823 yotk hypothetical protein yotk (db:pir2.dat) E69929 E69929 Bacillus subtilis 1423 -11531079 7000693824 yotk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:152244) (re:152429) (di:complement) BSUB0011 Z99114 g2634377 Bacillus subtilis 1423 -11531079 7500964640 yotk unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:133091) (re:133276) (di:direct) AF020713 AF020713 g3025660 Bacteriophage SPBc2 66797 -11531079

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800723	4645	26801	552	183

Description

6500727222 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotJ yotJ Bacillus subtilis 1423 -11531080 7000693821 yotj hypothetical protein yotj (db:pir2.dat) D69929 D69929 Bacillus subtilis 1423 -11531080 5500697851 yokg yokg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:2539) (re:2751) (di:direct) AF006665 AF006665 g2529451 Bacillus subtilis 1423 -11531080 7000693822 yotj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:152513) (re:152725) (di:complement) BSUB0011 Z99114 g2634378 Bacillus subtilis 1423 -11531080 7500964639 yotj unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:132795) (re:133007) (di:direct) AF020713 AF020713 g3025659 Bacteriophage SPBc2 66797 -11531080

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800744	4646	26802	762	253

Description

6500727223 yodw:yoti hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotI yotI Bacillus subtilis 1423 -11531081 7000693819 yoti hypothetical protein yoti (db:pir2.dat) C69929 C69929 Bacillus subtilis 1423 -11531081 7000693820 yoti (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yodw) (le:152791) (re:153153) (di:complement) BSUB0011 Z99114 g2634379 Bacillus subtilis 1423 -11531081 7500964638 yoti unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:132367) (re:132729) (di:direct) AF020713 AF020713 g3025658 Bacteriophage SPBc2 66797 -11531081

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800746	4647	26803	450	149

Description

6500727224 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotH yotH Bacillus subtilis 1423 -11531082 7000693817 yoth hypothetical protein yoth (db:pir2.dat) B69929 B69929 Bacillus subtilis 1423 -11531082 7000693818 yoth (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:153150) (re:153323) (di:complement) BSUB0011 Z99114 g2634380 Bacillus subtilis 1423 -11531082 7500964637 yoth unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:132197) (re:132370) (di:direct) AF020713 AF020713 g3025657 Bacteriophage SPBc2 66797 -11531082

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800748	4648	26804	456	151

Description

GTC ORF with score 127 to: (or:Rattus norvegicus) (sr:rattus norvegicus cdna to mrna) (db:genpept-rod) (de:rattus norvegicus calcium/calmodulin-dependent protein kinase imrna, complete cds.) (nt:calmodulin-binding protein;) (le:92) (re:1090) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800749	4649	26805	561	186

Description

6500727225 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotG yotG Bacillus subtilis 1423 -11531083 7000693815 yotg hypothetical protein yotg (db:pir2.dat) A69929 A69929 Bacillus subtilis 1423 -11531083 7000693816 yotg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:153339) (re:153656) (di:complement) BSUB0011 Z99114 g2634381 Bacillus subtilis 1423 -11531083 7500964636 yotg unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:131864) (re:132181) (di:direct) AF020713 AF020713 g3025656 Bacteriophage SPBc2 66797 -11531083

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800760	4650	26806	585	195

Description

6500727226 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotF yotF Bacillus subtilis 1423 -11531084 7000693813 yotf hypothetical protein yotf (db:pir2.dat) H69928 H69928 Bacillus subtilis 1423 -11531084 7000693814 yotf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:153669) (re:153746) (di:complement) BSUB0011 Z99114 g2634382 Bacillus subtilis 1423 -11531084 7500964635 yotf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:131774) (re:131851) (di:direct) AF020713 AF020713 g3025655 Bacteriophage SPBc2 66797 -11531084

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800764	4651	26807	708	236

Description

6500727227 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotE yotE Bacillus subtilis 1423 -11531085 7000693811 yote hypothetical protein yote (db:pir2.dat) G69928 G69928 Bacillus subtilis 1423 -11531085 7000693812 yote (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:153778) (re:153924) (di:complement) BSUB0011 Z99114 g2634383 Bacillus subtilis 1423 -11531085 7500964634 yote unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:131596) (re:131742) (di:direct) AF020713 AF020713 g3025654 Bacteriophage SPBc2 66797 -11531085

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800772	4652	26808	855	284

Description

6500727228 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotD yotD Bacillus subtilis 1423 -11531086 7000693809 yotd hypothetical protein yotd (db:pir2.dat) F69928 F69928 Bacillus subtilis 1423 -11531086 5500697848 yokd yokd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:1176) (re:1307) (di:direct) AF006665 AF006665 g2529448 Bacillus subtilis 1423 -11531086 7000693810 yotd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:153960) (re:154091) (di:complement) BSUB0011 Z99114 g2634384 Bacillus subtilis 1423 -11531086 7500964633 yotd unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:131429) (re:131560) (di:direct) AF020713 AF020713 g3025653 Bacteriophage SPBc2 66797 -11531086

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800774	4653	26809	432	144

Description

GTC ORF with score 94 to: (sr:human papillomavirus type 5 dna, from ev patient benign flat wart) (db:genpept-vrl) (de:human papillomoavirus type 5, complete genome.) (nt:orf e2 from bp 2699 to 4267; putative) (le:2723) (re:4267) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800775	4654	26810	840	279

Description

6500727229 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotC yotC Bacillus subtilis 1423 -11531087 7000693807 yotc hypothetical protein yotc (db:pir2.dat) E69928 E69928 Bacillus subtilis 1423 -11531087 5500697847 yokc yokc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:945) (re:1136) (di:direct) AF006665 AF006665 g2529447 Bacillus subtilis 1423 -11531087 7000693808 yotc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:154131) (re:154322) (di:complement) BSUB0011 Z99114 g2634385 Bacillus subtilis 1423 -11531087 7500964632 yotc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:131198) (re:131389) (di:direct) AF020713 AF020713 g3025652 Bacteriophage SPBc2 66797 -11531087

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800777	4655	26811	675	224

Description

6500727230 yodz:yotb hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yotB yotB Bacillus subtilis 1423 -11531088 7000693805 yotb probable phosphoesterase:yotb (cl:unassigned probable phosphoesterases:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) D69928 D69928 Bacillus subtilis 1423 -11531088 5500697846 yokb yokb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis 168 region at 182 min containing the cge genecluster.) (le:74) (re:901) (di:direct) AF006665 AF006665 g2529446 Bacillus subtilis 1423 -11531088 7000693806 yotb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:alternate gene name: yodz) (le:154366) (re:155193) (di:complement) BSUB0011 Z99114 g2634386 Bacillus subtilis 1423 -11531088 7500954188 yotb unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:130327) (re:131154) (di:direct) AF020713 AF020713 g3025651 Bacteriophage SPBc2 66797 -11531088

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800779	4656	26812	483	160

Description

GTC ORF with score 578 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1103.) (nt:similar to saccharomyces cerevisiae reduced) (le:<1) (re:813) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800793	4657	26813	555	184

Description

6500727231 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosZ yosZ Bacillus subtilis 1423 -11531089 7000693803 yosz hypothetical protein yosz (db:pir2.dat) C69928 C69928 Bacillus subtilis 1423 -11531089 7000693804 yosz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:155721) (re:155786) (di:complement) BSUB0011 Z99114 g2634388 Bacillus subtilis 1423 -11531089 7500964631 yosz unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:129734) (re:129799) (di:direct) AF020713 AF020713 g3025649 Bacteriophage SPBc2 66797 -11531089

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800805	4658	26814	465	154

Description

6500727232 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosX yosX Bacillus subtilis 1423 -11531090 7000693801 yosx hypothetical protein yosx (db:pir2.dat) B69928 B69928 Bacillus subtilis 1423 -11531090 5500698561 yojz unknown (db:genpept-bct1) (de:bacillus subtilis yojp gene, partial cds; yojq/s, yojr, yojt,yoju, yojv, yojw, yojx, yojy, yojz, and yoka genes, complete cds.) (nt:similar to tropomyosin 1 of drosophila) (le:6984) (re:7337) (di:direct) AF012906 AF012906 g2522414 Bacillus subtilis 1423 -11531090 7000693802 yosx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:155830) (re:156183) (di:complement) BSUB0011 Z99114 g2634389 Bacillus subtilis 1423 -11531090 7500964630 yosx unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:129337) (re:129690) (di:direct) AF020713 AF020713 g3025648 Bacteriophage SPBc2 66797 -11531090

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800840	4659	26815	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800853	4660	26816	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800860	4661	26817	369	123

Description

GTC ORF with score 101 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800865	4662	26818	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800872	4663	26819	597	198

Description

GTC ORF with score 196 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800878	4664	26820	423	140

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800888	4665	26821	468	155

Description

6500727233 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosW yosW Bacillus subtilis 1423 -11531091 7000693799 yosw hypothetical protein yosw (db:pir2.dat) A69928 A69928 Bacillus subtilis 1423 -11531091 7000693800 yosw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:156414) (re:156755) (di:complement) BSUB0011 Z99114 g2634390 Bacillus subtilis 1423 -11531091 7500964629 yosw unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:128765) (re:129106) (di:direct) AF020713 AF020713 g3025647 Bacteriophage SPBc2 66797 -11531091

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800890	4666	26822	516	171

Description

6500727234 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosV yosV Bacillus subtilis 1423 -11531092 7000693797 yosv hypothetical protein yosv (db:pir2.dat) H69927 H69927 Bacillus subtilis 1423 -11531092 5500698559 yojx unknown (db:genpept-bct1) (de:bacillus subtilis yojp gene, partial cds; yojq/s, yojr, yojt,yoju, yojv, yojw, yojx, yojy, yojz, and yoka genes, complete cds.) (le:5975) (re:6265) (di:direct) AF012906 AF012906 g2522412 Bacillus subtilis 1423 -11531092 7000693798 yosv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:156902) (re:157192) (di:complement) BSUB0011 Z99114 g2634391 Bacillus subtilis 1423 -11531092 7500964628 yosv unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:128328) (re:128618) (di:direct) AF020713 AF020713 g3025646 Bacteriophage SPBc2 66797 -11531092

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800891	4667	26823	195	64

Description

6500727235 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosU yosU Bacillus subtilis 1423 -11531093 7000693795 yosu hypothetical protein yosu (db:pir2.dat) G69927 G69927 Bacillus subtilis 1423 -11531093 7000693796 yosu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:157512) (re:157757) (di:direct) BSUB0011 Z99114 g2634392 Bacillus subtilis 1423 -11531093 7500964627 yosu unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:127763) (re:128008) (di:complement) AF020713 AF020713 g3025645 Bacteriophage SPBc2 66797 -11531093

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800892	4668	26824	234	77

Description

6500727236 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosT yosT Bacillus subtilis 1423 -11531094 7000693793 yost hypothetical protein yost (db:pir2.dat) F69927 F69927 Bacillus subtilis 1423 -11531094 5500698557 yojv unknown (db:genpept-bct1) (de:bacillus subtilis yojp gene, partial cds; yojq/s, yojr, yojt,yoju, yojv, yojw, yojx, yojy, yojz, and yoka genes, complete cds.) (le:4921) (re:5370) (di:direct) AF012906 AF012906 g2522410 Bacillus subtilis 1423 -11531094 7000693794 yost (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:157797) (re:158246) (di:complement) BSUB0011 Z99114 g2634393 Bacillus subtilis 1423 -11531094 7500964626 yost unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:127274) (re:127723) (di:direct) AF020713 AF020713 g3025644 Bacteriophage SPBc2 66797 -11531094

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800894	4669	26825	288	95

Description

6500727237 hypothetical protein:similar to thioredoxin (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosR yosR Bacillus subtilis 1423 -11531095 7000694685 yosr thioredoxin homolog yosr (cl:thioredoxin:thioredoxin homology) (db:pir2.dat) D69927 D69927 Bacillus subtilis 1423 -11531095 5500698555 yojt glutaredoxin-like protein homolog (db:genpept-bct1) (de:bacillus subtilis yojp gene, partial cds; yojq/s, yojr, yojt,yoju, yojv, yojw, yojx, yojy, yojz, and yoka genes, complete cds.) (nt:yojt; similar to glutaredoxin-like protein of) (le:4110) (re:4352) (di:direct) AF012906 AF012906 g2522312 Bacillus subtilis 1423 -11531095 7000694686 yosr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to thioredoxin) (le:158815) (re:159057) (di:complement) BSUB0011 Z99114 g2634395 Bacillus subtilis 1423 -11531095 7500965269 yosr thioredoxin (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:126463) (re:126705) (di:direct) AF020713 AF020713 g3025642 Bacteriophage SPBc2 66797 -11531095

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800895	4670	26826	393	130

Description

6500727238 hypothetical protein:similar to phage-related endodeoxyribonuclease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosQ yosQ Bacillus subtilis 1423 -11531096 7000694368 yosq phage-related endodeoxyribonuclease homolog yosq (db:pir2.dat) C69927 C69927 Bacillus subtilis 1423 -11531096 5500698554 yojr unknown (db:genpept-bct1) (de:bacillus subtilis yojp gene, partial cds; yojq/s, yojr, yojt,yoju, yojv, yojw, yojx, yojy, yojz, and yoka genes, complete cds.) (nt:similar to endodeoxyribonucleases; this region) (le:3008) (re:3529) (di:direct) AF012906 AF012906 g2522311 Bacillus subtilis 1423 -11531096 7000694369 yosq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to phage-related endodeoxyribonuclease) (le:159638) (re:160159) (di:complement) BSUB0011 Z99114 g2634396 Bacillus subtilis 1423 -11531096 7500965052 yosq (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to other intron-encoded site specific) (le:125361) (re:125882) (di:direct) AF020713 AF020713 g3025641 Bacteriophage SPBc2 66797 -11531096

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800903	4671	26827	666	222

Description

6500727239 hypothetical protein:similar to ribonucleoside-diphosphate reductase:alpha subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosO yosO Bacillus subtilis 1423 -11531097 7000694518 yoso ribonucleoside-diphosphate reductase alph homolog yoso (db:pir2.dat) A69927 A69927 Bacillus subtilis 1423 -11531097 7500965150 yoso (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to ribonucleoside-diphosphate reductase) (le:161181) (re:163541) (di:complement) BSUB0011 Z99114 g2634398 Bacillus subtilis 1423 -11531097

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800914	4672	26828	1254	418

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800921	4673	26829	531	176

Description

6500727240 hypothetical protein:similar to ribonucleoside-diphosphate reductase:alpha subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosN yosN Bacillus subtilis 1423 -11531098 7000694517 yosn ribonucleoside-diphosphate reductase alph homolog yosn (db:pir2.dat) H69926 H69926 Bacillus subtilis 1423 -11531098 7500965149 yosn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to ribonucleoside-diphosphate reductase) (le:163965) (re:164687) (di:complement) BSUB0011 Z99114 g2634399 Bacillus subtilis 1423 -11531098

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800943	4674	26830	855	284

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800946	4675	26831	873	291

Description

6500727241 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosM yosM Bacillus subtilis 1423 -11531099 7000692706 yosm conserved hypothetical protein yosm (db:pir2.dat) G69926 G69926 Bacillus subtilis 1423 -11531099 7000692707 yosm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:164650) (re:165039) (di:complement) BSUB0011 Z99114 g2634400 Bacillus subtilis 1423 -11531099 7500963794 bnrdi (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacillus subtilis nrdi (ymaa)) (le:120481) (re:120870) (di:direct) AF020713 AF020713 g3025638 Bacteriophage SPBc2 66797 -11531099

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800961	4676	26832	702	233

Description

6500727242 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosL yosL Bacillus subtilis 1423 -11531100 7000693791 yosl hypothetical protein yosl (db:pir2.dat) F69926 F69926 Bacillus subtilis 1423 -11531100 7000693792 yosl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:165045) (re:165398) (di:complement) BSUB0011 Z99114 g2634401 Bacillus subtilis 1423 -11531100 7500964625 yosl unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:120122) (re:120475) (di:direct) AF020713 AF020713 g3025637 Bacteriophage SPBc2 66797 -11531100

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501800965	4677	26833	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801104	4678	26834	441	146

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801113	4679	26835	222	73

Description

6500727243 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosK yosK Bacillus subtilis 1423 -11531101 7000693789 yosk hypothetical protein yosk (db:pir2.dat) E69926 E69926 Bacillus subtilis 1423 -11531101 7000693790 yosk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:165486) (re:165686) (di:complement) BSUB0011 Z99114 g2634402 Bacillus subtilis 1423 -11531101 7500964624 yosk unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:119834) (re:120034) (di:direct) AF020713 AF020713 g3025636 Bacteriophage SPBc2 66797 -11531101

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801117	4680	26836	549	182

Description

6500727244 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosJ yosJ Bacillus subtilis 1423 -11531102 7000693787 yosj hypothetical protein yosj (db:pir2.dat) D69926 D69926 Bacillus subtilis 1423 -11531102 7000693788 yosj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:165731) (re:165925) (di:complement) BSUB0011 Z99114 g2634403 Bacillus subtilis 1423 -11531102 7500964623 yosj unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:119595) (re:119789) (di:direct) AF020713 AF020713 g3025635 Bacteriophage SPBc2 66797 -11531102

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801120	4681	26837	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801127	4682	26838	183	60

Description

6500727245 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosI yosI Bacillus subtilis 1423 -11531103 7000693785 yosi hypothetical protein yosi (db:pir2.dat) C69926 C69926 Bacillus subtilis 1423 -11531103 7000693786 yosi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:165946) (re:166080) (di:complement) BSUB0011 Z99114 g2634404 Bacillus subtilis 1423 -11531103 7500964622 yosi unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:119440) (re:119574) (di:direct) AF020713 AF020713 g3025634 Bacteriophage SPBc2 66797 -11531103

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801130	4683	26839	195	65

Description

6500727246 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosH yosH Bacillus subtilis 1423 -11531104 7000693783 yosh hypothetical protein yosh (db:pir2.dat) B69926 B69926 Bacillus subtilis 1423 -11531104 7000693784 yosh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:166112) (re:166582) (di:complement) BSUB0011 Z99114 g2634405 Bacillus subtilis 1423 -11531104 7500964621 yosh unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:118938) (re:119408) (di:direct) AF020713 AF020713 g3025633 Bacteriophage SPBc2 66797 -11531104

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801142	4684	26840	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801148	4685	26841	1098	366

Description

6500727247 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosG yosG Bacillus subtilis 1423 -11531105 7000693781 yosg hypothetical protein yosg (db:pir2.dat) A69926 A69926 Bacillus subtilis 1423 -11531105 7000693782 yosg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:166643) (re:167005) (di:complement) BSUB0011 Z99114 g2634406 Bacillus subtilis 1423 -11531105 7500964620 yosg unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:118515) (re:118877) (di:direct) AF020713 AF020713 g3025632 Bacteriophage SPBc2 66797 -11531105

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801161	4686	26842	717	239

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801171	4687	26843	948	315

Description

GTC ORF with score 192 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c8c9.) (nt:spac8c9.14, len:539aa; similarity: to yhr206w,) (le:24919:25046:25892:26025) (re:24948:25135:25971:26082) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801173	4688	26844	435	144

Description

6500727248 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosF yosF Bacillus subtilis 1423 -11531106 7000693779 yosf hypothetical protein yosf (db:pir2.dat) H69925 H69925 Bacillus subtilis 1423 -11531106 7000693780 yosf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:167048) (re:167173) (di:complement) BSUB0011 Z99114 g2634407 Bacillus subtilis 1423 -11531106 7500964619 yosf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:118347) (re:118472) (di:direct) AF020713 AF020713 g3025631 Bacteriophage SPBc2 66797 -11531106

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801174	4689	26845	450	149

Description

6500727249 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosE yosE Bacillus subtilis 1423 -11531107 7000693777 yose hypothetical protein yose (db:pir2.dat) G69925 G69925 Bacillus subtilis 1423 -11531107 7000693778 yose (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:167187) (re:167534) (di:complement) BSUB0011 Z99114 g2634408 Bacillus subtilis 1423 -11531107 7500964618 yose unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:117986) (re:118333) (di:direct) AF020713 AF020713 g3025630 Bacteriophage SPBc2 66797 -11531107

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801185	4690	26846	351	116

Description

6500727250 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosD yosD Bacillus subtilis 1423 -11531108 7000693775 yosd hypothetical protein yosd (db:pir2.dat) F69925 F69925 Bacillus subtilis 1423 -11531108 7000693776 yosd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:167549) (re:167944) (di:complement) BSUB0011 Z99114 g2634409 Bacillus subtilis 1423 -11531108 7500964617 yosd unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:117576) (re:117971) (di:direct) AF020713 AF020713 g3025629 Bacteriophage SPBc2 66797 -11531108

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801202	4691	26847	498	165

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801216	4692	26848	1566	522

Description

6500727251 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosC yosC Bacillus subtilis 1423 -11531109 7000693773 yosc hypothetical protein yosc (db:pir2.dat) E69925 E69925 Bacillus subtilis 1423 -11531109 7000693774 yosc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:167983) (re:168525) (di:complement) BSUB0011 Z99114 g2634410 Bacillus subtilis 1423 -11531109 7500964616 yosc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:116995) (re:117537) (di:direct) AF020713 AF020713 g3025628 Bacteriophage SPBc2 66797 -11531109

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801221	4693	26849	426	141

Description

6500727252 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosB yosB Bacillus subtilis 1423 -11531110 7000693771 yosb hypothetical protein yosb (db:pir2.dat) D69925 D69925 Bacillus subtilis 1423 -11531110 7000693772 yosb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:168570) (re:168749) (di:complement) BSUB0011 Z99114 g2634411 Bacillus subtilis 1423 -11531110 7500964615 yosb unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:116771) (re:116950) (di:direct) AF020713 AF020713 g3025627 Bacteriophage SPBc2 66797 -11531110

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801224	4694	26850	501	166

Description

6500727253 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yosA yosA Bacillus subtilis 1423 -11531111 7000693769 yosa hypothetical protein yosa (db:pir2.dat) C69925 C69925 Bacillus subtilis 1423 -11531111 7000693770 yosa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:168880) (re:168999) (di:direct) BSUB0011 Z99114 g2634412 Bacillus subtilis 1423 -11531111 7500964614 yosa unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:116521) (re:116640) (di:complement) AF020713 AF020713 g3025626 Bacteriophage SPBc2 66797 -11531111

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801225	4695	26851	678	225

Description

6500727254 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorZ yorZ Bacillus subtilis 1423 -11531112 7000693767 yorz hypothetical protein yorz (db:pir2.dat) B69925 B69925 Bacillus subtilis 1423 -11531112 7000693768 yorz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:169103) (re:169315) (di:complement) BSUB0011 Z99114 g2634413 Bacillus subtilis 1423 -11531112 7500964613 yorz unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:116205) (re:116417) (di:direct) AF020713 AF020713 g3025625 Bacteriophage SPBc2 66797 -11531112

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801228	4696	26852	1098	365

Description

6500727255 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorY yorY Bacillus subtilis 1423 -11531113 7000693765 yory hypothetical protein yory (db:pir2.dat) A69925 A69925 Bacillus subtilis 1423 -11531113 7000693766 yory (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:169382) (re:169564) (di:complement) BSUB0011 Z99114 g2634414 Bacillus subtilis 1423 -11531113 7500964612 yory unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:115956) (re:116138) (di:direct) AF020713 AF020713 g3025624 Bacteriophage SPBc2 66797 -11531113

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801238	4697	26853	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801239	4698	26854	951	316

Description

6500727256 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorX yorX Bacillus subtilis 1423 -11531114 7000693763 yorx hypothetical protein yorx (db:pir2.dat) H69924 H69924 Bacillus subtilis 1423 -11531114 7000693764 yorx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:169577) (re:169804) (di:complement) BSUB0011 Z99114 g2634415 Bacillus subtilis 1423 -11531114 7500964611 yorx unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:115716) (re:115943) (di:direct) AF020713 AF020713 g3025623 Bacteriophage SPBc2 66797 -11531114

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801245	4699	26855	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801264	4700	26856	609	202

Description

GTC ORF with score 118 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c27f2.) (nt:coded for by c. elegans cdna yk86c6.3; coded for by) (le:34181:34408:34748) (re:34338:34533:34901) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801268	4701	26857	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801276	4702	26858	525	174

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801278	4703	26859	570	189

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801280	4704	26860	405	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801282	4705	26861	480	159

Description

6500727257 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorW yorW Bacillus subtilis 1423 -11531115 7000693761 yorw hypothetical protein yorw (db:pir2.dat) G69924 G69924 Bacillus subtilis 1423 -11531115 7000693762 yorw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:169844) (re:170209) (di:complement) BSUB0011 Z99114 g2634416 Bacillus subtilis 1423 -11531115 7500964610 yorw unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:115311) (re:115676) (di:direct) AF020713 AF020713 g3025622 Bacteriophage SPBc2 66797 -11531115

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801297	4706	26862	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801330	4707	26863	462	154

Description

6500727258 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorV yorV Bacillus subtilis 1423 -11531116 7000693759 yorv hypothetical protein yorv (db:pir2.dat) F69924 F69924 Bacillus subtilis 1423 -11531116 7000693760 yorv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:170212) (re:170430) (di:complement) BSUB0011 Z99114 g2634417 Bacillus subtilis 1423 -11531116 7500964609 yorv unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:115090) (re:115308) (di:direct) AF020713 AF020713 g3025621 Bacteriophage SPBc2 66797 -11531116

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801333	4708	26864	1551	516

Description

6500727259 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorT yorT Bacillus subtilis 1423 -11531117 7000693757 yort hypothetical protein yort (db:pir2.dat) E69924 E69924 Bacillus subtilis 1423 -11531117 7000693758 yort (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:171854) (re:171973) (di:complement) BSUB0011 Z99114 g2634419 Bacillus subtilis 1423 -11531117 7500964608 yort unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:113547) (re:113666) (di:direct) AF020713 AF020713 g3025619 Bacteriophage SPBc2 66797 -11531117

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801346	4709	26865	402	133

Description

6500727260 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorS yorS Bacillus subtilis 1423 -11531118 7000693755 yors hypothetical protein yors (db:pir2.dat) D69924 D69924 Bacillus subtilis 1423 -11531118 7000693756 yors (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:172005) (re:172523) (di:complement) BSUB0011 Z99114 g2634420 Bacillus subtilis 1423 -11531118 7500964607 yors unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:112997) (re:113515) (di:direct) AF020713 AF020713 g3025618 Bacteriophage SPBc2 66797 -11531118

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801350	4710	26866	183	60

Description

6500727261 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorR yorR Bacillus subtilis 1423 -11531119 7000693753 yorr hypothetical protein yorr (db:pir2.dat) C69924 C69924 Bacillus subtilis 1423 -11531119 7000693754 yorr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:172532) (re:173029) (di:complement) BSUB0011 Z99114 g2634421 Bacillus subtilis 1423 -11531119 7500964606 yorr unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:112491) (re:112988) (di:direct) AF020713 AF020713 g3025617 Bacteriophage SPBc2 66797 -11531119

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801370	4711	26867	372	124

Description

6500727262 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorQ yorQ Bacillus subtilis 1423 -11531120 7000693751 yorq hypothetical protein yorq (db:pir2.dat) B69924 B69924 Bacillus subtilis 1423 -11531120 7000693752 yorq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:173029) (re:173184) (di:complement) BSUB0011 Z99114 g2634422 Bacillus subtilis 1423 -11531120 7500964605 yorq unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:112336) (re:112491) (di:direct) AF020713 AF020713 g3025616 Bacteriophage SPBc2 66797 -11531120

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801371	4712	26868	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801374	4713	26869	975	324

Description

6500727263 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorP yorP Bacillus subtilis 1423 -11531121 7000693749 yorp hypothetical protein yorp (db:pir2.dat) A69924 A69924 Bacillus subtilis 1423 -11531121 7000693750 yorp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:173177) (re:173392) (di:complement) BSUB0011 Z99114 g2634423 Bacillus subtilis 1423 -11531121 7500964604 yorp unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:112128) (re:112343) (di:direct) AF020713 AF020713 g3025615 Bacteriophage SPBc2 66797 -11531121

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801375	4714	26870	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801383	4715	26871	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801388	4716	26872	1662	554

Description

6500727264 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorO yorO Bacillus subtilis 1423 -11531122 7000693747 yoro hypothetical protein yoro (db:pir2.dat) H69923 H69923 Bacillus subtilis 1423 -11531122 7000693748 yoro (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:173425) (re:173622) (di:complement) BSUB0011 Z99114 g2634424 Bacillus subtilis 1423 -11531122 7500964603 yoro unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:111898) (re:112095) (di:direct) AF020713 AF020713 g3025614 Bacteriophage SPBc2 66797 -11531122

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801402	4717	26873	483	160

Description

6500727265 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorN yorN Bacillus subtilis 1423 -11531123 7000693745 yorn hypothetical protein yorn (db:pir2.dat) G69923 G69923 Bacillus subtilis 1423 -11531123 7000693746 yorn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:173658) (re:173807) (di:complement) BSUB0011 Z99114 g2634425 Bacillus subtilis 1423 -11531123 7500964602 yorn unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:111713) (re:111862) (di:direct) AF020713 AF020713 g3025613 Bacteriophage SPBc2 66797 -11531123

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801417	4718	26874	390	129

Description

6500727266 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorM yorM Bacillus subtilis 1423 -11531124 7000692704 yorm conserved hypothetical protein yorm (db:pir2.dat) F69923 F69923 Bacillus subtilis 1423 -11531124 7000692705 yorm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:173923) (re:174639) (di:complement) BSUB0011 Z99114 g2634426 Bacillus subtilis 1423 -11531124 7500963793 yorm (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to c-moiety of b. subtilis yabe) (le:110881) (re:111597) (di:direct) AF020713 AF020713 g3025612 Bacteriophage SPBc2 66797 -11531124

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801435	4719	26875	276	92

Description

GTC ORF with score 90 to: (fn:salicylate synthesis) (db:genpept-bct2) (de:yersinia pestis trna-asn gene, complete sequence; cp4-likeintegrase (int), ybts (ybts), ybtx (ybtx), ybtq (ybtq), ybtp(ybtp), arac-like regulator ybta (ybta), ybt peptide ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801439	4720	26876	402	133

Description

GTC ORF with score 317 to: (sr:human) (db:genpept-pri3) (de:homo sapiens nitrilase homolog 1 (nit1) gene, alternatively splicedproduct, complete cds.) (nt:nit1; alternatively spliced) (le:679:1288:1636:2011:2321) (re:680:1383:1890:2114:2454) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801441	4721	26877	618	205

Description

GTC ORF with score 180 to: (fn:salicylate synthesis) (db:genpept-bct2) (de:yersinia pestis trna-asn gene, complete sequence; cp4-likeintegrase (int), ybts (ybts), ybtx (ybtx), ybtq (ybtq), ybtp(ybtp), arac-like regulator ybta (ybta), ybt peptide ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801446	4722	26878	969	323

Description

6500727267 hypothetical protein:similar to dna polymerase iii:alpha subunit (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorL yorL Bacillus subtilis 1423 -11531125 7000692938 yorl dna polymerase iii alpha subunit homolog yorl (db:pir2.dat) E69923 E69923 Bacillus subtilis 1423 -11531125 7000692939 yorl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to dna polymerase iii (alpha subunit)) (le:174667) (re:178584) (di:complement) BSUB0011 Z99114 g2634427 Bacillus subtilis 1423 -11531125 7500963952 yorl putative dna polymerase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:106936) (re:110853) (di:direct) AF020713 AF020713 g3025611 Bacteriophage SPBc2 66797 -11531125

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801461	4723	26879	720	240

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801468	4724	26880	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801480	4725	26881	477	158

Description

6500727268 hypothetical protein:similar to single-strand dna-specific exonuclease (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorK yorK Bacillus subtilis 1423 -11531126 7000694587 york single-strand dna-specific exonuclease homolog york (db:pir2.dat) D69923 D69923 Bacillus subtilis 1423 -11531126 7000694588 york (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to single-strand dna-specific exonuclease) (le:178597) (re:180327) (di:complement) BSUB0011 Z99114 g2634428 Bacillus subtilis 1423 -11531126 7500965187 york putative ss-dna-specific endonuclease (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:105193) (re:106923) (di:direct) AF020713 AF020713 g3025610 Bacteriophage SPBc2 66797 -11531126

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801510	4726	26882	1686	562

Description

6500727269 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorJ yorJ Bacillus subtilis 1423 -11531127 7000693743 yorj hypothetical protein yorj (db:pir2.dat) C69923 C69923 Bacillus subtilis 1423 -11531127 7000693744 yorj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:180327) (re:181463) (di:complement) BSUB0011 Z99114 g2634429 Bacillus subtilis 1423 -11531127 7500964601 yorj unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:104057) (re:105193) (di:direct) AF020713 AF020713 g3025609 Bacteriophage SPBc2 66797 -11531127

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801519	4727	26883	333	110

Description

6500727270 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorI yorI Bacillus subtilis 1423 -11531128 7000693741 yori hypothetical protein yori (db:pir2.dat) B69923 B69923 Bacillus subtilis 1423 -11531128 7000693742 yori (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:181479) (re:182993) (di:complement) BSUB0011 Z99114 g2634430 Bacillus subtilis 1423 -11531128 7500964600 yori putative replicative dna helicase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:102527) (re:104041) (di:direct) AF020713 AF020713 g3025608 Bacteriophage SPBc2 66797 -11531128

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801530	4728	26884	831	277

Description

6500727271 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorH yorH Bacillus subtilis 1423 -11531129 7000693739 yorh hypothetical protein yorh (db:pir2.dat) A69923 A69923 Bacillus subtilis 1423 -11531129 7000693740 yorh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:183008) (re:183478) (di:complement) BSUB0011 Z99114 g2634431 Bacillus subtilis 1423 -11531129 7500964599 yorh unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:102042) (re:102512) (di:direct) AF020713 AF020713 g3025607 Bacteriophage SPBc2 66797 -11531129

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801540	4729	26885	378	125

Description

6500727272 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorG yorG Bacillus subtilis 1423 -11531130 7000693737 yorg hypothetical protein yorg (db:pir2.dat) H69922 H69922 Bacillus subtilis 1423 -11531130 7000693738 yorg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:183521) (re:184492) (di:complement) BSUB0011 Z99114 g2634432 Bacillus subtilis 1423 -11531130 7500964598 yorg atp/gtp binding protein (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:101028) (re:101999) (di:direct) AF020713 AF020713 g3025606 Bacteriophage SPBc2 66797 -11531130

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801542	4730	26886	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801565	4731	26887	426	142

Description

6500727273 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorF yorF Bacillus subtilis 1423 -11531131 7000693735 yorf hypothetical protein yorf (db:pir2.dat) G69922 G69922 Bacillus subtilis 1423 -11531131 7000693736 yorf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:184575) (re:185489) (di:complement) BSUB0011 Z99114 g2634433 Bacillus subtilis 1423 -11531131 7500964597 yorf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:100031) (re:100945) (di:direct) AF020713 AF020713 g3025605 Bacteriophage SPBc2 66797 -11531131

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801571	4732	26888	501	166

Description

6500727274 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorE yorE Bacillus subtilis 1423 -11531132 7000693733 yore hypothetical protein yore (db:pir2.dat) F69922 F69922 Bacillus subtilis 1423 -11531132 7000693734 yore (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:185511) (re:185882) (di:complement) BSUB0011 Z99114 g2634434 Bacillus subtilis 1423 -11531132 7500964596 yore unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:99638) (re:100009) (di:direct) AF020713 AF020713 g3025604 Bacteriophage SPBc2 66797 -11531132

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801573	4733	26889	699	232

Description

GTC ORF with score 126 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t6a23 genomic sequence,complete sequence.) (nt:unknown protein) (le:30376:30906:31867:32237) (re:30479:31025:31981:32330) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801587	4734	26890	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801589	4735	26891	186	61

Description

6500727275 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorD yorD Bacillus subtilis 1423 -11531133 7000693731 yord hypothetical protein yord (db:pir2.dat) E69922 E69922 Bacillus subtilis 1423 -11531133 7000693732 yord (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:186056) (re:186370) (di:complement) BSUB0011 Z99114 g2634435 Bacillus subtilis 1423 -11531133 7500964595 yord (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacillus subtilis pbsx prophage xkdw) (le:99150) (re:99464) (di:direct) AF020713 AF020713 g3025603 Bacteriophage SPBc2 66797 -11531133

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801593	4736	26892	321	106

Description

6500727276 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorC yorC Bacillus subtilis 1423 -11531134 7000693729 yorc hypothetical protein yorc (db:pir2.dat) D69922 D69922 Bacillus subtilis 1423 -11531134 7000693730 yorc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:186447) (re:186827) (di:complement) BSUB0011 Z99114 g2634436 Bacillus subtilis 1423 -11531134 7500964594 yorc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:98693) (re:99073) (di:direct) AF020713 AF020713 g3025602 Bacteriophage SPBc2 66797 -11531134

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801594	4737	26893	363	120

Description

6500727277 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorB yorB Bacillus subtilis 1423 -11531135 7000693727 yorb hypothetical protein yorb (db:pir2.dat) C69922 C69922 Bacillus subtilis 1423 -11531135 7000693728 yorb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:186890) (re:187186) (di:complement) BSUB0011 Z99114 g2634437 Bacillus subtilis 1423 -11531135 7500964593 yorb unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:98334) (re:98630) (di:direct) AF020713 AF020713 g3025601 Bacteriophage SPBc2 66797 -11531135

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801595	4738	26894	693	231

Description

6500727278 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yorA yorA Bacillus subtilis 1423 -11531136 7000692702 yora conserved hypothetical protein yora (db:pir2.dat) B69922 B69922 Bacillus subtilis 1423 -11531136 7000692703 yora (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:187275) (re:189035) (di:complement) BSUB0011 Z99114 g2634438 Bacillus subtilis 1423 -11531136 7500963792 yora (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacillus subtilis yclg) (le:96485) (re:98245) (di:direct) AF020713 AF020713 g3025600 Bacteriophage SPBc2 66797 -11531136

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801603	4739	26895	291	96

Description

6500727279 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqZ yoqZ Bacillus subtilis 1423 -11531137 7000694386 yoqz phage-related replication protein homolog yoqz (cl:phage-related replication protein) (db:pir2.dat) A69922 A69922 Bacillus subtilis 1423 -11531137 7000694387 yoqz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to phage-related protein) (le:189032) (re:189856) (di:complement) BSUB0011 Z99114 g2634439 Bacillus subtilis 1423 -11531137 7500955716 yoqz (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacteriophage spp1 orf37.1 product) (le:95664) (re:96488) (di:direct) AF020713 AF020713 g3025599 Bacteriophage SPBc2 66797 -11531137

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801604	4740	26896	1185	394

Description

6500727280 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqY yoqY Bacillus subtilis 1423 -11531138 7000693725 yoqy hypothetical protein yoqy (db:pir2.dat) H69921 H69921 Bacillus subtilis 1423 -11531138 7000693726 yoqy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:189955) (re:190350) (di:complement) BSUB0011 Z99114 g2634440 Bacillus subtilis 1423 -11531138 7500964592 yoqy unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:95170) (re:95565) (di:direct) AF020713 AF020713 g3025598 Bacteriophage SPBc2 66797 -11531138

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801612	4741	26897	879	292

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801623	4742	26898	465	154

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801625	4743	26899	1548	515

Description

6500727281 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqX yoqX Bacillus subtilis 1423 -11531139 7000693723 yoqx hypothetical protein yoqx (db:pir2.dat) G69921 G69921 Bacillus subtilis 1423 -11531139 7000693724 yoqx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:190405) (re:190626) (di:complement) BSUB0011 Z99114 g2634441 Bacillus subtilis 1423 -11531139 7500964591 yoqx unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:94894) (re:95115) (di:direct) AF020713 AF020713 g3025597 Bacteriophage SPBc2 66797 -11531139

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801631	4744	26900	222	73

Description

6500727282 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqW yoqW Bacillus subtilis 1423 -11531140 7000692700 yoqw conserved hypothetical protein yoqw (db:pir2.dat) F69921 F69921 Bacillus subtilis 1423 -11531140 7000692701 yoqw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins) (le:190697) (re:191371) (di:direct) BSUB0011 Z99114 g2634442 Bacillus subtilis 1423 -11531140 7500963791 yoqw (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to escherichia coli yedg) (le:94149) (re:94823) (di:complement) AF020713 AF020713 g3025596 Bacteriophage SPBc2 66797 -11531140

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801633	4745	26901	414	137

Description

6500727283 hypothetical protein:similar to dna ligase (gtcfc:14.1) (ec:6.5.1.1) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqV yoqV Bacillus subtilis 1423 -11531141 7000692931 yoqv dna ligase homolog yoqv (db:pir2.dat) E69921 E69921 Bacillus subtilis 1423 -11531141 7000692932 yoqv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to dna ligase) (le:191441) (re:192253) (di:direct) BSUB0011 Z99114 g2634443 Bacillus subtilis 1423 -11531141 7500963948 yoqv (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to part of dna ligases) (le:93267) (re:94079) (di:complement) AF020713 AF020713 g3025595 Bacteriophage SPBc2 66797 -11531141

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801634	4746	26902	285	95

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801652	4747	26903	456	151

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801677	4748	26904	912	303

Description

6500727284 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqU yoqU Bacillus subtilis 1423 -11531142 7000693721 yoqu hypothetical protein yoqu (db:pir2.dat) D69921 D69921 Bacillus subtilis 1423 -11531142 7000693722 yoqu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:192319) (re:192732) (di:complement) BSUB0011 Z99114 g2634444 Bacillus subtilis 1423 -11531142 7500964590 yoqu unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:92788) (re:93201) (di:direct) AF020713 AF020713 g3025594 Bacteriophage SPBc2 66797 -11531142

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801678	4749	26905	735	244

Description

GTC ORF with score 259 to: (sr:streptomyces hygroscopicus (strain:sf1293) dna) (db:genpept-bct2) (de:streptomyces hygroscopicus gene for carboxyphosphonoenolpyruvatephosphonomutase, complete cds.) (le:168) (re:1055) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801681	4750	26906	312	103

Description

6500727285 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqT yoqT Bacillus subtilis 1423 -11531143 7000693719 yoqt hypothetical protein yoqt (db:pir2.dat) C69921 C69921 Bacillus subtilis 1423 -11531143 7000693720 yoqt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:192898) (re:193047) (di:direct) BSUB0011 Z99114 g2634445 Bacillus subtilis 1423 -11531143 7500964589 yoqt unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:92473) (re:92622) (di:complement) AF020713 AF020713 g3025593 Bacteriophage SPBc2 66797 -11531143

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801682	4751	26907	402	133

Description

GTC ORF with score 128 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome i bac f22k20 genomic sequence,complete sequence.) (nt:highly similar to gp|x67953|47149 and others) (le:70755:71205:71478) (re:71123:71380:71502) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801685	4752	26908	339	112

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801692	4753	26909	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801701	4754	26910	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801707	4755	26911	1098	365

Description

6500727286 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqS yoqS Bacillus subtilis 1423 -11531144 7000693717 yoqs hypothetical protein yoqs (db:pir2.dat) B69921 B69921 Bacillus subtilis 1423 -11531144 7000693718 yoqs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:193124) (re:193471) (di:complement) BSUB0011 Z99114 g2634446 Bacillus subtilis 1423 -11531144 7500964588 yoqs unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:92049) (re:92396) (di:direct) AF020713 AF020713 g3025592 Bacteriophage SPBc2 66797 -11531144

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801717	4756	26912	774	257

Description

GTC ORF with score 178 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f4b14 (essaiiproject).) (nt:contains eukaryotic rna polymerase ii heptapeptide) (le:24678:24953:25138) (re:24846:25024:28199) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801718	4757	26913	561	186

Description

6500727287 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqR yoqR Bacillus subtilis 1423 -11531145 7000693715 yoqr hypothetical protein yoqr (db:pir2.dat) A69921 A69921 Bacillus subtilis 1423 -11531145 7000693716 yoqr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:193473) (re:193829) (di:complement) BSUB0011 Z99114 g2634447 Bacillus subtilis 1423 -11531145 7500964587 yoqr unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:91691) (re:92047) (di:direct) AF020713 AF020713 g3025591 Bacteriophage SPBc2 66797 -11531145

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801744	4758	26914	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801747	4759	26915	924	308

Description

6500727288 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqP yoqP Bacillus subtilis 1423 -11531146 7000693713 yoqp hypothetical protein yoqp (db:pir2.dat) H69920 H69920 Bacillus subtilis 1423 -11531146 7000693714 yoqp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:193789) (re:194130) (di:complement) BSUB0011 Z99114 g2634448 Bacillus subtilis 1423 -11531146 7500964586 yoqp unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:91390) (re:91731) (di:direct) AF020713 AF020713 g3025590 Bacteriophage SPBc2 66797 -11531146

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801778	4760	26916	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801782	4761	26917	900	299

Description

6500727289 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqO yoqO Bacillus subtilis 1423 -11531147 7000693711 yoqo hypothetical protein yoqo (db:pir2.dat) G69920 G69920 Bacillus subtilis 1423 -11531147 7000693712 yoqo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:194244) (re:194618) (di:direct) BSUB0011 Z99114 g2634449 Bacillus subtilis 1423 -11531147 7500964585 yoqo unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:90902) (re:91276) (di:complement) AF020713 AF020713 g3025589 Bacteriophage SPBc2 66797 -11531147

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801821	4762	26918	1023	340

Description

6500727290 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqN yoqN Bacillus subtilis 1423 -11531148 7000693709 yoqn hypothetical protein yoqn (db:pir2.dat) F69920 F69920 Bacillus subtilis 1423 -11531148 7000693710 yoqn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:194635) (re:194853) (di:complement) BSUB0011 Z99114 g2634450 Bacillus subtilis 1423 -11531148 7500964584 yoqn unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:90667) (re:90885) (di:direct) AF020713 AF020713 g3025588 Bacteriophage SPBc2 66797 -11531148

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801822	4763	26919	1062	354

Description

6500727291 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqM yoqM Bacillus subtilis 1423 -11531149 7000693707 yoqm hypothetical protein yoqm (db:pir2.dat) E69920 E69920 Bacillus subtilis 1423 -11531149 7000693708 yoqm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:195057) (re:195335) (di:direct) BSUB0011 Z99114 g2634451 Bacillus subtilis 1423 -11531149 7500964583 yoqm unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:90185) (re:90463) (di:complement) AF020713 AF020713 g3025587 Bacteriophage SPBc2 66797 -11531149

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801830	4764	26920	219	72

Description

GTC ORF with score 115 to: (fn:suppressor of abf2 (him1)) (sr:baker's yeast) (db:genpept-pln2) (de:saccharomyces cerevisiae putative carrier protein (shm1) gene,complete cds.) (nt:mitochondrial integral membrane protein) (le:474) (re:1376) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801831	4765	26921	201	66

Description

6500727292 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqL yoqL Bacillus subtilis 1423 -11531150 7000693705 yoql hypothetical protein yoql (db:pir2.dat) D69920 D69920 Bacillus subtilis 1423 -11531150 6000691070 yoql (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:195460) (re:196152) (di:complement) BSUB0011 Z99114 g2634452 Bacillus subtilis 1423 -11531150 7000693706 yoql (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:90) (re:782) (di:complement) BSUB0012 Z99115 g2634479 Bacillus subtilis 1423 -11531150 7500964582 yoql unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:89368) (re:90060) (di:direct) AF020713 AF020713 g3025586 Bacteriophage SPBc2 66797 -11531150

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801834	4766	26922	237	78

Description

GTC ORF with score 256 to: (fn:suppressor of abf2 (him1)) (sr:baker's yeast) (db:genpept-pln2) (de:saccharomyces cerevisiae putative carrier protein (shm1) gene,complete cds.) (nt:mitochondrial integral membrane protein) (le:474) (re:1376) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801838	4767	26923	357	118

Description

GTC ORF with score 450 to: (fn:suppressor of abf2 (him1)) (sr:baker's yeast) (db:genpept-pln2) (de:saccharomyces cerevisiae putative carrier protein (shm1) gene,complete cds.) (nt:mitochondrial integral membrane protein) (le:474) (re:1376) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801845	4768	26924	837	279

Description

6500727293 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqK yoqK Bacillus subtilis 1423 -11531151 7000693703 yoqk hypothetical protein yoqk (db:pir2.dat) C69920 C69920 Bacillus subtilis 1423 -11531151 6000691072 yoqk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:196192) (re:196395) (di:complement) BSUB0011 Z99114 g2634453 Bacillus subtilis 1423 -11531151 7000693704 yoqk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:822) (re:1025) (di:complement) BSUB0012 Z99115 g2634480 Bacillus subtilis 1423 -11531151 7500964581 yoqk unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:89125) (re:89328) (di:direct) AF020713 AF020713 g3025585 Bacteriophage SPBc2 66797 -11531151

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801853	4769	26925	1047	348

Description

6500727294 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqJ yoqJ Bacillus subtilis 1423 -11531152 7000692698 yoqj conserved hypothetical protein yoqj (db:pir2.dat) B69920 B69920 Bacillus subtilis 1423 -11531152 6000691074 yoqj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:196415) (re:196930) (di:complement) BSUB0011 Z99114 g2634454 Bacillus subtilis 1423 -11531152 7000692699 yoqj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:1045) (re:1560) (di:complement) BSUB0012 Z99115 g2634481 Bacillus subtilis 1423 -11531152 7500963790 yoqj (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacillus subtilis ypsa) (le:88590) (re:89105) (di:direct) AF020713 AF020713 g3025584 Bacteriophage SPBc2 66797 -11531152

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801864	4770	26926	1110	369

Description

6500727295 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqI yoqI Bacillus subtilis 1423 -11531153 7000693701 yoqi hypothetical protein yoqi (db:pir2.dat) A69920 A69920 Bacillus subtilis 1423 -11531153 6000691076 yoqi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:197141) (re:197335) (di:complement) BSUB0011 Z99114 g2634455 Bacillus subtilis 1423 -11531153 7000693702 yoqi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:1771) (re:1965) (di:complement) BSUB0012 Z99115 g2634482 Bacillus subtilis 1423 -11531153 7500964580 yoqi unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:88185) (re:88379) (di:direct) AF020713 AF020713 g3025583 Bacteriophage SPBc2 66797 -11531153

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801877	4771	26927	987	328

Description

6500727296 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqH yoqH Bacillus subtilis 1423 -11531154 7000693699 yoqh hypothetical protein yoqh (db:pir2.dat) H69919 H69919 Bacillus subtilis 1423 -11531154 6000691078 yoqh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:197384) (re:197836) (di:complement) BSUB0011 Z99114 g2634456 Bacillus subtilis 1423 -11531154 7000693700 yoqh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:2014) (re:2466) (di:complement) BSUB0012 Z99115 g2634483 Bacillus subtilis 1423 -11531154 7500964579 yoqh unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:87684) (re:88136) (di:direct) AF020713 AF020713 g3025582 Bacteriophage SPBc2 66797 -11531154

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801885	4772	26928	1320	439

Description

GTC ORF with score 881 to: (sr:acinetobacter sp. (strain ncib 9871) dna, clone puc2d3) (db:genpept-bct1) (de:acinetobacter sp. cyclohexanone monooxygenase gene, complete cds.) (nt:cyclohexanone monoxygenase) (le:391) (re:2022) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801889	4773	26929	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801895	4774	26930	1680	560

Description

6500727297 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqG yoqG Bacillus subtilis 1423 -11531155 7000693697 yoqg hypothetical protein yoqg (db:pir2.dat) G69919 G69919 Bacillus subtilis 1423 -11531155 6000691080 yoqg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:197919) (re:198176) (di:complement) BSUB0011 Z99114 g2634457 Bacillus subtilis 1423 -11531155 7000693698 yoqg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:2549) (re:2806) (di:complement) BSUB0012 Z99115 g2634484 Bacillus subtilis 1423 -11531155 7500964578 yoqg unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:87344) (re:87601) (di:direct) AF020713 AF020713 g3025581 Bacteriophage SPBc2 66797 -11531155

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801904	4775	26931	354	117

Description

6500727298 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqF yoqF Bacillus subtilis 1423 -11531156 7000693695 yoqf hypothetical protein yoqf (db:pir2.dat) F69919 F69919 Bacillus subtilis 1423 -11531156 6000691082 yoqf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:198221) (re:198424) (di:complement) BSUB0011 Z99114 g2634458 Bacillus subtilis 1423 -11531156 7000693696 yoqf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:2851) (re:3054) (di:complement) BSUB0012 Z99115 g2634485 Bacillus subtilis 1423 -11531156 7500964577 yoqf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:87096) (re:87299) (di:direct) AF020713 AF020713 g3025580 Bacteriophage SPBc2 66797 -11531156

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801907	4776	26932	735	244

Description

6500727299 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqE yoqE Bacillus subtilis 1423 -11531157 7000693693 yoqe hypothetical protein yoqe (db:pir2.dat) E69919 E69919 Bacillus subtilis 1423 -11531157 6000691084 yoqe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:198433) (re:198597) (di:complement) BSUB0011 Z99114 g2634459 Bacillus subtilis 1423 -11531157 7000693694 yoqe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:3063) (re:3227) (di:complement) BSUB0012 Z99115 g2634486 Bacillus subtilis 1423 -11531157 7500964576 yoqe unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:86923) (re:87087) (di:direct) AF020713 AF020713 g3025579 Bacteriophage SPBc2 66797 -11531157

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801908	4777	26933	291	97

Description

6500727300 hypothetical protein:similar to phage-related dna-binding protein anti-repressor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqD yoqD Bacillus subtilis 1423 -11531158 7000694366 yoqd phage-related dna-binding protein anti-rep homolog yoqd (db:pir2.dat) D69919 D69919 Bacillus subtilis 1423 -11531158 6000691086 yoqd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to phage-related dna-binding protein) (le:198651) (re:199406) (di:complement) BSUB0011 Z99114 g2634460 Bacillus subtilis 1423 -11531158 7000694367 yoqd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phage-related dna-binding protein) (le:3281) (re:4036) (di:complement) BSUB0012 Z99115 g2634487 Bacillus subtilis 1423 -11531158 7500965051 yoqd putative antirepressor (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:86114) (re:86869) (di:direct) AF020713 AF020713 g3025578 Bacteriophage SPBc2 66797 -11531158

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801910	4778	26934	222	73

Description

6500727301 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqC yoqC Bacillus subtilis 1423 -11531159 7000693691 yoqc hypothetical protein yoqc (db:pir2.dat) C69919 C69919 Bacillus subtilis 1423 -11531159 6000691088 yoqc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:199447) (re:199854) (di:complement) BSUB0011 Z99114 g2634461 Bacillus subtilis 1423 -11531159 7000693692 yoqc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:4077) (re:4484) (di:complement) BSUB0012 Z99115 g2634488 Bacillus subtilis 1423 -11531159 7500964575 yoqc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:85666) (re:86073) (di:direct) AF020713 AF020713 g3025577 Bacteriophage SPBc2 66797 -11531159

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801911	4779	26935	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801912	4780	26936	438	145

Description

6500727302 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqB yoqB Bacillus subtilis 1423 -11531160 7000693689 yoqb hypothetical protein yoqb (db:pir2.dat) B69919 B69919 Bacillus subtilis 1423 -11531160 6000691090 yoqb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:199861) (re:200199) (di:complement) BSUB0011 Z99114 g2634462 Bacillus subtilis 1423 -11531160 7000693690 yoqb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:4491) (re:4829) (di:complement) BSUB0012 Z99115 g2634489 Bacillus subtilis 1423 -11531160 7500964574 yoqb unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:85321) (re:85659) (di:direct) AF020713 AF020713 g3025576 Bacteriophage SPBc2 66797 -11531160

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801913	4781	26937	912	303

Description

6500727303 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yoqA yoqA Bacillus subtilis 1423 -11531161 7000693687 yoqa hypothetical protein yoqa (db:pir2.dat) A69919 A69919 Bacillus subtilis 1423 -11531161 6000691092 yoqa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:200196) (re:200546) (di:complement) BSUB0011 Z99114 g2634463 Bacillus subtilis 1423 -11531161 7000693688 yoqa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:4826) (re:5176) (di:complement) BSUB0012 Z99115 g2634490 Bacillus subtilis 1423 -11531161 7500964573 yoqa unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:84974) (re:85324) (di:direct) AF020713 AF020713 g3025575 Bacteriophage SPBc2 66797 -11531161

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801939	4782	26938	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801944	4783	26939	345	114

Description

GTC ORF with score 95 to: (fn:putative lectin-like protein involved in) (sr:saccharomyces cerevisiae (sub_species:pastorianus, strain:kms004) (db:genpept) (de:saccharomyces cerevisiae gene for flocculin, partial cds.) (le:<1) (re:2550) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801945	4784	26940	726	241

Description

6500727304 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopZ yopZ Bacillus subtilis 1423 -11531162 7000693685 yopz hypothetical protein yopz (db:pir2.dat) H69918 H69918 Bacillus subtilis 1423 -11531162 6000691094 yopz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:200559) (re:200762) (di:complement) BSUB0011 Z99114 g2634464 Bacillus subtilis 1423 -11531162 7000693686 yopz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:5189) (re:5392) (di:complement) BSUB0012 Z99115 g2634491 Bacillus subtilis 1423 -11531162 7500964572 yopz unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:84758) (re:84961) (di:direct) AF020713 AF020713 g3025574 Bacteriophage SPBc2 66797 -11531162

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801948	4785	26941	1584	528

Description

6500727305 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopY yopY Bacillus subtilis 1423 -11531163 7000693683 yopy hypothetical protein yopy (db:pir2.dat) G69918 G69918 Bacillus subtilis 1423 -11531163 6000691096 yopy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:200776) (re:201054) (di:complement) BSUB0011 Z99114 g2634465 Bacillus subtilis 1423 -11531163 7000693684 yopy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:5406) (re:5684) (di:complement) BSUB0012 Z99115 g2634492 Bacillus subtilis 1423 -11531163 7500964571 yopy unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:84466) (re:84744) (di:direct) AF020713 AF020713 g3025573 Bacteriophage SPBc2 66797 -11531163

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801964	4786	26942	828	275

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801968	4787	26943	633	210

Description

6500727306 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopX yopX Bacillus subtilis 1423 -11531164 7000693681 yopx hypothetical protein yopx (db:pir2.dat) F69918 F69918 Bacillus subtilis 1423 -11531164 6000691098 yopx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:201051) (re:201455) (di:complement) BSUB0011 Z99114 g2634466 Bacillus subtilis 1423 -11531164 7000693682 yopx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:5681) (re:6085) (di:complement) BSUB0012 Z99115 g2634493 Bacillus subtilis 1423 -11531164 7500964570 yopx unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:84065) (re:84469) (di:direct) AF020713 AF020713 g3025572 Bacteriophage SPBc2 66797 -11531164

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801977	4788	26944	675	224

Description

6500727307 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopW yopW Bacillus subtilis 1423 -11531165 7000693679 yopw hypothetical protein yopw (db:pir2.dat) E69918 E69918 Bacillus subtilis 1423 -11531165 6000691100 yopw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:201452) (re:201787) (di:complement) BSUB0011 Z99114 g2634467 Bacillus subtilis 1423 -11531165 7000693680 yopw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:6082) (re:6417) (di:complement) BSUB0012 Z99115 g2634494 Bacillus subtilis 1423 -11531165 7500964569 yopw unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:83733) (re:84068) (di:direct) AF020713 AF020713 g3025571 Bacteriophage SPBc2 66797 -11531165

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801983	4789	26945	687	228

Description

6500727308 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopV yopV Bacillus subtilis 1423 -11531166 7000693677 yopv hypothetical protein yopv (db:pir2.dat) D69918 D69918 Bacillus subtilis 1423 -11531166 6000691102 yopv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:201876) (re:202070) (di:complement) BSUB0011 Z99114 g2634468 Bacillus subtilis 1423 -11531166 7000693678 yopv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:6506) (re:6700) (di:complement) BSUB0012 Z99115 g2634495 Bacillus subtilis 1423 -11531166 7500964568 yopv unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:83450) (re:83644) (di:direct) AF020713 AF020713 g3025570 Bacteriophage SPBc2 66797 -11531166

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801984	4790	26946	363	120

Description

6500727309 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopU yopU Bacillus subtilis 1423 -11531167 7000693675 yopu hypothetical protein yopu (db:pir2.dat) C69918 C69918 Bacillus subtilis 1423 -11531167 6000691104 yopu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:202182) (re:202379) (di:complement) BSUB0011 Z99114 g2634469 Bacillus subtilis 1423 -11531167 7000693676 yopu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:6812) (re:7009) (di:complement) BSUB0012 Z99115 g2634496 Bacillus subtilis 1423 -11531167 7500964567 yopu unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:83141) (re:83338) (di:direct) AF020713 AF020713 g3025569 Bacteriophage SPBc2 66797 -11531167

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801997	4791	26947	324	107

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501801998	4792	26948	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802031	4793	26949	387	128

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802039	4794	26950	357	118

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802046	4795	26951	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802048	4796	26952	924	307

Description

GTC ORF with score 803 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1007.) (nt:similar to saccharomyces cerevisiae ornithine) (le:<1) (re:1093) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802056	4797	26953	222	73

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802064	4798	26954	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802068	4799	26955	468	156

Description

6500727310 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopT yopT Bacillus subtilis 1423 -11531168 7000693673 yopt hypothetical protein yopt (db:pir2.dat) B69918 B69918 Bacillus subtilis 1423 -11531168 6000691106 yopt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:202449) (re:202667) (di:complement) BSUB0011 Z99114 g2634470 Bacillus subtilis 1423 -11531168 7000693674 yopt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:7079) (re:7297) (di:complement) BSUB0012 Z99115 g2634497 Bacillus subtilis 1423 -11531168 7500964566 yopt unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:82853) (re:83071) (di:direct) AF020713 AF020713 g3025568 Bacteriophage SPBc2 66797 -11531168

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802093	4800	26956	639	212

Description

6500727311 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopS yopS Bacillus subtilis 1423 -11531169 7000692696 yops conserved hypothetical protein yops (cl:hypothetical protein yotl) (db:pir2.dat) A69918 A69918 Bacillus subtilis 1423 -11531169 6000691108 yops (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (nt:similar to hypothetical proteins from b. subtilis) (le:202850) (re:203074) (di:direct) BSUB0011 Z99114 g2634471 Bacillus subtilis 1423 -11531169 7000692697 yops (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:7480) (re:7704) (di:direct) BSUB0012 Z99115 g2634498 Bacillus subtilis 1423 -11531169 7500955946 yops unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:82446) (re:82670) (di:complement) AF020713 AF020713 g3025567 Bacteriophage SPBc2 66797 -11531169

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802094	4801	26957	660	219

Description

6500727312 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopR yopR Bacillus subtilis 1423 -11531170 7000693671 yopr hypothetical protein yopr (db:pir2.dat) H69917 H69917 Bacillus subtilis 1423 -11531170 6000691110 yopr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:203263) (re:204240) (di:complement) BSUB0011 Z99114 g2634472 Bacillus subtilis 1423 -11531170 7000693672 yopr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:7893) (re:8870) (di:complement) BSUB0012 Z99115 g2634499 Bacillus subtilis 1423 -11531170 7500964565 yopr unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:81280) (re:82257) (di:direct) AF020713 AF020713 g3025566 Bacteriophage SPBc2 66797 -11531170

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802105	4802	26958	1119	372

Description

6500727313 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopQ yopQ Bacillus subtilis 1423 -11531171 7000693669 yopq hypothetical protein yopq (db:pir2.dat) G69917 G69917 Bacillus subtilis 1423 -11531171 6000691112 yopq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:204264) (re:205646) (di:complement) BSUB0011 Z99114 g2634473 Bacillus subtilis 1423 -11531171 7000693670 yopq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:8894) (re:10276) (di:complement) BSUB0012 Z99115 g2634500 Bacillus subtilis 1423 -11531171 7500964564 yopq unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:79874) (re:81256) (di:direct) AF020713 AF020713 g3025565 Bacteriophage SPBc2 66797 -11531171

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802116	4803	26959	291	96

Description

6500727314 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopP yopP Bacillus subtilis 1423 -11531172 7000693667 yopp hypothetical protein yopp (db:pir2.dat) F69917 F69917 Bacillus subtilis 1423 -11531172 6000691114 yopp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:205753) (re:206829) (di:complement) BSUB0011 Z99114 g2634474 Bacillus subtilis 1423 -11531172 7000693668 yopp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:10383) (re:11459) (di:complement) BSUB0012 Z99115 g2634501 Bacillus subtilis 1423 -11531172 7500964563 yopp unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:78691) (re:79767) (di:direct) AF020713 AF020713 g3025564 Bacteriophage SPBc2 66797 -11531172

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802119	4804	26960	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802121	4805	26961	561	186

Description

6500727315 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopO yopO Bacillus subtilis 1423 -11531173 7000693665 yopo hypothetical protein yopo (db:pir2.dat) E69917 E69917 Bacillus subtilis 1423 -11531173 6000691116 yopo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:206819) (re:207031) (di:complement) BSUB0011 Z99114 g2634475 Bacillus subtilis 1423 -11531173 7000693666 yopo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:11449) (re:11661) (di:complement) BSUB0012 Z99115 g2634502 Bacillus subtilis 1423 -11531173 7500964562 yopo unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:78489) (re:78701) (di:direct) AF020713 AF020713 g3025563 Bacteriophage SPBc2 66797 -11531173

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802122	4806	26962	444	147

Description

6500727316 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopN yopN Bacillus subtilis 1423 -11531174 7500964561 yopn (de:hypothetical 12.1 kd protein in mtbp-sunt intergenic region) (db:swissprot) YOPN_BACSU O34369 BACILLUS SUBTILIS 1423 -11531174 7502851703 yopn (de:hypothetical 12.1 kd protein in mtbp-sunt intergenic region) (db:swissprot) YOPN_BACSU O34369 BACTERIOPHAGE SPBC2 66797 -11531174 7000693663 yopn hypothetical protein yopn (db:pir2.dat) D69917 D69917 Bacillus subtilis 1423 -11531174 6000691118 yopn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:207079) (re:207396) (di:complement) BSUB0011 Z99114 g2634476 Bacillus subtilis 1423 -11531174 7000693664 yopn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:11709) (re:12026) (di:complement) BSUB0012 Z99115 g2634503 Bacillus subtilis 1423 -11531174 7502851704 yopn unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:78124) (re:78441) (di:direct) AF020713 AF020713 g3025562 Bacteriophage SPBc2 66797 -11531174

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802152	4807	26963	1179	392

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802174	4808	26964	996	331

Description

GTC ORF with score 454 to: (db:genpept) (de:aureobasidium pullulans cosmid ppsr-22 hydroxylase, multidrugresistance-like protein (apmdr1), and peptide synthetase genes,complete cds.) (le:13308:13350:13743:13878) (re:19541:19541:19541:19541) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802176	4809	26965	891	297

Description

6500727317 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopM yopM Bacillus subtilis 1423 -11531175 7000693661 yopm hypothetical protein yopm (db:pir2.dat) C69917 C69917 Bacillus subtilis 1423 -11531175 6000691120 yopm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.) (le:207399) (re:207599) (di:complement) BSUB0011 Z99114 g2634477 Bacillus subtilis 1423 -11531175 7000693662 yopm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:12029) (re:12229) (di:complement) BSUB0012 Z99115 g2634504 Bacillus subtilis 1423 -11531175 7500964560 yopm unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:77921) (re:78121) (di:direct) AF020713 AF020713 g3025561 Bacteriophage SPBc2 66797 -11531175

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802182	4810	26966	960	319

Description

6500727318 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopL yopL Bacillus subtilis 1423 -11531176 7000693659 yopl hypothetical protein yopl (db:pir2.dat) B69917 B69917 Bacillus subtilis 1423 -11531176 7000693660 yopl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:12556) (re:12681) (di:complement) BSUB0012 Z99115 g2634505 Bacillus subtilis 1423 -11531176 7500964559 yopl unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:77469) (re:77594) (di:direct) AF020713 AF020713 g3025560 Bacteriophage SPBc2 66797 -11531176

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802188	4811	26967	723	240

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802201	4812	26968	426	141

Description

GTC ORF with score 220 to: (sr:gibberella zeae (sub_species:graminearum, strain:f15) dna) (db:genpept-pln2) (de:gibberella zeae genes for trichothecene 3-o-acetyltransferase,utp-ammonia ligase and phosphate permease, complete cds.) (le:6588:7075:7622) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802203	4813	26969	615	205

Description

GTC ORF with score 244 to: (sr:gibberella zeae (sub_species:graminearum, strain:f15) dna) (db:genpept-pln2) (de:gibberella zeae genes for trichothecene 3-o-acetyltransferase,utp-ammonia ligase and phosphate permease, complete cds.) (le:6588:7075:7622) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802213	4814	26970	744	247

Description

6500727319 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopK yopK Bacillus subtilis 1423 -11531177 7000693657 yopk hypothetical protein yopk (db:pir2.dat) A69917 A69917 Bacillus subtilis 1423 -11531177 7000693658 yopk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:12695) (re:13855) (di:complement) BSUB0012 Z99115 g2634506 Bacillus subtilis 1423 -11531177 7500964558 yopk unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:76295) (re:77455) (di:direct) AF020713 AF020713 g3025559 Bacteriophage SPBc2 66797 -11531177

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802220	4815	26971	426	141

Description

6500727320 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopJ yopJ Bacillus subtilis 1423 -11531178 7000693655 yopj hypothetical protein yopj (db:pir2.dat) H69916 H69916 Bacillus subtilis 1423 -11531178 7000693656 yopj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:14032) (re:14448) (di:complement) BSUB0012 Z99115 g2634507 Bacillus subtilis 1423 -11531178 7500964557 yopj unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:75702) (re:76118) (di:direct) AF020713 AF020713 g3025558 Bacteriophage SPBc2 66797 -11531178

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802227	4816	26972	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802231	4817	26973	1146	381

Description

6500727321 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopI yopI Bacillus subtilis 1423 -11531179 7000693653 yopi hypothetical protein yopi (db:pir2.dat) G69916 G69916 Bacillus subtilis 1423 -11531179 7000693654 yopi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:14450) (re:14983) (di:complement) BSUB0012 Z99115 g2634508 Bacillus subtilis 1423 -11531179 7500964556 yopi unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:75167) (re:75700) (di:direct) AF020713 AF020713 g3025557 Bacteriophage SPBc2 66797 -11531179

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802233	4818	26974	408	135

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802240	4819	26975	987	329

Description

6500727322 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopH yopH Bacillus subtilis 1423 -11531180 7000693651 yoph hypothetical protein yoph (db:pir2.dat) F69916 F69916 Bacillus subtilis 1423 -11531180 7000693652 yoph (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:15010) (re:15546) (di:complement) BSUB0012 Z99115 g2634509 Bacillus subtilis 1423 -11531180 7500964555 yoph putative atp/gtp-binding protein (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:74604) (re:75140) (di:direct) AF020713 AF020713 g3025556 Bacteriophage SPBc2 66797 -11531180

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802250	4820	26976	231	77

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802258	4821	26977	393	130

Description

GTC ORF with score 162 to: (sr:drosophila melanogaster cdna to mrna) (db:genpept-inv) (de:drosophila melanogaster ethanolamine kinase (easily shocked) mrna,complete cds.) (nt:mutant phenotype includes paralysis, excitability) (le:223) (re:1710) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802261	4822	26978	186	61

Description

6500727323 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopG yopG Bacillus subtilis 1423 -11531181 7000693649 yopg hypothetical protein yopg (db:pir2.dat) E69916 E69916 Bacillus subtilis 1423 -11531181 7000693650 yopg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:15585) (re:15716) (di:complement) BSUB0012 Z99115 g2634510 Bacillus subtilis 1423 -11531181 7500964554 yopg unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:74434) (re:74565) (di:direct) AF020713 AF020713 g3025555 Bacteriophage SPBc2 66797 -11531181

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802263	4823	26979	303	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802267	4824	26980	405	135

Description

6500727324 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopF yopF Bacillus subtilis 1423 -11531182 7000693647 yopf hypothetical protein yopf (db:pir2.dat) D69916 D69916 Bacillus subtilis 1423 -11531182 7000693648 yopf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:15727) (re:15942) (di:complement) BSUB0012 Z99115 g2634511 Bacillus subtilis 1423 -11531182 7500964553 yopf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:74208) (re:74423) (di:direct) AF020713 AF020713 g3025554 Bacteriophage SPBc2 66797 -11531182

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802268	4825	26981	396	131

Description

6500727325 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopE yopE Bacillus subtilis 1423 -11531183 7000693645 yope hypothetical protein yope (db:pir2.dat) C69916 C69916 Bacillus subtilis 1423 -11531183 7000693646 yope (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:15946) (re:16197) (di:complement) BSUB0012 Z99115 g2634512 Bacillus subtilis 1423 -11531183 7500964552 yope unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:73953) (re:74204) (di:direct) AF020713 AF020713 g3025553 Bacteriophage SPBc2 66797 -11531183

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802279	4826	26982	228	75

Description

6500727326 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopD yopD Bacillus subtilis 1423 -11531184 7000692694 yopd conserved hypothetical protein yopd (cl:conserved hypothetical protein ynef) (db:pir2.dat) B69916 B69916 Bacillus subtilis 1423 -11531184 7000692695 yopd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:16784) (re:17179) (di:complement) BSUB0012 Z99115 g2634513 Bacillus subtilis 1423 -11531184 7500963789 yopd (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacillus subtilis ywla) (le:72971) (re:73366) (di:direct) AF020713 AF020713 g3025552 Bacteriophage SPBc2 66797 -11531184

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802280	4827	26983	873	291

Description

6500727327 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopC yopC Bacillus subtilis 1423 -11531185 7000693643 yopc hypothetical protein yopc (db:pir2.dat) A69916 A69916 Bacillus subtilis 1423 -11531185 7000693644 yopc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:17237) (re:18565) (di:complement) BSUB0012 Z99115 g2634514 Bacillus subtilis 1423 -11531185 7500964551 yopc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:71585) (re:72913) (di:direct) AF020713 AF020713 g3025551 Bacteriophage SPBc2 66797 -11531185

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802281	4828	26984	408	135

Description

6500727328 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopB yopB Bacillus subtilis 1423 -11531186 7000693641 yopb hypothetical protein yopb (db:pir2.dat) H69915 H69915 Bacillus subtilis 1423 -11531186 7000693642 yopb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:18673) (re:18900) (di:complement) BSUB0012 Z99115 g2634515 Bacillus subtilis 1423 -11531186 7500964550 yopb unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:71250) (re:71477) (di:direct) AF020713 AF020713 g3025550 Bacteriophage SPBc2 66797 -11531186

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802283	4829	26985	420	139

Description

6500727329 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yopA yopA Bacillus subtilis 1423 -11531187 7000693639 yopa hypothetical protein yopa (db:pir2.dat) G69915 G69915 Bacillus subtilis 1423 -11531187 7000693640 yopa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:19161) (re:20477) (di:complement) BSUB0012 Z99115 g2634516 Bacillus subtilis 1423 -11531187 7500964549 yopa unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:69673) (re:70989) (di:direct) AF020713 AF020713 g3025549 Bacteriophage SPBc2 66797 -11531187

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802289	4830	26986	1149	382

Description

6500727330 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonX yonX Bacillus subtilis 1423 -11531188 7000693637 yonx hypothetical protein yonx (db:pir2.dat) F69915 F69915 Bacillus subtilis 1423 -11531188 7000693638 yonx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:20834) (re:21340) (di:complement) BSUB0012 Z99115 g2634517 Bacillus subtilis 1423 -11531188 7500964548 yonx unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:68810) (re:69316) (di:direct) AF020713 AF020713 g3025548 Bacteriophage SPBc2 66797 -11531188

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802293	4831	26987	204	67

Description

6500727331 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonV yonV Bacillus subtilis 1423 -11531189 7000693635 yonv hypothetical protein yonv (db:pir2.dat) E69915 E69915 Bacillus subtilis 1423 -11531189 7000693636 yonv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:21668) (re:22900) (di:complement) BSUB0012 Z99115 g2634518 Bacillus subtilis 1423 -11531189 7500964547 yonv unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:67250) (re:68482) (di:direct) AF020713 AF020713 g3025547 Bacteriophage SPBc2 66797 -11531189

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802298	4832	26988	468	155

Description

6500727332 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonU yonU Bacillus subtilis 1423 -11531190 7000693633 yonu hypothetical protein yonu (db:pir2.dat) D69915 D69915 Bacillus subtilis 1423 -11531190 7000693634 yonu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:22982) (re:23170) (di:complement) BSUB0012 Z99115 g2634519 Bacillus subtilis 1423 -11531190 7500964546 yonu unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:66980) (re:67168) (di:direct) AF020713 AF020713 g3025546 Bacteriophage SPBc2 66797 -11531190

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802305	4833	26989	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802316	4834	26990	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802328	4835	26991	267	88

Description

6500727333 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonT yonT Bacillus subtilis 1423 -11531191 7000693631 yont hypothetical protein yont (db:pir2.dat) C69915 C69915 Bacillus subtilis 1423 -11531191 7000693632 yont (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:23485) (re:23661) (di:complement) BSUB0012 Z99115 g2634520 Bacillus subtilis 1423 -11531191 7500964545 yont unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:66489) (re:66665) (di:direct) AF020713 AF020713 g3025545 Bacteriophage SPBc2 66797 -11531191

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802386	4836	26992	945	314

Description

6500727334 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonS yonS Bacillus subtilis 1423 -11531192 7000693629 yons hypothetical protein yons (db:pir2.dat) B69915 B69915 Bacillus subtilis 1423 -11531192 7000693630 yons (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:24036) (re:24647) (di:complement) BSUB0012 Z99115 g2634521 Bacillus subtilis 1423 -11531192 7500964544 yons unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:65503) (re:66114) (di:direct) AF020713 AF020713 g3025544 Bacteriophage SPBc2 66797 -11531192

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802395	4837	26993	438	145

Description

6500727335 hypothetical protein:similar to transcriptional regulator:phage-related:xre family (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonR yonR Bacillus subtilis 1423 -11531193 7000694780 yonr transcription regulator phage-related homolog yonr (cl:probable transcription repressor yowr) (db:pir2.dat) A69915 A69915 Bacillus subtilis 1423 -11531193 7000694781 yonr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to transcriptional regulator) (le:24762) (re:25088) (di:complement) BSUB0012 Z99115 g2634522 Bacillus subtilis 1423 -11531193 7500965343 yonr putative spbeta phage repressor (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:65062) (re:65388) (di:direct) AF020713 AF020713 g3025543 Bacteriophage SPBc2 66797 -11531193

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802400	4838	26994	291	96

Description

6500727336 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonP yonP Bacillus subtilis 1423 -11531194 7000693627 yonp hypothetical protein yonp (db:pir2.dat) H69914 H69914 Bacillus subtilis 1423 -11531194 7000693628 yonp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:26041) (re:26235) (di:direct) BSUB0012 Z99115 g2634523 Bacillus subtilis 1423 -11531194 7500964543 yonp unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:63915) (re:64109) (di:complement) AF020713 AF020713 g3025542 Bacteriophage SPBc2 66797 -11531194

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802403	4839	26995	540	179

Description

6500727337 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonO yonO Bacillus subtilis 1423 -11531195 7000693625 yono hypothetical protein yono (db:pir2.dat) G69914 G69914 Bacillus subtilis 1423 -11531195 7000693626 yono (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:26275) (re:28794) (di:direct) BSUB0012 Z99115 g2634524 Bacillus subtilis 1423 -11531195 7500964542 yono unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:61356) (re:63875) (di:complement) AF020713 AF020713 g3025541 Bacteriophage SPBc2 66797 -11531195

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802410	4840	26996	510	169

Description

6500727338 hypothetical protein:similar to hu-related dna-binding protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonN yonN Bacillus subtilis 1423 -11531196 7000693112 yonn probable dna-binding protein hu:hu-related dna-binding protein homolog yonn (cl:bacterial dna-binding protein) (db:pir2.dat) F69914 F69914 Bacillus subtilis 1423 -11531196 7000693113 yonn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hu-related dna-binding protein) (le:29038) (re:29316) (di:direct) BSUB0012 Z99115 g2634525 Bacillus subtilis 1423 -11531196 7500954783 yonn histone-like prokaryotic dna-binding protein (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:60834) (re:61112) (di:complement) AF020713 AF020713 g3025540 Bacteriophage SPBc2 66797 -11531196

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802411	4841	26997	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802422	4842	26998	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802430	4843	26999	498	166

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802431	4844	27000	1305	434

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802444	4845	27001	1203	401

Description

6500727339 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonK yonK Bacillus subtilis 1423 -11531197 7000693623 yonk hypothetical protein yonk (db:pir2.dat) E69914 E69914 Bacillus subtilis 1423 -11531197 7000693624 yonk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:30998) (re:31189) (di:direct) BSUB0012 Z99115 g2634526 Bacillus subtilis 1423 -11531197 7500964541 yonk unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:58961) (re:59152) (di:complement) AF020713 AF020713 g3025539 Bacteriophage SPBc2 66797 -11531197

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802451	4846	27002	1275	425

Description

GTC ORF with score 1242 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0224 gene, complete cds.) (nt:similar to putative atp-dependent rna helicase) (le:137) (re:3820) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802465	4847	27003	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802469	4848	27004	231	76

Description

6500727340 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonJ yonJ Bacillus subtilis 1423 -11531198 7000693621 yonj hypothetical protein yonj (db:pir2.dat) D69914 D69914 Bacillus subtilis 1423 -11531198 7000693622 yonj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:31206) (re:32423) (di:direct) BSUB0012 Z99115 g2634527 Bacillus subtilis 1423 -11531198 7500964540 yonj unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:57727) (re:58944) (di:complement) AF020713 AF020713 g3025538 Bacteriophage SPBc2 66797 -11531198

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802480	4849	27005	300	99

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802495	4850	27006	618	

Description

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802500	4851	27007	681	226

Description

6500727341 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonI yonI Bacillus subtilis 1423 -11531199 7000693619 yoni hypothetical protein yoni (db:pir2.dat) C69914 C69914 Bacillus subtilis 1423 -11531199 7000693620 yoni (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:32457) (re:32867) (di:complement) BSUB0012 Z99115 g2634528 Bacillus subtilis 1423 -11531199 7500964539 yoni unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:57283) (re:57693) (di:direct) AF020713 AF020713 g3025537 Bacteriophage SPBc2 66797 -11531199

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802506	4852	27008	516	171

Description

6500727342 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonH yonH Bacillus subtilis 1423 -11531200 7000693617 yonh hypothetical protein yonh (db:pir2.dat) B69914 B69914 Bacillus subtilis 1423 -11531200 7000693618 yonh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:33086) (re:33586) (di:direct) BSUB0012 Z99115 g2634529 Bacillus subtilis 1423 -11531200 7500964538 yonh unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:56564) (re:57064) (di:complement) AF020713 AF020713 g3025536 Bacteriophage SPBc2 66797 -11531200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802520	4853	27009	603	200

Description

6500727343 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonG yonG Bacillus subtilis 1423 -11531201 7000693615 yong hypothetical protein yong (db:pir2.dat) A69914 A69914 Bacillus subtilis 1423 -11531201 7000693616 yong (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:33689) (re:34609) (di:direct) BSUB0012 Z99115 g2634530 Bacillus subtilis 1423 -11531201 7500964537 yong unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:55541) (re:56461) (di:complement) AF020713 AF020713 g3025535 Bacteriophage SPBc2 66797 -11531201

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802521	4854	27010	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802526	4855	27011	690	230

Description

6500727344 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) *yonF yonF* Bacillus subtilis 1423 -11531202 7000693613 yonf hypothetical protein yonf (db:pir2.dat) H69913 H69913 Bacillus subtilis 1423 -11531202 7000693614 yonf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:34596) (re:36365) (di:direct) BSUB0012 Z99115 g2634531 Bacillus subtilis 1423 -11531202 7500964536 yonf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:53785) (re:55554) (di:complement) AF020713 AF020713 g3025534 Bacteriophage SPBc2 66797 -11531202

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802527	4856	27012	231	76

Description

6500727345 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) *yonE yonE* Bacillus subtilis 1423 -11531203 7000693611 yone hypothetical protein yone (db:pir2.dat) G69913 G69913 Bacillus subtilis 1423 -11531203 7000693612 yone (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:36383) (re:37903) (di:direct) BSUB0012 Z99115 g2634532 Bacillus subtilis 1423 -11531203 7500964535 yone unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:52247) (re:53767) (di:complement) AF020713 AF020713 g3025533 Bacteriophage SPBc2 66797 -11531203

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802528	4857	27013	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802529	4858	27014	951	316

Description

6500727346 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonD yonD Bacillus subtilis 1423 -11531204 7000693609 yond hypothetical protein yond (db:pir2.dat) F69913 F69913 Bacillus subtilis 1423 -11531204 7000693610 yond (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:37934) (re:39370) (di:direct) BSUB0012 Z99115 g2634533 Bacillus subtilis 1423 -11531204 7500964534 yond unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:50780) (re:52216) (di:complement) AF020713 AF020713 g3025532 Bacteriophage SPBc2 66797 -11531204

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802548	4859	27015	579	192

Description

6500727347 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonC yonC Bacillus subtilis 1423 -11531205 7000693607 yonc hypothetical protein yonc (db:pir2.dat) E69913 E69913 Bacillus subtilis 1423 -11531205 7000693608 yonc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:39395) (re:39931) (di:direct) BSUB0012 Z99115 g2634534 Bacillus subtilis 1423 -11531205 7500964533 yonc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:50219) (re:50755) (di:complement) AF020713 AF020713 g3025531 Bacteriophage SPBc2 66797 -11531205

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802563	4860	27016	1161	386

Description

6500727348 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonB yonB Bacillus subtilis 1423 -11531206 7000693605 yonb hypothetical protein yonb (db:pir2.dat) D69913 D69913 Bacillus subtilis 1423 -11531206 7000693606 yonb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:39970) (re:40986) (di:direct) BSUB0012 Z99115 g2634535 Bacillus subtilis 1423 -11531206 7500964532 yonb unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:49164) (re:50180) (di:complement) AF020713 AF020713 g3025530 Bacteriophage SPBc2 66797 -11531206

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802564	4861	27017	378	125

Description

6500727349 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yonA yonA Bacillus subtilis 1423 -11531207 7000693603 yona hypothetical protein yona (db:pir2.dat) C69913 C69913 Bacillus subtilis 1423 -11531207 7000693604 yona (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:41022) (re:41492) (di:direct) BSUB0012 Z99115 g2634536 Bacillus subtilis 1423 -11531207 7500964531 yona unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:48658) (re:49128) (di:complement) AF020713 AF020713 g3025529 Bacteriophage SPBc2 66797 -11531207

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802565	4862	27018	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802568	4863	27019	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802579	4864	27020	885	294

Description

6500727350 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomZ yomZ Bacillus subtilis 1423 -11531208 7000693601 yomz hypothetical protein yomz (db:pir2.dat) B69913 B69913 Bacillus subtilis 1423 -11531208 7000693602 yomz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:41507) (re:41902) (di:direct) BSUB0012 Z99115 g2634537 Bacillus subtilis 1423 -11531208 7500964530 yomz unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:48248) (re:48643) (di:complement) AF020713 AF020713 g3025528 Bacteriophage SPBc2 66797 -11531208

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802591	4865	27021	540	179

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802600	4866	27022	417	138

Description

6500727351 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomY yomY Bacillus subtilis 1423 -11531209 7000693599 yomy hypothetical protein yomy (db:pir2.dat) A69913 A69913 Bacillus subtilis 1423 -11531209 7000693600 yomy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:41899) (re:42153) (di:direct) BSUB0012 Z99115 g2634538 Bacillus subtilis 1423 -11531209 7500964529 yomy unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:47997) (re:48251) (di:complement) AF020713 AF020713 g3025527 Bacteriophage SPBc2 66797 -11531209

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802601	4867	27023	1383	460

Description

6500727352 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomX yomX Bacillus subtilis 1423 -11531210 7000693597 yomx hypothetical protein yomx (db:pir2.dat) H69912 H69912 Bacillus subtilis 1423 -11531210 7000693598 yomx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:42137) (re:42787) (di:direct) BSUB0012 Z99115 g2634539 Bacillus subtilis 1423 -11531210 7500964528 yomx unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:47363) (re:48013) (di:complement) AF020713 AF020713 g3025526 Bacteriophage SPBc2 66797 -11531210

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802628	4868	27024	750	249

Description

6500727353 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomW yomW Bacillus subtilis 1423 -11531211 7000693595 yomw hypothetical protein yomw (db:pir2.dat) G69912 G69912 Bacillus subtilis 1423 -11531211 7000693596 yomw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:42784) (re:43290) (di:direct) BSUB0012 Z99115 g2634540 Bacillus subtilis 1423 -11531211 7500964527 yomw unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:46860) (re:47366) (di:complement) AF020713 AF020713 g3025525 Bacteriophage SPBc2 66797 -11531211

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802634	4869	27025	201	66

Description

6500727354 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomV yomV Bacillus subtilis 1423 -11531212 7000693593 yomv hypothetical protein yomv (db:pir2.dat) F69912 F69912 Bacillus subtilis 1423 -11531212 7000693594 yomv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:43287) (re:43997) (di:direct) BSUB0012 Z99115 g2634541 Bacillus subtilis 1423 -11531212 7500964526 yomv unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:46153) (re:46863) (di:complement) AF020713 AF020713 g3025524 Bacteriophage SPBc2 66797 -11531212

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802644	4870	27026	378	125

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802656	4871	27027	1509	502

Description

6500727355 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomU yomU Bacillus subtilis 1423 -11531213 7000693591 yomu hypothetical protein yomu (db:pir2.dat) E69912 E69912 Bacillus subtilis 1423 -11531213 7000693592 yomu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:44040) (re:44837) (di:direct) BSUB0012 Z99115 g2634542 Bacillus subtilis 1423 -11531213 7500964525 yomu unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:45313) (re:46110) (di:complement) AF020713 AF020713 g3025523 Bacteriophage SPBc2 66797 -11531213

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802664	4872	27028	192	63

Description

6500727356 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomT yomT Bacillus subtilis 1423 -11531214 7000693589 yomt hypothetical protein yomt (db:pir2.dat) D69912 D69912 Bacillus subtilis 1423 -11531214 7000693590 yomt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:45466) (re:45693) (di:direct) BSUB0012 Z99115 g2634543 Bacillus subtilis 1423 -11531214 7500964524 yomt unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:44457) (re:44684) (di:complement) AF020713 AF020713 g3025521 Bacteriophage SPBc2 66797 -11531214

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802687	4873	27029	315	104

Description

6500727357 hypothetical protein:similar to phage-related lytic exoenzyme (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomS yomS Bacillus subtilis 1423 -11531215 7000694372 yoms phage-related lytic exoenzyme homolog yoms (db:pir2.dat) C69912 C69912 Bacillus subtilis 1423 -11531215 7000694373 yoms (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phage-related lytic exoenzyme) (le:45757) (re:46113) (di:direct) BSUB0012 Z99115 g2634544 Bacillus subtilis 1423 -11531215 7500965053 yoms (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to yqxg of b. subtilis skin element and) (le:44037) (re:44393) (di:complement) AF020713 AF020713 g3025520 Bacteriophage SPBc2 66797 -11531215

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802698	4874	27030	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802700	4875	27031	324	107

Description

6500727358 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomR yomR Bacillus subtilis 1423 -11531216 7000694384 yomr phage-related protein homolog yomr (db:pir2.dat) B69912 B69912 Bacillus subtilis 1423 -11531216 7000694385 yomr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phage-related protein) (le:46115) (re:47332) (di:direct) BSUB0012 Z99115 g2634545 Bacillus subtilis 1423 -11531216 7500965059 yomr (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to yqcc of b. subtilis skin element and) (le:42818) (re:44035) (di:complement) AF020713 AF020713 g3025519 Bacteriophage SPBc2 66797 -11531216

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802704	4876	27032	201	66

Description

6500727359 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomQ yomQ Bacillus subtilis 1423 -11531217 7000693587 yomq hypothetical protein yomq (db:pir2.dat) A69912 A69912 Bacillus subtilis 1423 -11531217 7000693588 yomq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:47343) (re:47693) (di:direct) BSUB0012 Z99115 g2634546 Bacillus subtilis 1423 -11531217 7500964523 yomq (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to xkdw of b. subtilis prophage pbsx) (le:42457) (re:42807) (di:complement) AF020713 AF020713 g3025518 Bacteriophage SPBc2 66797 -11531217

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802723	4877	27033	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802727	4878	27034	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802730	4879	27035	216	71

Description

6500727360 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomP yomP Bacillus subtilis 1423 -11531218 7000694382 yomp phage-related protein homolog yomp (db:pir2.dat) H69911 H69911 Bacillus subtilis 1423 -11531218 7000694383 yomp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phage-related protein) (le:47690) (re:47881) (di:direct) BSUB0012 Z99115 g2634547 Bacillus subtilis 1423 -11531218 7500965058 yomp (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to yqce of b. subtilis skin element and) (le:42269) (re:42460) (di:complement) AF020713 AF020713 g3025517 Bacteriophage SPBc2 66797 -11531218

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802735	4880	27036	342	114

Description

6500727361 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomO yomO Bacillus subtilis 1423 -11531219 7000693585 yomo hypothetical protein yomo (db:pir2.dat) G69911 G69911 Bacillus subtilis 1423 -11531219 7000693586 yomo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:47931) (re:48431) (di:direct) BSUB0012 Z99115 g2634548 Bacillus subtilis 1423 -11531219 7500964522 yomo unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:41719) (re:42219) (di:complement) AF020713 AF020713 g3025516 Bacteriophage SPBc2 66797 -11531219

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802736	4881	27037	450	149

Description

6500727362 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomN yomN Bacillus subtilis 1423 -11531220 7000693583 yomn hypothetical protein yomn (db:pir2.dat) F69911 F69911 Bacillus subtilis 1423 -11531220 7000693584 yomn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:48415) (re:48834) (di:direct) BSUB0012 Z99115 g2634549 Bacillus subtilis 1423 -11531220 7500964521 unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:41316) (re:41735) (di:complement) AF020713 AF020713 g3025515 Bacteriophage SPBc2 66797 -11531220

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802737	4882	27038	633	210

Description

6500727363 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomM yomM Bacillus subtilis 1423 -11531221 7000693581 yomm hypothetical protein yomm (db:pir2.dat) E69911 E69911 Bacillus subtilis 1423 -11531221 7000693582 yomm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:48848) (re:49849) (di:direct) BSUB0012 Z99115 g2634550 Bacillus subtilis 1423 -11531221 7500964520 yomm unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:40301) (re:41302) (di:complement) AF020713 AF020713 g3025514 Bacteriophage SPBc2 66797 -11531221

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802751	4883	27039	264	87

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802754	4884	27040	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802756	4885	27041	300	100

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802757	4886	27042	270	89

Description

6500727364 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yozP yozP Bacillus subtilis 1423 -11531222 7000693841 yozp hypothetical protein yozp (db:pir2.dat) D69932 D69932 Bacillus subtilis 1423 -11531222 7500964654 yozp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:49852) (re:50181) (di:complement) BSUB0012 Z99115 g2634551 Bacillus subtilis 1423 -11531222

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802762	4887	27043	525	174

Description

GTC ORF with score 219 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, essa i contig fragment no.2.) (nt:similar to unknown protein in escherichia coli k-12) (le:179874:180123:180931) (re:180061:180882:181604) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802765	4888	27044	183	60

Description

6500727365 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomL yomL Bacillus subtilis 1423 -11531223 7000692692 yoml conserved hypothetical protein yoml (db:pir2.dat) D69911 D69911 Bacillus subtilis 1423 -11531223 7000692693 yoml (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:50357) (re:51043) (di:complement) BSUB0012 Z99115 g2634552 Bacillus subtilis 1423 -11531223 7500963788 yoml unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:39107) (re:39793) (di:direct) AF020713 AF020713 g3025513 Bacteriophage SPBc2 66797 -11531223

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802780	4889	27045	432	143

Description

6500727366 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomK yomK Bacillus subtilis 1423 -11531224 7000693579 yomk hypothetical protein yomk (db:pir2.dat) C69911 C69911 Bacillus subtilis 1423 -11531224 7000693580 yomk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:51590) (re:52036) (di:direct) BSUB0012 Z99115 g2634553 Bacillus subtilis 1423 -11531224 7500964519 yomk unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:38114) (re:38560) (di:complement) AF020713 AF020713 g3025512 Bacteriophage SPBc2 66797 -11531224

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802802	4890	27046	1884	628

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802811	4891	27047	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802813	4892	27048	1149	382

Description

6500727367 hypothetical protein:similar to phage-related immunity protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomJ yomJ Bacillus subtilis 1423 -11531225 7000694370 yomj phage-related immunity protein homolog yomj (cl:phage sp-beta immunity protein) (db:pir2.dat) B69911 B69911 Bacillus subtilis 1423 -11531225 326747 yomj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phage-related immunity protein) (le:52118) (re:52801) (di:direct) BSUB0012 Z99115 g2634554 Bacillus subtilis 1423 -11531225 7000694371 yomj immunity protein d (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:37349) (re:38032) (di:complement) AF020713 AF020713 g3025511 Bacteriophage SPBc2 66797 -11531225 7500955725 d d (db:genpept-phg) (de:bacteriophage phi-3t immunity protein (d) gene, complete cds.) (nt:immunity protein; homologous to sp-beta immunity) (le:135) (re:818) (di:direct) BPU50554 U50554 g1256254 Bacteriophage phi-3T 10736 -11531225

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802817	4893	27049	474	157

Description

6500727368 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomI yomI Bacillus subtilis 1423 -11531226 7000693577 yomi hypothetical protein yomi (db:pir2.dat) A69911 A69911 Bacillus subtilis 1423 -11531226 7000693578 yomi (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:52855) (re:59712) (di:direct) BSUB0012 Z99115 g2634555 Bacillus subtilis 1423 -11531226 7500964518 yomi putative transglycosylase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:30438) (re:37295) (di:complement) AF020713 AF020713 g3025510 Bacteriophage SPBc2 66797 -11531226

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802823	4894	27050	954	317

Description

6500727369 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomH yomH Bacillus subtilis 1423 -11531227 7000693575 yomh hypothetical protein yomh (db:pir2.dat) H69910 H69910 Bacillus subtilis 1423 -11531227 7000693576 yomh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:59763) (re:60521) (di:direct) BSUB0012 Z99115 g2634556 Bacillus subtilis 1423 -11531227 7500964517 yomh unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:29629) (re:30387) (di:complement) AF020713 AF020713 g3025509 Bacteriophage SPBc2 66797 -11531227

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802833	4895	27051	243	81

Description

6500727370 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomG yomG Bacillus subtilis 1423 -11531228 7000693573 yomg hypothetical protein yomg (db:pir2.dat) G69910 G69910 Bacillus subtilis 1423 -11531228 7000693574 yomg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:60533) (re:63160) (di:direct) BSUB0012 Z99115 g2634557 Bacillus subtilis 1423 -11531228 7500964516 yomg yomg (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:26990) (re:29617) (di:complement) AF020713 AF020713 g3025508 Bacteriophage SPBc2 66797 -11531228

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802851	4896	27052	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802854	4897	27053	768	255

Description

6500727371 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomF yomF Bacillus subtilis 1423 -11531229 7000693571 yomf hypothetical protein yomf (db:pir2.dat) F69910 F69910 Bacillus subtilis 1423 -11531229 7000693572 yomf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:63176) (re:63997) (di:direct) BSUB0012 Z99115 g2634558 Bacillus subtilis 1423 -11531229 7500964515 yomf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:26153) (re:26974) (di:complement) AF020713 AF020713 g3025507 Bacteriophage SPBc2 66797 -11531229

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802861	4898	27054	669	222

Description

6500727372 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomE yomE Bacillus subtilis 1423 -11531230 7000693569 yome hypothetical protein yome (db:pir2.dat) E69910 E69910 Bacillus subtilis 1423 -11531230 7000693570 yome (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:64034) (re:65968) (di:direct) BSUB0012 Z99115 g2634559 Bacillus subtilis 1423 -11531230 7500964514 yome unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:24182) (re:26116) (di:complement) AF020713 AF020713 g3025506 Bacteriophage SPBc2 66797 -11531230

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802862	4899	27055	651	216

Description

6500727373 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomD yomD Bacillus subtilis 1423 -11531231 7000693567 yomd hypothetical protein yomd (db:pir2.dat) D69910 D69910 Bacillus subtilis 1423 -11531231 7000693568 yomd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:66138) (re:66962) (di:direct) BSUB0012 Z99115 g2634560 Bacillus subtilis 1423 -11531231 7500964513 yomd unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:23188) (re:24012) (di:complement) AF020713 AF020713 g3025505 Bacteriophage SPBc2 66797 -11531231

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802863	4900	27056	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802894	4901	27057	462	153

Description

6500727374 hypothetical protein:similar to n-acetylmuramoyl-l-alanine amidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomC yomC Bacillus subtilis 1423 -11531232 7000694280 yomc n-acetylmuramoyl-l-alanine amidase homolog yomc (db:pir2.dat) C69910 C69910 Bacillus subtilis 1423 -11531232 7000694281 yomc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to n-acetylmuramoyl-l-alanine amidase) (le:67190) (re:68293) (di:direct) BSUB0012 Z99115 g2634561 Bacillus subtilis 1423 -11531232 7000694282 blya n-acetylmuramoyl-l-alanine amidase (db:genpept-bct2) (de:bacillus subtilis 168 prophage spbeta n-acetylmuramoyl-l-alanineamidase (blya), holin-like protein (bhla), holin-like protein(bhlb), and yolk genes, complete cds; and yolj gene, partial cds.) (le:432) (re:1535) (di:direct) AF021803 AF021803 g2997595 Bacillus subtilis 1423 -11531232 7500964993 yomc n-acetylmuramoyl-l-alanine amidase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:21857) (re:22960) (di:complement) AF020713 AF020713 g3025504 Bacteriophage SPBc2 66797 -11531232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802899	4902	27058	888	296

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802908	4903	27059	402	133

Description

6500727375 hypothetical protein:similar to bacteriocin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomB yomB Bacillus subtilis 1423 -11531233 7000692255 yomb bacteriocin homolog yomb (cl:uvib protein) (db:pir2.dat) B69910 B69910 Bacillus subtilis 1423 -11531233 7000692256 yomb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to bacteriocin) (le:68381) (re:68593) (di:direct) BSUB0012 Z99115 g2634562 Bacillus subtilis 1423 -11531233 7000692257 bhla holin-like protein (db:genpept-bct2) (de:bacillus subtilis 168 prophage spbeta n-acetylmuramoyl-l-alanineamidase (blya), holin-like protein (bhla), holin-like protein(bhlb), and yolk genes, complete cds; and yolj gene, partial cds.) (le:1623) (re:1835) (di:direct) AF021803 AF021803 g2997596 Bacillus subtilis 1423 -11531233 7500955844 yomb possibly involved in bacteriocin production or (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:21557) (re:21769) (di:complement) AF020713 AF020713 g3025503 Bacteriophage SPBc2 66797 -11531233

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802913	4904	27060	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802916	4905	27061	228	75

Description

6500727376 hypothetical protein:similar to holin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yomA yomA Bacillus subtilis 1423 -11531234 7000693102 yoma holin homolog yoma (db:pir2.dat) A69910 A69910 Bacillus subtilis 1423 -11531234 7000693103 yoma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to holin) (le:68604) (re:68870) (di:direct) BSUB0012 Z99115 g2634563 Bacillus subtilis 1423 -11531234 7000693104 bhlb holin-like protein (db:genpept-bct2) (de:bacillus subtilis 168 prophage spbeta n-acetylmuramoyl-l-alanineamidase (blya), holin-like protein (bhla), holin-like protein(bhlb), and yolk genes, complete cds; and yolj gene, partial cds.) (le:1846) (re:2112) (di:direct) AF021803 AF021803 g2997597 Bacillus subtilis 1423 -11531234 7500964053 yoma unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:21280) (re:21546) (di:complement) AF020713 AF020713 g3025502 Bacteriophage SPBc2 66797 -11531234

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802934	4906	27062	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802939	4907	27063	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802951	4908	27064	384	127

Description

6500727377 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolK yolK Bacillus subtilis 1423 -11531235 7000692689 yolk probable protein-disulfide oxidoreductase:yolk (cl:protein-disulfide oxidoreductase dsbb) (ec:1.8.4.-) (db:pir2.dat) H69909 H69909 Bacillus subtilis 1423 -11531235 7000692690 yolk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:68926) (re:69372) (di:complement) BSUB0012 Z99115 g2634564 Bacillus subtilis 1423 -11531235 7000692691 yolk unknown protein (db:genpept-bct2) (de:bacillus subtilis 168 prophage spbeta n-acetylmuramoyl-l-alanineamidase (blya), holin-like protein (bhla), holin-like protein(bhlb), and yolk genes, complete cds; and yolj gene, partial cds.) (le:2168) (re:2614) (di:complement) AF021803 AF021803 g2997598 Bacillus subtilis 1423 -11531235 7500955850 yolk putative disulfide oxidoreductase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:20778) (re:21224) (di:direct) AF020713 AF020713 g3025501 Bacteriophage SPBc2 66797 -11531235

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802955	4909	27065	189	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802957	4910	27066	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802970	4911	27067	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802993	4912	27068	1530	510

Description

GTC ORF with score 486 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8543.) (nt:ylr319c; weak similarity to poly (adp-ribose)) (le:14332) (re:16698) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501802998	4913	27069	207	68

Description

GTC ORF with score 123 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t06b20 genomic sequence,complete sequence.) (nt:yeast hypothetical protein ydb1_schpo isolog) (le:74887:75256:76460:76808) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803015	4914	27070	717	238

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803017	4915	27071	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803019	4916	27072	396	131

Description

6500727378 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolJ yolJ Bacillus subtilis 1423 -11531236 7000692687 yolj conserved hypothetical protein yolj (db:pir2.dat) G69909 G69909 Bacillus subtilis 1423 -11531236 7000692688 yolj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:69369) (re:70637) (di:complement) BSUB0012 Z99115 g2634565 Bacillus subtilis 1423 -11531236 7500963787 yolj unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:19513) (re:20781) (di:direct) AF020713 AF020713 g3025500 Bacteriophage SPBc2 66797 -11531236

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803029	4917	27073	483	160

Description

6500727379 hypothetical protein:similar to thioredoxin (gtcfc:9.13) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolI yolI Bacillus subtilis 1423 -11531237 7000694683 yoli thioredoxin homolog yoli (db:pir2.dat) F69909 F69909 Bacillus subtilis 1423 -11531237 7000694684 yoli (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to thioredoxin) (le:70637) (re:71050) (di:complement) BSUB0012 Z99115 g2634566 Bacillus subtilis 1423 -11531237 7500965268 yoli putative thioredoxin (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:19100) (re:19513) (di:direct) AF020713 AF020713 g3025499 Bacteriophage SPBc2 66797 -11531237

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803031	4918	27074	669	222

Description

6500727380 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolF yolF Bacillus subtilis 1423 -11531238 7000693565 yolf hypothetical protein yolf (cl:hypothetical protein yolf) (db:pir2.dat) E69909 E69909 Bacillus subtilis 1423 -11531238 7000693566 yolf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:73689) (re:74006) (di:complement) BSUB0012 Z99115 g2634569 Bacillus subtilis 1423 -11531238 7500955899 yolf unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:16144) (re:16461) (di:direct) AF020713 AF020713 g3025496 Bacteriophage SPBc2 66797 -11531238

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803062	4919	27075	267	88

Description

6500727381 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolD yolD Bacillus subtilis 1423 -11531239 7000692685 yold conserved hypothetical protein yold (db:pir2.dat) D69909 D69909 Bacillus subtilis 1423 -11531239 7000692686 yold (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:75351) (re:75683) (di:complement) BSUB0012 Z99115 g2634571 Bacillus subtilis 1423 -11531239 7500963786 yold unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:14467) (re:14799) (di:direct) AF020713 AF020713 g3025494 Bacteriophage SPBc2 66797 -11531239

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803063	4920	27076	648	215

Description

6500727382 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolC yolC Bacillus subtilis 1423 -11531240 7000693563 yolc hypothetical protein yolc (db:pir2.dat) C69909 C69909 Bacillus subtilis 1423 -11531240 7000693564 yolc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:75857) (re:76192) (di:direct) BSUB0012 Z99115 g2634572 Bacillus subtilis 1423 -11531240 7500964512 yolc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:13958) (re:14293) (di:complement) AF020713 AF020713 g3025493 Bacteriophage SPBc2 66797 -11531240

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803065	4921	27077	201	66

Description

6500727383 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolB yolB Bacillus subtilis 1423 -11531241 7000694380 yolb phage-related protein homolog yolb (db:pir2.dat) B69909 B69909 Bacillus subtilis 1423 -11531241 7000694381 yolb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phage-related protein) (le:76235) (re:76591) (di:complement) BSUB0012 Z99115 g2634573 Bacillus subtilis 1423 -11531241 7500965057 yolb unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:13559) (re:13915) (di:direct) AF020713 AF020713 g3025492 Bacteriophage SPBc2 66797 -11531241

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803067	4922	27078	303	100

Description

6500727384 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yolA yolA Bacillus subtilis 1423 -11531242 7000693561 yola hypothetical protein yola (db:pir2.dat) A69909 A69909 Bacillus subtilis 1423 -11531242 7000693562 yola (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:76597) (re:77064) (di:complement) BSUB0012 Z99115 g2634574 Bacillus subtilis 1423 -11531242 7500964511 yola unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:13086) (re:13553) (di:direct) AF020713 AF020713 g3025491 Bacteriophage SPBc2 66797 -11531242

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803087	4923	27079	1581	527

Description

6500727385 hypothetical protein:similar to phage-related protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokL yokL Bacillus subtilis 1423 -11531243 7000694378 yokl phage-related protein homolog yokl (cl:hypothetical protein yoaa) (db:pir2.dat) H69908 H69908 Bacillus subtilis 1423 -11531243 7000694379 yokl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to phage-related protein) (le:77690) (re:78223) (di:complement) BSUB0012 Z99115 g2634575 Bacillus subtilis 1423 -11531243 7500955880 yokl unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:11927) (re:12460) (di:direct) AF020713 AF020713 g3025490 Bacteriophage SPBc2 66797 -11531243

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803103	4924	27080	531	176

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803119	4925	27081	873	290

Description

6500727386 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokK yokK Bacillus subtilis 1423 -11531244 7000693559 yokk hypothetical protein yokk (db:pir2.dat) G69908 G69908 Bacillus subtilis 1423 -11531244 7000693560 yokk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:78259) (re:78837) (di:complement) BSUB0012 Z99115 g2634576 Bacillus subtilis 1423 -11531244 7500964510 yokk unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:11313) (re:11891) (di:direct) AF020713 AF020713 g3025489 Bacteriophage SPBc2 66797 -11531244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803122	4926	27082	429	142

Description

6500727387 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokJ yokJ Bacillus subtilis 1423 -11531245 7000693557 yokj hypothetical protein yokj (db:pir2.dat) F69908 F69908 Bacillus subtilis 1423 -11531245 7000693558 yokj (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:78901) (re:79398) (di:complement) BSUB0012 Z99115 g2634577 Bacillus subtilis 1423 -11531245 7500964509 yokj unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:10752) (re:11249) (di:direct) AF020713 AF020713 g3025488 Bacteriophage SPBc2 66797 -11531245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803123	4927	27083	378	125

Description

6500727388 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokI yokI Bacillus subtilis 1423 -11531246 7000692683 yoki conserved hypothetical protein yoki (db:pir2.dat) E69908 E69908 Bacillus subtilis 1423 -11531246 7000692684 yoki (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:79407) (re:81122) (di:complement) BSUB0012 Z99115 g2634578 Bacillus subtilis 1423 -11531246 7500963785 yoki (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacillus subtilis skin element yqcg) (le:9028) (re:10743) (di:direct) AF020713 AF020713 g3025487 Bacteriophage SPBc2 66797 -11531246

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803125	4928	27084	456	151

Description

6500727389 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokH yokH Bacillus subtilis 1423 -11531247 7000692681 yokh conserved hypothetical protein yokh (db:pir2.dat) D69908 D69908 Bacillus subtilis 1423 -11531247 7000692682 yokh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:81222) (re:81779) (di:complement) BSUB0012 Z99115 g2634579 Bacillus subtilis 1423 -11531247 7500963784 yokh unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:8371) (re:8928) (di:direct) AF020713 AF020713 g3025486 Bacteriophage SPBc2 66797 -11531247

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803128	4929	27085	426	141

Description

6500727390 hypothetical protein:similar to delta-endotoxin (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokG yokG Bacillus subtilis 1423 -11531248 7000692910 yokg delta-endotoxin homolog yokg (db:pir2.dat) C69908 C69908 Bacillus subtilis 1423 -11531248 7000692911 yokg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to delta-endotoxin) (le:82303) (re:83376) (di:complement) BSUB0012 Z99115 g2634580 Bacillus subtilis 1423 -11531248 7500963931 yokg (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to bacillus thuringiensis delta-endotoxins) (le:6774) (re:7847) (di:direct) AF020713 AF020713 g3025485 Bacteriophage SPBc2 66797 -11531248

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803129	4930	27086	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803131	4931	27087	882	293

Description

6500727391 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokF yokF Bacillus subtilis 1423 -11531249 7000692679 yokf conserved hypothetical protein yokf (cl:micrococcal nuclease) (db:pir2.dat) B69908 B69908 Bacillus subtilis 1423 -11531249 7000692680 yokf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:83678) (re:84568) (di:direct) BSUB0012 Z99115 g2634581 Bacillus subtilis 1423 -11531249 7500963783 yokf putative dnase/rnase endonuclease (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:putative lipoprotein) (le:5582) (re:6472) (di:complement) AF020713 AF020713 g3025484 Bacteriophage SPBc2 66797 -11531249

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803138	4932	27088	612	203

Description

6500727392 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokE yokE Bacillus subtilis 1423 -11531250 7000693555 yoke hypothetical protein yoke (db:pir2.dat) A69908 A69908 Bacillus subtilis 1423 -11531250 7000693556 yoke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:84582) (re:85064) (di:direct) BSUB0012 Z99115 g2634582 Bacillus subtilis 1423 -11531250 7500964508 yoke unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:5086) (re:5568) (di:complement) AF020713 AF020713 g3025483 Bacteriophage SPBc2 66797 -11531250

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803144	4933	27089	225	74

Description

6500727393 hypothetical protein:similar to aminoglycoside n3-acetyltransferase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokD yokD Bacillus subtilis 1423 -11531251 7000692205 yokd aminoglycoside n3-acetyltransferase homolog yokd (db:pir2.dat) H69907 H69907 Bacillus subtilis 1423 -11531251 7000692206 yokd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to aminoglycoside n3'-acetyltransferase) (le:85368) (re:86186) (di:direct) BSUB0012 Z99115 g2634583 Bacillus subtilis 1423 -11531251 7500963413 yokd (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (nt:similar to aminoglycoside n3'-acetyltransferases) (le:3964) (re:4782) (di:complement) AF020713 AF020713 g3025482 Bacteriophage SPBc2 66797 -11531251

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803147	4934	27090	384	128

Description

6500727394 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokC yokC Bacillus subtilis 1423 -11531252 7000693553 yokc hypothetical protein yokc (db:pir2.dat) G69907 G69907 Bacillus subtilis 1423 -11531252 7000693554 yokc (fn:unknown) . (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:86837) (re:87352) (di:complement) BSUB0012 Z99115 g2634584 Bacillus subtilis 1423 -11531252 7500964507 yokc unknown (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:2798) (re:3313) (di:direct) AF020713 AF020713 g3025481 Bacteriophage SPBc2 66797 -11531252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803164	4935	27091	1512	504

Description

6500727395 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokB yokB Bacillus subtilis 1423 -11531253 7000693551 yokb hypothetical protein yokb (db:pir2.dat) F69907 F69907 Bacillus subtilis 1423 -11531253 7000693552 yokb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:87559) (re:88269) (di:complement) BSUB0012 Z99115 g2634585 Bacillus subtilis 1423 -11531253 7500964506 yokb putative lipoprotein (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:1881) (re:2591) (di:direct) AF020713 AF020713 g3025480 Bacteriophage SPBc2 66797 -11531253

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803184	4936	27092	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803199	4937	27093	405	134

Description

6500727396 hypothetical protein:similar to dna recombinase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yokA yokA Bacillus subtilis 1423 -11531254 7000692942 yoka dna recombinase homolog yoka (db:pir2.dat) E69907 E69907 Bacillus subtilis 1423 -11531254 7000692943 yoka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to dna recombinase) (le:88472) (re:90109) (di:direct) BSUB0012 Z99115 g2634586 Bacillus subtilis 1423 -11531254 7500963954 yoka site-specific recombinase (db:genpept-phg) (de:bacteriophage spbc2 complete genome.) (le:41) (re:1678) (di:complement) AF020713 AF020713 g3025479 Bacteriophage SPBc2 66797 -11531254

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803208	4938	27094	603	200

Description

5000689254 hypothetical protein:hypothetical protein in ilva 3region:fragment (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypqP ypqP Bacillus subtilis 1423 -11531255 115674 ypqp (de:hypothetical protein in ilva 3'region (fragment)) (db:swissprot) YPQP_BACSU P54183 BACILLUS SUBTILIS 1423 -11531255 7000688261 ypqp capsular polysaccharide homolog ypqp (db:pir2.dat) A69941 A69941 Bacillus subtilis 1423 -11531255 217112 ypqp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:this orf is interrupted by insertion of the spbetta) (le:34398) (re:35021) (di:complement) BACYACA L77246 g1256655 Bacillus subtilis 1423 -11531255 7500952280 ypqp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to capsular polysaccharide biosynthesis;) (le:<90131) (re:90754) (di:direct) BSUB0012 Z99115 g2634587 Bacillus subtilis 1423 -11531255 6500727397 hypothetical protein:hypothetical protein in ilva 3region:fragment (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypqP ypqP Bacillus subtilis 1423 -11531255

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803210	4939	27095	1266	421

Description

5000689252 hypothetical protein:hypothetical 16.6 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppQ yppQ Bacillus subtilis 1423 -11531256 115669 yppq (de:hypothetical 16.6 kd protein in ilva 3'region) (db:swissprot) YPPQ_BACSU P54155 BACILLUS SUBTILIS 1423 -11531256 7000688258 yppq transcription regulator pilb family homolog yppq (cl:hypthetical protein ycl033c) (db:pir2.dat) F69940 F69940 Bacillus subtilis 1423 -11531256 217111 yppq (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:54.8% identity with neisseria gonorrhoeae) (le:33923) (re:34354) (di:direct) BACYACA L77246 g1256654 Bacillus subtilis 1423 -11531256 7500952277 yppq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to transcriptional regulator (pilb family)) (le:90798) (re:91229) (di:complement) BSUB0012 Z99115 g2634588 Bacillus subtilis 1423 -11531256 6500727398 hypothetical protein:hypothetical 16.6 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppQ yppQ Bacillus subtilis 1423 -11531256

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803225	4940	27096	600	199

Description

5000689251 hypothetical protein:putative peptide methionine sulfoxide reductase:peptide met:o reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppP yppP Bacillus subtilis 1423 -11531257 90135 yppp (de:reductase)) (db:swissprot) PMSR_BACSU P54154 BACILLUS SUBTILIS 1423 -11531257 7000686156 yppp peptide methionine sulfoxide reductase homolog yppp (cl:peptide methionine sulfoxide reductase) (db:pir2.dat) E69940 E69940 Bacillus subtilis 1423 -11531257 217110 yppp dna-binding protein (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:42.4% identity with the lycopersicon esculentum) (le:33389) (re:33922) (di:direct) BACYACA L77246 g1256653 Bacillus subtilis 1423 -11531257 7500888210 yppp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to peptide methionine sulfoxide reductase) (le:91230) (re:91763) (di:complement) BSUB0012 Z99115 g2634589 Bacillus subtilis 1423 -11531257 6500727399 hypothetical protein:putative peptide methionine sulfoxide reductase:peptide met:o reductase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppP yppP Bacillus subtilis 1423 -11531257

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803235	4941	27097	330	109

Description

5000689246 hypothetical protein:hypothetical transcriptional regulator in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypoP ypoP Bacillus subtilis 1423 -11531258 115661 ypop (de:hypothetical transcriptional regulator in uvrx-ilva intergenic region) (db:swissprot) YPOP_BACSU P54182 BACILLUS SUBTILIS 1423 -11531258 7000688251 ypop transcription regulator marr family homolog ypop (db:pir2.dat) F69939 F69939 Bacillus subtilis 1423 -11531258 217109 ypop (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:25% identity to the e.coli regulatory protein mpra;) (le:32832) (re:33257) (di:complement) BACYACA L77246 g1256652 Bacillus subtilis 1423 -11531258 7500952270 ypop (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to transcriptional regulator (marr family)) (le:91895) (re:92320) (di:direct) BSUB0012 Z99115 g2634590 Bacillus subtilis 1423 -11531258 6500727400 hypothetical protein:hypothetical transcriptional regulator in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypoP ypoP Bacillus subtilis 1423 -11531258

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803251	4942	27098	186	62

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803276	4943	27099	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803278	4944	27100	840	279

Description

5000689245 hypothetical protein:hypothetical 48.5 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypnP ypnP Bacillus subtilis 1423 -11531259 115645 ypnp (de:hypothetical 48.5 kd protein in ilva 3'region) (db:swissprot) YPNP_BACSU P54181 BACILLUS SUBTILIS 1423 -11531259 7000688249 ypnp conserved hypothetical protein ypnp (db:pir2.dat) D69939 D69939 Bacillus subtilis 1423 -11531259 217108 ypnp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:21% identity with the nadh-dehydrogenase) (le:31445) (re:32782) (di:direct) BACYACA L77246 g1256651 Bacillus subtilis 1423 -11531259 7500952268 ypnp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:92370) (re:93707) (di:complement) BSUB0012 Z99115 g2634591 Bacillus subtilis 1423 -11531259 6500727401 hypothetical protein:hypothetical 48.5 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypnP ypnP Bacillus subtilis 1423 -11531259

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803280	4945	27101	1074	357

Description

5000689244 hypothetical protein:hypothetical 7.7 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmT ypmT Bacillus subtilis 1423 -11531260 115643 ypmt (de:hypothetical 7.7 kd protein in ilva 3'region) (db:swissprot) YPMT_BACSU P54180 BACILLUS SUBTILIS 1423 -11531260 7000688248 ypmt hypothetical protein ypmt (db:pir2.dat) C69939 C69939 Bacillus subtilis 1423 -11531260 217107 ypmt (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:31179) (re:31373) (di:direct) BACYACA L77246 g1256650 Bacillus subtilis 1423 -11531260 7500952267 ypmt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:93779) (re:93973) (di:complement) BSUB0012 Z99115 g2634592 Bacillus subtilis 1423 -11531260 6500727402 hypothetical protein:hypothetical 7.7 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmT ypmT Bacillus subtilis 1423 -11531260

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803282	4946	27102	423	140

Description

5000689243 hypothetical protein:hypothetical 21.1 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmS ypmS Bacillus subtilis 1423 -11531261 115642 ypms (de:hypothetical 21.1 kd protein in ilva 3'region) (db:swissprot) YPMS_BACSU P54179 BACILLUS SUBTILIS 1423 -11531261 7000688247 ypms conserved hypothetical protein ypms (db:pir2.dat) B69939 B69939 Bacillus subtilis 1423 -11531261 217106 ypms (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:30603) (re:31166) (di:direct) BACYACA L77246 g1256649 Bacillus subtilis 1423 -11531261 7500952266 ypms (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:93986) (re:94549) (di:complement) BSUB0012 Z99115 g2634593 Bacillus subtilis 1423 -11531261 6500727403 hypothetical protein:hypothetical 21.1 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmS ypmS Bacillus subtilis 1423 -11531261

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803290	4947	27103	612	203

Description

6500727404 yzja:ypmr hypothetical protein:hypothetical 28.9 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmR ypmR Bacillus subtilis 1423 -11531262 115641 ypmr (de:hypothetical 28.9 kd protein in ilva 3'region) (db:swissprot) YPMR_BACSU P40766 BACILLUS SUBTILIS 1423 -11531262 7000688246 ypmr conserved hypothetical protein ypmr (db:pir2.dat) A69939 A69939 Bacillus subtilis 1423 -11531262 217105 ypmr (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:29826) (re:30593) (di:direct) BACYACA L77246 g1256648 Bacillus subtilis 1423 -11531262 7500952265 ypmr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: yzja; similar to hypothetical) (le:94559) (re:95326) (di:complement) BSUB0012 Z99115 g2634594 Bacillus subtilis 1423 -11531262 5000689242 (de:(ypmr) (pn:hypothetical 28) (gtcfc:13.07) (ec:) (ypmr_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) ypmR ypmR Bacillus subtilis 1423 10057367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803299	4948	27104	1422	473

Description

5000689241 hypothetical protein:hypothetical 21.6 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmQ ypmQ Bacillus subtilis 1423 -11531263 115640 ypmq (de:hypothetical 21.6 kd protein in ilva 3'region) (db:swissprot) YPMQ_BACSU P54178 BACILLUS SUBTILIS 1423 -11531263 7000688245 ypmq conserved hypothetical protein ypmq (db:pir2.dat) H69938 H69938 Bacillus subtilis 1423 -11531263 217104 ypmq (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:29% identity with a pseudomonas stutzeri) (le:29167) (re:29748) (di:direct) BACYACA L77246 g1256647 Bacillus subtilis 1423 -11531263 7500952264 ypmq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:95404) (re:95985) (di:complement) BSUB0012 Z99115 g2634595 Bacillus subtilis 1423 -11531263 6500727405 hypothetical protein:hypothetical 21.6 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmQ ypmQ Bacillus subtilis 1423 -11531263

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803300	4949	27105	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803317	4950	27106	1116	371

Description

GTC ORF with score 157 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8083.) (nt:similar to kluyveromyces lactis deoxyribonucleic) (le:23775) (re:26219) (di:complement)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803332	4951	27107	222	73

Description

5000689240 hypothetical protein:hypothetical 10.2 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmP ypmP Bacillus subtilis 1423 -11531264 115639 ypmp (de:hypothetical 10.2 kd protein in ilva 3'region) (db:swissprot) YPMP_BACSU P54177 BACILLUS SUBTILIS 1423 -11531264 7000688244 ypmp hypothetical protein ypmp (db:pir2.dat) G69938 G69938 Bacillus subtilis 1423 -11531264 217103 ypmp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:28768) (re:29019) (di:direct) BACYACA L77246 g1256646 Bacillus subtilis 1423 -11531264 7500952263 ypmp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:96133) (re:96384) (di:complement) BSUB0012 Z99115 g2634596 Bacillus subtilis 1423 -11531264 6500727406 hypothetical protein:hypothetical 10.2 kd protein in ilva 3region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmP ypmP Bacillus subtilis 1423 -11531264

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803335	4952	27108	462	153

Description

5000689236 hypothetical protein:putative sigma 1-dependent transcriptional regulator in dfra-ilva intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yplP yplP Bacillus subtilis 1423 -11531265 115633 yplp (de:intergenic region) (db:swissprot) YPLP_BACSU P54156 BACILLUS SUBTILIS 1423 -11531265 7000688241 yplp transcription regulator sigma-1-dependent homolog yplp (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) C69938 C69938 Bacillus subtilis 1423 -11531265 217101 yplp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:37.0% identity over 119 aa to the e.coli ornithine) (le:26170) (re:27165) (di:complement) BACYACA L77246 g1256644 Bacillus subtilis 1423 -11531265 7500952260 yplp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to transcriptional regulator) (le:97987) (re:98982) (di:direct) BSUB0012 Z99115 g2634598 Bacillus subtilis 1423 -11531265 6500727407 hypothetical protein:putative sigma 1-dependent transcriptional regulator in dfra-ilva intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yplP yplP Bacillus subtilis 1423 -11531265

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803339	4953	27109	435	144

Description

5000689237 hypothetical protein:hemolysin iii homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yplQ yplQ Bacillus subtilis 1423 -11531266 77128 yplq (de:hemolysin iii homolog) (db:swissprot) HLY3_BACSU P54175 BACILLUS SUBTILIS 1423 -11531266 7000685537 yplq hemolysin iii homolog homolog yplq (cl:hemolysin iii yplq) (db:pir2.dat) D69938 D69938 Bacillus subtilis 1423 -11531266 217100 yplq (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:20.2% identity with nadh dehydrogenase of the) (le:25508) (re:26149) (di:complement) BACYACA L77246 g1256643 Bacillus subtilis 1423 -11531266 7500883388 yplq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hemolysin iii homolog) (le:99003) (re:99644) (di:direct) BSUB0012 Z99115 g2634599 Bacillus subtilis 1423 -11531266 6500727408 hypothetical protein:hemolysin iii homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yplQ yplQ Bacillus subtilis 1423 -11531266

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803341	4954	27110	492	163

Description

5000689235 hypothetical protein:hypothetical 23.3 kd protein in dfra-ilva intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypkP ypkP Bacillus subtilis 1423 -11531267 115628 ypkp (de:hypothetical 23.3 kd protein in dfra-ilva intergenic region) (db:swissprot) YPKP_BACSU P54174 BACILLUS SUBTILIS 1423 -11531267 7000688240 ypkp hypothetical protein ypkp (db:pir2.dat) B69938 B69938 Bacillus subtilis 1423 -11531267 217099 ypkp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:24849) (re:25469) (di:direct) BACYACA L77246 g1256642 Bacillus subtilis 1423 -11531267 7500952259 ypkp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:99683) (re:100303) (di:complement) BSUB0012 Z99115 g2634600 Bacillus subtilis 1423 -11531267 6500727409 hypothetical protein:hypothetical 23.3 kd protein in dfra-ilva intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypkP ypkP Bacillus subtilis 1423 -11531267

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803359	4955	27111	1590	530

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803367	4956	27112	1062	354

Description

5000689234 hypothetical protein:hypothetical 19.9 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjQ ypjQ Bacillus subtilis 1423 -11531268 115622 ypjq (de:hypothetical 19.9 kd protein in ilvd-thyb intergenic region) (db:swissprot) YPJQ_BACSU P54173 BACILLUS SUBTILIS 1423 -11531268 7000688239 ypjq conserved hypothetical protein ypjq (db:pir2.dat) A69938 A69938 Bacillus subtilis 1423 -11531268 217096 ypjq (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:22934) (re:23467) (di:direct) BACYACA L77246 g1256639 Bacillus subtilis 1423 -11531268 7500952256 ypjq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:101685) (re:102218) (di:complement) BSUB0012 Z99115 g2634603 Bacillus subtilis 1423 -11531268 6500727410 hypothetical protein:hypothetical 19.9 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjQ ypjQ Bacillus subtilis 1423 -11531268

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803386	4957	27113	306	101

Description

5000689233 hypothetical protein:hypothetical 23.7 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjP ypjP Bacillus subtilis 1423 -11531269 115621 ypjp (de:hypothetical 23.7 kd protein in ilvd-thyb intergenic region) (db:swissprot) YPJP_BACSU P54172 BACILLUS SUBTILIS 1423 -11531269 7000688238 ypjp hypothetical protein ypjp (db:pir2.dat) H69937 H69937 Bacillus subtilis 1423 -11531269 217095 ypjp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:22305) (re:22916) (di:direct) BACYACA L77246 g1256638 Bacillus subtilis 1423 -11531269 7500952255 ypjp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:102236) (re:102847) (di:complement) BSUB0012 Z99115 g2634604 Bacillus subtilis 1423 -11531269 6500727411 hypothetical protein:hypothetical 23.7 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjP ypjP Bacillus subtilis 1423 -11531269

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803387	4958	27114	414	138

Description

5000689230 hypothetical protein:hypothetical 19.0 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypiP ypiP Bacillus subtilis 1423 -11531270 115606 ypip (de:hypothetical 19.0 kd protein in ilvd-thyb intergenic region) (db:swissprot) YPIP_BACSU P54171 BACILLUS SUBTILIS 1423 -11531270 7000688229 ypip hypothetical protein ypip (db:pir2.dat) H69936 H69936 Bacillus subtilis 1423 -11531270 217094 ypip (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:21527) (re:22045) (di:direct) BACYACA L77246 g1256637 Bacillus subtilis 1423 -11531270 7500952242 ypip (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:103107) (re:103625) (di:complement) BSUB0012 Z99115 g2634605 Bacillus subtilis 1423 -11531270 6500727412 hypothetical protein:hypothetical 19.0 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypiP ypiP Bacillus subtilis 1423 -11531270

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803390	4959	27115	1575	524

Description

5000689227 hypothetical protein:hypothetical 15.9 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphP yphP Bacillus subtilis 1423 -11531271 115594 yphp (de:hypothetical 15.9 kd protein in ilvd-thyb intergenic region) (db:swissprot) YPHP_BACSU P54170 BACILLUS SUBTILIS 1423 -11531271 7000688225 yphp conserved hypothetical protein yphp (db:pir2.dat) D69936 D69936 Bacillus subtilis 1423 -11531271 217093 yphp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:20796) (re:21230) (di:direct) BACYACA L77246 g1256636 Bacillus subtilis 1423 -11531271 7500952236 yphp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:103922) (re:104356) (di:complement) BSUB0012 Z99115 g2634606 Bacillus subtilis 1423 -11531271 6500727413 hypothetical protein:hypothetical 15.9 kd protein in ilvd-thyb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphP yphP Bacillus subtilis 1423 -11531271

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803392	4960	27116	420	139

Description

5000689222 hypothetical protein:hypothetical 42.6 kd protein in bsaa-ilvd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypgR ypgR Bacillus subtilis 1423 -11531272 115575 ypgr (de:hypothetical 42.6 kd protein in bsaa-ilvd intergenic region) (db:swissprot) YPGR_BACSU P54169 BACILLUS SUBTILIS 1423 -11531272 7000688219 ypgr conserved hypothetical protein ypgr (db:pir2.dat) F69935 F69935 Bacillus subtilis 1423 -11531272 217091 ypgr (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:25.8% identity over 120 aa with the synenococcus) (le:17591) (re:18724) (di:direct) BACYACA L77246 g1256634 Bacillus subtilis 1423 -11531272 7500952201 ypgr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:106428) (re:107561) (di:complement) BSUB0012 Z99115 g2634608 Bacillus subtilis 1423 -11531272 6500727414 hypothetical protein:hypothetical 42.6 kd protein in bsaa-ilvd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypgR ypgR Bacillus subtilis 1423 -11531272

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803403	4961	27117	429	142

Description

5000689221 hypothetical protein:hypothetical 23.1 kd protein in bsaa-ilvd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypgQ ypgQ Bacillus subtilis 1423 -11531273 115574 ypgq (de:hypothetical 23.1 kd protein in bsaa-ilvd intergenic region) (db:swissprot) YPGQ_BACSU P54168 BACILLUS SUBTILIS 1423 -11531273 7000688218 ypgq conserved hypothetical protein ypgq (cl:conserved hypothetical protein af0994) (db:pir2.dat) E69935 E69935 Bacillus subtilis 1423 -11531273 217090 ypgq (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:16914) (re:17531) (di:direct) BACYACA L77246 g1256633 Bacillus subtilis 1423 -11531273 7500952200 ypgq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:107621) (re:108238) (di:complement) BSUB0012 Z99115 g2634609 Bacillus subtilis 1423 -11531273 6500727415 hypothetical protein:hypothetical 23.1 kd protein in bsaa-ilvd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypgQ ypgQ Bacillus subtilis 1423 -11531273

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803404	4962	27118	399	132

Description

GTC ORF with score 166 to: (fn:involved in rhamnolipids synthesis) (db:genpept-bct2) (de:pseudomonas aeruginosa ctra, beta-ketoacyl reductase (rhlg), andregulator protein (rcsf) genes, complete cds.) (nt:rhlg) (le:1723) (re:2757) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803407	4963	27119	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803421	4964	27120	663	220

Description

5000689219 hypothetical protein:hypothetical 43.6 kd protein in cpsd-metb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypfP ypfP Bacillus subtilis 1423 -11531274 115568 ypfp (de:hypothetical 43.6 kd protein in cpsd-metb intergenic region) (db:swissprot) YPFP_BACSU P54166 BACILLUS SUBTILIS 1423 -11531274 7000688216 ypfp cell wall synthesis homolog ypfp (db:pir2.dat) C69935 C69935 Bacillus subtilis 1423 -11531274 217087 ypfp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:13788) (re:14936) (di:complement) BACYACA L77246 g1256630 Bacillus subtilis 1423 -11531274 7500952198 ypfp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to cell wall synthesis) (le:110216) (re:111364) (di:direct) BSUB0012 Z99115 g2634612 Bacillus subtilis 1423 -11531274 6500727416 hypothetical protein:hypothetical 43.6 kd protein in cpsd-metb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypfP ypfP Bacillus subtilis 1423 -11531274

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803439	4965	27121	534	177

Description

6500727417 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypzA ypzA Bacillus subtilis 1423 -11531275 7000693842 ypza hypothetical protein ypza (db:pir2.dat) E69943 E69943 Bacillus subtilis 1423 -11531275 7500964655 ypza (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:112197) (re:112466) (di:direct) BSUB0012 Z99115 g2634615 Bacillus subtilis 1423 -11531275

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803453	4966	27122	444	147

Description

5000689218 hypothetical protein:hypothetical 7.2 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypeQ ypeQ Bacillus subtilis 1423 -11531276 115560 ypeq (de:hypothetical 7.2 kd protein in bcsa-degr intergenic region) (db:swissprot) YPEQ_BACSU P54165 BACILLUS SUBTILIS 1423 -11531276 7000688211 ypeq hypothetical protein ypeq (db:pir2.dat) G69934 G69934 Bacillus subtilis 1423 -11531276 217084 ypeq (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:12476) (re:12658) (di:direct) BACYACA L77246 g1256627 Bacillus subtilis 1423 -11531276 7500952189 ypeq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:112494) (re:112676) (di:complement) BSUB0012 Z99115 g2634616 Bacillus subtilis 1423 -11531276 6500727418 hypothetical protein:hypothetical 7.2 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypeQ ypeQ Bacillus subtilis 1423 -11531276

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803478	4967	27123	594	197

Description

5000689217 hypothetical protein:hypothetical 13.7 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypeP ypeP Bacillus subtilis 1423 -11531277 115559 ypep (de:hypothetical 13.7 kd protein in bcsa-degr intergenic region) (db:swissprot) YPEP_BACSU P54164 BACILLUS SUBTILIS 1423 -11531277 7000688210 ypep hypothetical protein ypep (db:pir2.dat) F69934 F69934 Bacillus subtilis 1423 -11531277 217083 ypep (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:12121) (re:12483) (di:direct) BACYACA L77246 g1256626 Bacillus subtilis 1423 -11531277 7500952188 ypep (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:112669) (re:113031) (di:complement) BSUB0012 Z99115 g2634617 Bacillus subtilis 1423 -11531277 6500727419 hypothetical protein:hypothetical 13.7 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypeP ypeP Bacillus subtilis 1423 -11531277

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803502	4968	27124	690	229

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803503	4969	27125	759	252

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803514	4970	27126	381	126

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803520	4971	27127	663	220

Description

5000689214 hypothetical protein:hypothetical 25.7 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdP ypdP Bacillus subtilis 1423 -11531278 115541 ypdp (de:hypothetical 25.7 kd protein in bcsa-degr intergenic region) (db:swissprot) YPDP_BACSU P54163 BACILLUS SUBTILIS 1423 -11531278 7000688207 ypdp conserved hypothetical protein ypdp (cl:archaeoglobus fulgidus conserved hypothetical protein af2110) (db:pir2.dat) C69934 C69934 Bacillus subtilis 1423 -11531278 217082 ypdp (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:11031) (re:11720) (di:complement) BACYACA L77246 g1256625 Bacillus subtilis 1423 -11531278 7500952183 ypdp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:113432) (re:114121) (di:direct) BSUB0012 Z99115 g2634618 Bacillus subtilis 1423 -11531278 6500727420 hypothetical protein:hypothetical 25.7 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdP ypdP Bacillus subtilis 1423 -11531278

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803521	4972	27128	246	82

Description

GTC ORF with score 214 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1341.) (nt:similar to saccharomyces cerevisiae orf ycr028) (le:<1) (re:916) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803537	4973	27129	1149	383

Description

5000689215 hypothetical protein:hypothetical 14.7 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdQ ypdQ Bacillus subtilis 1423 -11531279 115542 ypdq (de:hypothetical 14.7 kd protein in bcsa-degr intergenic region) (db:swissprot) YPDQ_BACSU P54162 BACILLUS SUBTILIS 1423 -11531279 7000688208 ypdq cell wall enzyme homolog ypdq (cl:enterococcus faecalis ebsb protein) (db:pir2.dat) D69934 D69934 Bacillus subtilis 1423 -11531279 217081 ypdq (fn:cell wall assembly) (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:41% identity over 125 aa to cell wall enzyme of) (le:10633) (re:11031) (di:complement) BACYACA L77246 g1256624 Bacillus subtilis 1423 -11531279 7500952184 ypdq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to cell wall enzyme) (le:114121) (re:114519) (di:direct) BSUB0012 Z99115 g2634619 Bacillus subtilis 1423 -11531279 6500727421 hypothetical protein:hypothetical 14.7 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdQ ypdQ Bacillus subtilis 1423 -11531279

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803547	4974	27130	294	97

Description

6500727422 hypothetical protein:potential 5-3 exonuclease (gtcfc:14.1) (ec:3.1.11.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypcP ypcP Bacillus subtilis 1423 -11531280 115530 ypcp (ec:3.1.11.-) (de:potential 5'-3' exonuclease,) (db:swissprot) YPCP_BACSU P54161 BACILLUS SUBTILIS 1423 -11531280 7000688204 ypcp 5-3 exonuclease homolog ypcp (db:pir2.dat) H69933 H69933 Bacillus subtilis 1423 -11531280 217080 ypcp exodeoxyribonuclease (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:36.1% identity with 219 aa at the 5' end of the) (le:9565) (re:10455) (di:direct) BACYACA L77246 g1256623 Bacillus subtilis 1423 -11531280 7500952180 ypcp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to 5'-3' exonuclease) (le:114697) (re:115587) (di:complement) BSUB0012 Z99115 g2634620 Bacillus subtilis 1423 -11531280 5000689443 (de:(ypcp) (pn:potential 5"-3" exonuclease) (gtcfc:13.07) (ec:3.1.11.-) (ypcp_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) ypcP ypcP Bacillus subtilis 1423 10057256

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803568	4975	27131	456	152

Description

5000689210 hypothetical protein:hypothetical 9.9 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbS ypbS Bacillus subtilis 1423 -11531281 115517 ypbs (de:hypothetical 9.9 kd protein in bcsa-degr intergenic region) (db:swissprot) YPBS_BACSU P54160 BACILLUS SUBTILIS 1423 -11531281 7000688202 ypbs hypothetical protein ypbs (db:pir2.dat) F69933 F69933 Bacillus subtilis 1423 -11531281 217079 ypbs (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:putative) (le:8986) (re:9243) (di:direct) BACYACA L77246 g1256622 Bacillus subtilis 1423 -11531281 7500952177 ypbs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:115909) (re:116166) (di:complement) BSUB0012 Z99115 g2634621 Bacillus subtilis 1423 -11531281 6500727423 hypothetical protein:hypothetical 9.9 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbS ypbS Bacillus subtilis 1423 -11531281

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803574	4976	27132	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803596	4977	27133	216	71

Description

5000689209 hypothetical protein:hypothetical 137.4 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbR ypbR Bacillus subtilis 1423 -11531282 115516 ypbr (de:hypothetical 137.4 kd protein in bcsa-degr intergenic region) (db:swissprot) YPBR_BACSU P54159 BACILLUS SUBTILIS 1423 -11531282 7000688201 ypbr hypothetical protein ypbr (db:pir2.dat) E69933 E69933 Bacillus subtilis 1423 -11531282 217078 ypbr (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:26.7% of identity in 165 aa to a thermophilic) (le:5340) (re:8921) (di:direct) BACYACA L77246 g1256621 Bacillus subtilis 1423 -11531282 7500952176 ypbr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:116231) (re:119812) (di:complement) BSUB0012 Z99115 g2634622 Bacillus subtilis 1423 -11531282 6500727424 hypothetical protein:hypothetical 137.4 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbR ypbR Bacillus subtilis 1423 -11531282

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803597	4978	27134	360	119

Description

5000689208 hypothetical protein:hypothetical 19.3 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbQ ypbQ Bacillus subtilis 1423 -11531283 110365 ypbq (de:hypothetical 19.3 kd protein in bcsa-degr intergenic region) (db:swissprot) YBPQ_BACSU P54158 BACILLUS SUBTILIS 1423 -11531283 7000687388 ypbq conserved hypothetical protein ypbq (db:pir2.dat) D69933 D69933 Bacillus subtilis 1423 -11531283 217077 ypbq (db:genpept-bct1) (de:bacillus subtilis (yac10-9 clone) dna region between the sera andkdg loci.) (nt:33.3% of identity in 60 aa with the sacharomyces) (le:4498) (re:5004) (di:direct) BACYACA L77246 g1256620 Bacillus subtilis 1423 -11531283 7500896919 ypbq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:120148) (re:120654) (di:complement) BSUB0012 Z99115 g2634623 Bacillus subtilis 1423 -11531283 6500727425 hypothetical protein:hypothetical 19.3 kd protein in bcsa-degr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbQ ypbQ Bacillus subtilis 1423 -11531283

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803608	4979	27135	192	63

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803629	4980	27136	348	115

Description

5000689262 hypothetical protein:hypothetical 58.2 kd protein in kdgt-xpt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypwA ypwA Bacillus subtilis 1423 -11531284 115773 ypwa (de:hypothetical 58.2 kd protein in kdgt-xpt intergenic region) (db:swissprot) YPWA_BACSU P50848 BACILLUS SUBTILIS 1423 -11531284 7000688281 ypwa carboxypeptidase homolog ypwa (cl:thermus aquaticus carboxypeptidase taq) (db:pir2.dat) D69943 D69943 Bacillus subtilis 1423 -11531284 7500952314 ypwa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to carboxypeptidase) (le:124057) (re:125562) (di:complement) BSUB0012 Z99115 g2634627 Bacillus subtilis 1423 -11531284 6500727426 hypothetical protein:hypothetical 58.2 kd protein in kdgt-xpt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypwA ypwA Bacillus subtilis 1423 -11531284

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803641	4981	27137	1638	546

Description

5000689261 hypothetical protein:probable atp-dependent helicase in cotd-kdud intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypvA ypvA Bacillus subtilis 1423 -11531285 115770 ypva (de:probable atp-dependent helicase in cotd-kdud intergenic region) (db:swissprot) YPVA_BACSU P50831 BACILLUS SUBTILIS 1423 -11531285 7000688280 ypva atp-dependent helicase homolog ypva (db:pir2.dat) C69943 C69943 Bacillus subtilis 1423 -11531285 216504 ypua (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:33.3% of... BACPONAYPP L47838 g1146185 Bacillus subtilis 1423 -11531285 7500952313 ypva (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to atp-dependent helicase) (le:131190) (re:133115) (di:complement) BSUB0012 Z99115 g2634634 Bacillus subtilis 1423 -11531285 6500727427 hypothetical protein:probable atp-dependent helicase in cotd-kdud intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypvA ypvA Bacillus subtilis 1423 -11531285

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803655	4982	27138	450	149

Description

5000689260 hypothetical protein:hypothetical 7.1 kd protein in cotd-kdud intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yptA yptA Bacillus subtilis 1423 -11531286 115737 ypta (de:hypothetical 7.1 kd protein in cotd-kdud intergenic region precursor) (db:swissprot) YPTA_BACSU P50841 BACILLUS SUBTILIS 1423 -11531286 7000688268 ypta hypothetical protein ypta (db:pir2.dat) G69941 G69941 Bacillus subtilis 1423 -11531286 216503 ypta (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146184 Bacillus subtilis 1423 -11531286 7500952297 ypta (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:133217) (re:133408) (di:complement) BSUB0012 Z99115 g2634635 Bacillus subtilis 1423 -11531286 6500727428 hypothetical protein:hypothetical 7.1 kd protein in cotd-kdud intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yptA yptA Bacillus subtilis 1423 -11531286

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803659	4983	27139	366	121

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803661	4984	27140	387	128

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803668	4985	27141	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803685	4986	27142	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803690	4987	27143	510	169

Description

5000689259 hypothetical protein:hypothetical 43.5 kd protein in cotd-kdud intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypsC ypsC Bacillus subtilis 1423 -11531287 115701 ypsc (de:hypothetical 43.5 kd protein in cotd-kdud intergenic region precursor) (db:swissprot) YPSC_BACSU P50840 BACILLUS SUBTILIS 1423 -11531287 7000688266 ypsc conserved hypothetical protein ypsc (db:pir2.dat) F69941 F69941 Bacillus subtilis 1423 -11531287 216502 ypsc (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146183 Bacillus subtilis 1423 -11531287 7500952290 ypsc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:133777) (re:134934) (di:complement) BSUB0012 Z99115 g2634636 Bacillus subtilis 1423 -11531287 6500727429 hypothetical protein:hypothetical 43.5 kd protein in cotd-kdud intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypsC ypsC Bacillus subtilis 1423 -11531287

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803692	4988	27144	483	160

Description

5000689258 hypothetical protein:hypothetical 11.6 kd protein in cotd-kdud intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypsB ypsB Bacillus subtilis 1423 -11531288 115700 ypsb (de:hypothetical 11.6 kd protein in cotd-kdud intergenic region) (db:swissprot) YPSB_BACSU P50839 BACILLUS SUBTILIS 1423 -11531288 7000688265 ypsb hypothetical protein ypsb (db:pir2.dat) E69941 E69941 Bacillus subtilis 1423 -11531288 216501 ypsb (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146182 Bacillus subtilis 1423 -11531288 7500952289 ypsb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:135481) (re:135777) (di:complement) BSUB0012 Z99115 g2634637 Bacillus subtilis 1423 -11531288 6500727430 hypothetical protein:hypothetical 11.6 kd protein in cotd-kdud intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypsB ypsB Bacillus subtilis 1423 -11531288

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803693	4989	27145	306	101

Description

5000689257 hypothetical protein:hypothetical 21.1 kd protein in cotd-kdud intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypsA ypsA Bacillus subtilis 1423 -11531289 115699 ypsa (de:hypothetical 21.1 kd protein in cotd-kdud intergenic region) (db:swissprot) YPSA_BACSU P50838 BACILLUS SUBTILIS 1423 -11531289 7000688264 ypsa conserved hypothetical protein ypsa (db:pir2.dat) D69941 D69941 Bacillus subtilis 1423 -11531289 216500 ypsa (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146181 Bacillus subtilis 1423 -11531289 7500952288 ypsa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins from b. subtilis) (le:135855) (re:136397) (di:complement) BSUB0012 Z99115 g2634638 Bacillus subtilis 1423 -11531289 6500727431 hypothetical protein:hypothetical 21.1 kd protein in cotd-kdud intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypsA ypsA Bacillus subtilis 1423 -11531289

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803696	4990	27146	411	137

Description

5000689256 hypothetical protein:hypothetical 48.0 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yprB yprB Bacillus subtilis 1423 -11531290 115687 yprb (de:hypothetical 48.0 kd protein in pona-cotd intergenic region) (db:swissprot) YPRB_BACSU P50837 BACILLUS SUBTILIS 1423 -11531290 7000688263 yprb hypothetical protein yprb (db:pir2.dat) C69941 C69941 Bacillus subtilis 1423 -11531290 216498 yprb (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146179 Bacillus subtilis 1423 -11531290 7500952285 yprb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:137026) (re:138267) (di:complement) BSUB0012 Z99115 g2634640 Bacillus subtilis 1423 -11531290 6500727432 hypothetical protein:hypothetical 48.0 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yprB yprB Bacillus subtilis 1423 -11531290

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803711	4991	27147	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803713	4992	27148	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803737	4993	27149	708	235

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803756	4994	27150	249	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803768	4995	27151	600	199

Description

5000689255 hypothetical protein:hypothetical helicase in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yprA yprA Bacillus subtilis 1423 -11531291 115684 ypra (de:hypothetical helicase in pona-cotd intergenic region) (db:swissprot) YPRA_BACSU P50830 BACILLUS SUBTILIS 1423 -11531291 7000688262 ypra atp-dependent helicase homolog ypra (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) B69941 B69941 Bacillus subtilis 1423 -11531291 216497 ypra helicase (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:27.7% of... BACPONAYPP L47838 g1146178 Bacillus subtilis 1423 -11531291 7500952284 ypra (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to atp-dependent helicase) (le:138283) (re:140532) (di:complement) BSUB0012 Z99115 g2634641 Bacillus subtilis 1423 -11531291 6500727433 hypothetical protein:hypothetical helicase in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yprA yprA Bacillus subtilis 1423 -11531291

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803775	4996	27152	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803799	4997	27153	2364	787

Description

5000689253 hypothetical protein:hypothetical 16.3 kd protein in pona-cotd intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypqA ypqA Bacillus subtilis 1423 -11531292 115671 ypqa (de:hypothetical 16.3 kd protein in pona-cotd intergenic region precursor) (db:swissprot) YPQA_BACSU P50836 BACILLUS SUBTILIS 1423 -11531292 7000688259 ypqa hypothetical protein ypqa (db:pir2.dat) G69940 G69940 Bacillus subtilis 1423 -11531292 216495 ypqa (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146176 Bacillus subtilis 1423 -11531292 7500952278 ypqa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:141279) (re:141698) (di:direct) BSUB0012 Z99115 g2634643 Bacillus subtilis 1423 -11531292 6500727434 hypothetical protein:hypothetical 16.3 kd protein in pona-cotd intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypqA ypqA Bacillus subtilis 1423 -11531292

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803803	4998	27154	276	91

Description

5000689250 hypothetical protein:hypothetical 14.5 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppG yppG Bacillus subtilis 1423 -11531293 115668 yppg (de:hypothetical 14.5 kd protein in pona-cotd intergenic region) (db:swissprot) YPPG_BACSU P50835 BACILLUS SUBTILIS 1423 -11531293 7000688257 yppg hypothetical protein yppg (db:pir2.dat) D69940 D69940 Bacillus subtilis 1423 -11531293 216494 yppg (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146175 Bacillus subtilis 1423 -11531293 7500952276 yppg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:141719) (re:142096) (di:complement) BSUB0012 Z99115 g2634644 Bacillus subtilis 1423 -11531293 6500727435 hypothetical protein:hypothetical 14.5 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppG yppG Bacillus subtilis 1423 -11531293

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803808	4999	27155	579	193

Description

5000689249 hypothetical protein:hypothetical 7.3 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppF yppF Bacillus subtilis 1423 -11531294 115667 yppf (de:hypothetical 7.3 kd protein in pona-cotd intergenic region) (db:swissprot) YPPF_BACSU P50834 BACILLUS SUBTILIS 1423 -11531294 7000688256 yppf hypothetical protein yppf (db:pir2.dat) C69940 C69940 Bacillus subtilis 1423 -11531294 216493 yppf (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146174 Bacillus subtilis 1423 -11531294 7500952275 yppf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:142284) (re:142472) (di:direct) BSUB0012 Z99115 g2634645 Bacillus subtilis 1423 -11531294 6500727436 hypothetical protein:hypothetical 7.3 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppF yppF Bacillus subtilis 1423 -11531294

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803809	5000	27156	480	159

Description

5000689248 hypothetical protein:hypothetical 14.5 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppE yppE Bacillus subtilis 1423 -11531295 115666 yppe (de:hypothetical 14.5 kd protein in pona-cotd intergenic region) (db:swissprot) YPPE_BACSU P50833 BACILLUS SUBTILIS 1423 -11531295 7000688255 yppe hypothetical protein yppe (db:pir2.dat) B69940 B69940 Bacillus subtilis 1423 -11531295 216492 yppe (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146173 Bacillus subtilis 1423 -11531295 7500952274 yppe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:142511) (re:142882) (di:complement) BSUB0012 Z99115 g2634646 Bacillus subtilis 1423 -11531295 6500727437 hypothetical protein:hypothetical 14.5 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppE yppE Bacillus subtilis 1423 -11531295

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803817	5001	27157	624	207

Description

5000689247 hypothetical protein:hypothetical 9.5 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppD yppD Bacillus subtilis 1423 -11531296 115665 yppd (de:hypothetical 9.5 kd protein in pona-cotd intergenic region) (db:swissprot) YPPD_BACSU P50832 BACILLUS SUBTILIS 1423 -11531296 7000688254 yppd hypothetical protein yppd (db:pir2.dat) A69940 A69940 Bacillus subtilis 1423 -11531296 216491 yppd (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146172 Bacillus subtilis 1423 -11531296 7500952273 yppd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:142928) (re:143173) (di:complement) BSUB0012 Z99115 g2634647 Bacillus subtilis 1423 -11531296 6500727438 hypothetical protein:hypothetical 9.5 kd protein in pona-cotd intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppD yppD Bacillus subtilis 1423 -11531296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803828	5002	27158	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803831	5003	27159	681	226

Description

6500727439 jopc:yppc hypothetical protein:hypothetical 38.5 kd protein in pona-cotd intergenic region:orfx (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppC yppC Bacillus subtilis 1423 -11531297 115663 yppc (de:hypothetical 38.5 kd protein in pona-cotd intergenic region (orfx)) (db:swissprot) YPPC_BACSU P39791 BACILLUS SUBTILIS 1423 -11531297 7000688253 yppc hypothetical protein yppc (db:pir2.dat) H69939 H69939 Bacillus subtilis 1423 -11531297 216490 yppc (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:putative... BACPONAYPP L47838 g1146171 Bacillus subtilis 1423 -11531297 7500952272 yppc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jopc) (le:143501) (re:144463) (di:complement) BSUB0012 Z99115 g2634648 Bacillus subtilis 1423 -11531297 5000689614 (de:(yppc) (pn:hypothetical 38:hypothetical protein in pona 5"region:orfx:fragment) (gtcfc:13.07) (ec:) (yppc_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yppC yppC Bacillus subtilis 1423 10057389

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803832	5004	27160	228	75

Description

6500727440 jopb:prfa:yppb hypothetical protein:hypothetical 24.0 kd protein in pona-cotd intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yppB yppB Bacillus subtilis 1423 -11531298 115662 yppb:prfa (de:hypothetical 24.0 kd protein in pona-cotd intergenic region (orf1)) (db:swissprot) YPPB_BACSU P39792 BACILLUS SUBTILIS 1423 -11531298 7000688252 yppb conserved hypothetical protein yppb (db:pir2.dat) I40528 I40528 Bacillus subtilis 1423 -11531298 7500952271 yppb (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) pona gene, yppbcdefg genes,ypqae genes, yprab genes, cotd gene, ypsabc genes, rnap gene, yptagene, ypua gene, kdudi genes, kdgrkat genes, ypwa gene, completecds's.) (nt:50.3% of... BACPONAYPP L47838 g1146170 Bacillus subtilis 1423 -11531298 216489 unknown (db:genpept-bct1) (de:bacillus subtilis 168 penicillin-binding proteins 1a and 1b (pona)gene, complete cds, orfx gene, partial cds, orf1 and orfy genes,complete cds.) (nt:orf1) (le:683) (re:1303) (di:direct) BSU11883 U11883 g520540 Bacillus subtilis 1423 -11531298 219803 yppb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jopb; similar to hypothetical) (le:144504) (re:145124) (di:direct) BSUB0012 Z99115 g2634649 Bacillus subtilis 1423 -11531298 170061 yppb conserved hypothetical protein yppb (db:pir) I40528 I40528 Bacillus subtilis 1423 -11531298 5000689613 (de:(yppb) (pn:hypothetical 24) (gn:prfa) (gtcfc:13.07) (ec:) (yppb_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yppB yppB Bacillus subtilis 1423 10057388

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803841	5005	27161	192	63

Description

6500727441 jooc:ypoc hypothetical protein:hypothetical 19.3 kd protein in pona-nth intergenic region:orfy (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypoC ypoC Bacillus subtilis 1423 -11531299 115653 ypoc:jooc (de:hypothetical 19.3 kd protein in pona-nth intergenic region (orfy)) (db:swissprot) YPOC_BACSU P39789 BACILLUS SUBTILIS 1423 -11531299 7000688250 ypoc:jooc hypothetical protein ypoc:hypothetical protein y pona operon:jooc protein (db:pir2.dat) I40526 I40526 Bacillus subtilis 1423 -11531299 7500952269 ypoc (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146250 Bacillus subtilis 1423 -11531299 217172 jooc unknown (db:genpept-bct1) (de:bacillus subtilis 168 asparaginyl-trna synthetase (asns) andendonuclease iii (joob) genes, partial cds and dnad protein (dnad)and (jooc) genes, complete cds.) (le:1702) (re:2196) (di:direct) BSU11289 U11289 g533100 Bacillus subtilis 1423 -11531299 219793 unknown (db:genpept-bct1) (de:bacillus subtilis 168 penicillin-binding proteins 1a and 1b (pona)gene, complete cds, orfx gene, partial cds, orf1 and orfy genes,complete cds.) (nt:orfy) (le:4145) (re:4639) (di:complement) BSU11883 U11883 g520542 Bacillus subtilis 1423 -11531299 219805 ypoc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jooc) (le:147966) (re:148460) (di:complement) BSUB0012 Z99115 g2634651 Bacillus subtilis 1423 -11531299 170304 ypoc:jooc hypothetical protein ypoc:hypothetical protein y pona operon:jooc protein (db:pir) I40526 I40526 Bacillus subtilis 1423 -11531299 5000689612 (de:(ypoc) (pn:hypothetical 19) (gn:jooc) (gtcfc:13.07) (ec:) (ypoc_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ypoC ypoC Bacillus subtilis 1423 10057379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803858	5006	27162	558	185

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803868	5007	27163	207	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803873	5008	27164	684	227

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803911	5009	27165	294	97

Description

5000689239 hypothetical protein:hypothetical 17.9 kd protein in ding-aspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmB ypmB Bacillus subtilis 1423 -11531300 115635 ypmb (de:hypothetical 17.9 kd protein in ding-aspb intergenic region) (db:swissprot) YPMB_BACSU P54396 BACILLUS SUBTILIS 1423 -11531300 7000688243 ypmb hypothetical protein ypmb (db:pir2.dat) F69938 F69938 Bacillus subtilis 1423 -11531300 217167 ypmb (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146245 Bacillus subtilis 1423 -11531300 7500952262 ypmb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:152566) (re:153051) (di:complement) BSUB0012 Z99115 g2634656 Bacillus subtilis 1423 -11531300 6500727442 hypothetical protein:hypothetical 17.9 kd protein in ding-aspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmB ypmB Bacillus subtilis 1423 -11531300

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803916	5010	27166	708	235

Description

5000689238 hypothetical protein:hypothetical 6.6 kd protein in ding-aspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmA ypmA Bacillus subtilis 1423 -11531301 115634 ypma (de:hypothetical 6.6 kd protein in ding-aspb intergenic region) (db:swissprot) YPMA_BACSU P54395 BACILLUS SUBTILIS 1423 -11531301 7000688242 ypma hypothetical protein ypma (db:pir2.dat) E69938 E69938 Bacillus subtilis 1423 -11531301 217166 ypma (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146244 Bacillus subtilis 1423 -11531301 7500952261 ypma (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:153060) (re:153230) (di:complement) BSUB0012 Z99115 g2634657 Bacillus subtilis 1423 -11531301 6500727443 hypothetical protein:hypothetical 6.6 kd protein in ding-aspb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypmA ypmA Bacillus subtilis 1423 -11531301

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803930	5011	27167	669	222

Description

GTC ORF with score 496 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completecds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803934	5012	27168	420	139

Description

GTC ORF with score 500 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completecds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803940	5013	27169	1188	396

Description

GTC ORF with score 2013 to: (fn:required for conidial pigmentation) (db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene, completecds.) (nt:alb1) (le:598:932:1268:4755:5584) (re:884:1220:4699:5510:7260) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803942	5014	27170	591	196

Description

6500727444 jojh:ypjh hypothetical protein:hypothetical 42.0 kd protein in dapb-paps intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjH ypjH Bacillus subtilis 1423 -11531302 115620 ypjh:jojh (de:hypothetical 42.0 kd protein in dapb-paps intergenic region) (db:swissprot) YPJH_BACSU P42982 BACILLUS SUBTILIS 1423 -11531302 7000688237 ypjh lipopolysaccharide biosynthesis-related pr homolog ypjh (db:pir2.dat) G69937 G69937 Bacillus subtilis 1423 -11531302 217159 ypjh (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:21.4% o... BACYPIA L47709 g1146237 Bacillus subtilis 1423 -11531302 7500952254 ypjh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jojh; similar to) (le:160780) (re:161913) (di:complement) BSUB0012 Z99115 g2634664 Bacillus subtilis 1423 -11531302 5000689611 (de:(ypjh) (pn:hypothetical 42:hypothetical 24) (gn:jojh) (gtcfc:13.07) (ec:) (ypjh_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ypjH ypjH Bacillus subtilis 1423 10057346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803950	5015	27171	438	146

Description

6500727445 jojg:ypjg hypothetical protein:hypothetical 24.8 kd protein in dapb-paps intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjG ypjG Bacillus subtilis 1423 -11531303 115619 ypjg:jojg (de:hypothetical 24.8 kd protein in dapb-paps intergenic region) (db:swissprot) YPJG_BACSU P42981 BACILLUS SUBTILIS 1423 -11531303 7000688236 ypjg conserved hypothetical protein ypjg (db:pir2.dat) F69937 F69937 Bacillus subtilis 1423 -11531303 216256 jojg unknown (sr:bacillus subtilis (sub_strain 168, strain marburg) dna) (db:genpept-bct1) (de:bacillus subtilis dihydropicolinate reductase (joje) gene, completecds; poly(a) polymerase (joji) gene, complete cds; biotinacetyl-coa-carboxylase ligase (bira) gene, com... BACJOJC L38424 g755605 Bacillus subtilis 1423 -11531303 217158 ypjg (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146236 Bacillus subtilis 1423 -11531303 7500952253 ypjg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jojg; similar to hypothetical) (le:161945) (re:162619) (di:complement) BSUB0012 Z99115 g2634665 Bacillus subtilis 1423 -11531303 5000689610 (de:(ypjg) (pn:hypothetical 24) (gn:jojg) (gtcfc:13.07) (ec:) (ypjg_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ypjG ypjG Bacillus subtilis 1423 10057345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803951	5016	27172	687	228

Description

6500727446 jojf:mgsa:ypjf hypothetical protein:methylglyoxal synthase (gtcfc:14.1) (ec:4.2.99.11) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjF ypjF Bacillus subtilis 1423 -11531304 115618 mgsa (ec:4.2.99.11) (de:methylglyoxal synthase,) (db:swissprot) MGSA_BACSU P42980 BACILLUS SUBTILIS 1423 -11531304 7000685839 ypjf conserved hypothetical protein ypjf (cl:escherichia coli yccg protein) (db:pir2.dat) E69937 E69937 Bacillus subtilis 1423 -11531304 216255 jojf unknown (sr:bacillus subtilis (sub_strain 168, strain marburg) dna) (db:genpept-bct1) (de:bacillus subtilis dihydropicolinate reductase (joje) gene, completecds; poly(a) polymerase (joji) gene, complete cds; biotinacetyl-coa-carboxylase ligase (bira) gene, com... BACJOJC L38424 g755604 Bacillus subtilis 1423 -11531304 217157 ypjf (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146235 Bacillus subtilis 1423 -11531304 7500885604 ypjf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jojf; similar to hypothetical) (le:162612) (re:163025) (di:complement) BSUB0012 Z99115 g2634666 Bacillus subtilis 1423 -11531304 5000689609 (de:(ypjf) (pn:hypothetical 15) (gn:jojf) (gtcfc:13.07) (ec:) (ypjf_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ypjF ypjF Bacillus subtilis 1423 10057344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803955	5017	27173	780	260

Description

6500727447 jojd:ypjd hypothetical protein:hypothetical 13.0 kd protein in qcrc-dapb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjD ypjD Bacillus subtilis 1423 -11531305 115617 ypjd:jojd (de:hypothetical 13.0 kd protein in qcrc-dapb intergenic region) (db:swissprot) YPJD_BACSU P42979 BACILLUS SUBTILIS 1423 -11531305 7000688234 ypjd hypothetical protein ypjd (db:pir2.dat) D69937 D69937 Bacillus subtilis 1423 -11531305 216253 jojd unknown (sr:bacillus subtilis (sub_strain 168, strain marburg) dna) (db:genpept-bct1) (de:bacillus subtilis dihydropicolinate reductase (joje) gene, completecds; poly(a) polymerase (joji) gene, complete cds; biotinacetyl-coa-carboxylase ligase (bira) gene, com... BACJOJC L38424 g755602 Bacillus subtilis 1423 -11531305 217155 ypjd (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146233 Bacillus subtilis 1423 -11531305 7500952247 ypjd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jojd) (le:163856) (re:164191) (di:complement) BSUB0012 Z99115 g2634668 Bacillus subtilis 1423 -11531305 5000689608 (de:(ypjd) (pn:hypothetical 13) (gn:jojd) (gtcfc:13.07) (ec:) (ypjd_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ypjD ypjD Bacillus subtilis 1423 10057343

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803958	5018	27174	663	220

Description

6500727448 jojc:ypjc hypothetical protein:hypothetical 23.6 kd protein in qcrc-dapb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjC ypjC Bacillus subtilis 1423 -11531306 115616 ypjc:jojc (de:hypothetical 23.6 kd protein in qcrc-dapb intergenic region) (db:swissprot) YPJC_BACSU P42978 BACILLUS SUBTILIS 1423 -11531306 7000688233 ypjc conserved hypothetical protein ypjc (cl:conserved hypothetical protein yitt) (db:pir2.dat) C69937 C69937 Bacillus subtilis 1423 -11531306 216252 jojc unknown (sr:bacillus subtilis (sub_strain 168, strain marburg) dna) (db:genpept-bct1) (de:bacillus subtilis dihydropicolinate reductase (joje) gene, completecds; poly(a) polymerase (joji) gene, complete cds; biotinacetyl-coa-carboxylase ligase (bira) gene, com... BACJOJC L38424 g755601 Bacillus subtilis 1423 -11531306 217154 ypjc (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146232 Bacillus subtilis 1423 -11531306 7500952246 ypjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jojc; similar to hypothetical) (le:164556) (re:165203) (di:direct) BSUB0012 Z99115 g2634669 Bacillus subtilis 1423 -11531306 5000689607 (de:(ypjc) (pn:hypothetical 23) (gn:jojc) (gtcfc:13.07) (ec:) (ypjc_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) ypjC ypjC Bacillus subtilis 1423 10057342

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803961	5019	27175	576	191

Description

5000689232 hypothetical protein:hypothetical 30.6 kd protein in qcrc-dapb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjB ypjB Bacillus subtilis 1423 -11531307 115615 ypjb (de:hypothetical 30.6 kd protein in qcrc-dapb intergenic region precursor) (db:swissprot) YPJB_BACSU P54393 BACILLUS SUBTILIS 1423 -11531307 7000688232 ypjb hypothetical protein ypjb (db:pir2.dat) B69937 B69937 Bacillus subtilis 1423 -11531307 217153 ypjb (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146231 Bacillus subtilis 1423 -11531307 7500952245 ypjb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:165245) (re:166039) (di:complement) BSUB0012 Z99115 g2634670 Bacillus subtilis 1423 -11531307 6500727449 hypothetical protein:hypothetical 30.6 kd protein in qcrc-dapb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjB ypjB Bacillus subtilis 1423 -11531307

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803976	5020	27176	273	90

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803984	5021	27177	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501803989	5022	27178	537	179

Description

5000689231 hypothetical protein:hypothetical 21.3 kd protein in qcrc-dapb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjA ypjA Bacillus subtilis 1423 -11531308 115613 ypja (de:hypothetical 21.3 kd protein in qcrc-dapb intergenic region) (db:swissprot) YPJA_BACSU P54392 BACILLUS SUBTILIS 1423 -11531308 7000688230 ypja hypothetical protein ypja (db:pir2.dat) A69937 A69937 Bacillus subtilis 1423 -11531308 217152 ypja (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146230 Bacillus subtilis 1423 -11531308 7500952243 ypja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:166108) (re:166665) (di:complement) BSUB0012 Z99115 g2634671 Bacillus subtilis 1423 -11531308 6500727450 hypothetical protein:hypothetical 21.3 kd protein in qcrc-dapb intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypjA ypjA Bacillus subtilis 1423 -11531308

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804010	5023	27179	294	97

Description

6500727451 hypothetical protein:hypothetical 17.3 kd protein in qcra 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypiF ypiF Bacillus subtilis 1423 -11531309 115604 ypif (de:hypothetical 17.3 kd protein in qcra-aroe intergenic region) (db:swissprot) YPIF_BACSU P54391 BACILLUS SUBTILIS 1423 -11531309 7000688228 ypif hypothetical protein ypif (db:pir2.dat) G69936 G69936 Bacillus subtilis 1423 -11531309 217148 ypif (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146226 Bacillus subtilis 1423 -11531309 7500952241 ypif (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:168936) (re:169382) (di:complement) BSUB0012 Z99115 g2634675 Bacillus subtilis 1423 -11531309

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804011	5024	27180	333	110

Description

5000689229 hypothetical protein:hypothetical 21.4 kd protein in qcra 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypiB ypiB Bacillus subtilis 1423 -11531310 115603 ypib (de:hypothetical 21.4 kd protein in qcra-aroe intergenic region) (db:swissprot) YPIB_BACSU P54390 BACILLUS SUBTILIS 1423 -11531310 7000688227 ypib hypothetical protein ypib (db:pir2.dat) F69936 F69936 Bacillus subtilis 1423 -11531310 217147 ypib (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146225 Bacillus subtilis 1423 -11531310 7500952240 ypib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:169437) (re:169976) (di:complement) BSUB0012 Z99115 g2634676 Bacillus subtilis 1423 -11531310 6500727452 hypothetical protein:hypothetical 21.4 kd protein in qcra 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypiB ypiB Bacillus subtilis 1423 -11531310

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804012	5025	27181	462	153

Description

5000689228 hypothetical protein:hypothetical 48.3 kd protein in qcra 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypiA ypiA Bacillus subtilis 1423 -11531311 115602 ypia (de:hypothetical 48.3 kd protein in qcra-aroe intergenic region) (db:swissprot) YPIA_BACSU P54389 BACILLUS SUBTILIS 1423 -11531311 7000688226 ypia conserved hypothetical protein ypia (cl:tetratricopeptide repeat homology) (db:pir2.dat) E69936 E69936 Bacillus subtilis 1423 -11531311 217146 ypia (fn:hypothetical) (db:genpept-bct1) (de:bacillus subtilis (clone yac15-6b) ypiabf genes, qcrabc genes,ypjabcdefghi genes, bira gene, panbcd genes, ding gene, ypmb gene,aspb gene, asns gene, dnad gene, nth gene and ypoc gene, completecds's.) (nt:putativ... BACYPIA L47709 g1146224 Bacillus subtilis 1423 -11531311 7500952239 ypia (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:170048) (re:171319) (di:complement) BSUB0012 Z99115 g2634677 Bacillus subtilis 1423 -11531311 6500727453 hypothetical protein:hypothetical 48.3 kd protein in qcra 5region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypiA ypiA Bacillus subtilis 1423 -11531311

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804013	5026	27182	189	62

Description

6500727454 johf:yphf hypothetical protein:hypothetical 27.7 kd protein in gpsa-spoiva intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphF yphF Bacillus subtilis 1423 -11531312 115593 yphf:johf (de:hypothetical 27.7 kd protein in gpsa-spoiva intergenic region (orf1)) (db:swissprot) YPHF_BACSU P39911 BACILLUS SUBTILIS 1423 -11531312 7000688224 yphf hypothetical protein yphf:orfx upstream of spoiva (db:pir2.dat) C69936 C69936 Bacillus subtilis 1423 -11531312 7500952225 yphf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: johf) (le:191551) (re:192285) (di:complement) BSUB0012 Z99115 g2634699 Bacillus subtilis 1423 -11531312 216728 yphf (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146222 Bacillus subtilis 1423 -11531312 5000689606 yphf (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146222 Bacillus subtilis 1423 -11531312

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804020	5027	27183	396	131

Description

5000689226 hypothetical protein:hypothetical 7.5 kd protein in gpsa-spoiva intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphE yphE Bacillus subtilis 1423 -11531313 115592 yphe (de:hypothetical 7.5 kd protein in gpsa-spoiva intergenic region) (db:swissprot) YPHE_BACSU P50744 BACILLUS SUBTILIS 1423 -11531313 7000688223 yphe hypothetical protein yphe (db:pir2.dat) B69936 B69936 Bacillus subtilis 1423 -11531313 7500952220 yphe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:192307) (re:192510) (di:complement) BSUB0012 Z99115 g2634700 Bacillus subtilis 1423 -11531313 216727 yphe (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146221 Bacillus subtilis 1423 -11531313 7502851705 yphe (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146221 Bacillus subtilis 1423 -11531313 6500727455 hypothetical protein:hypothetical 7.5 kd protein in gpsa-spoiva intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphE yphE Bacillus subtilis 1423 -11531313

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804023	5028	27184	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804024	5029	27185	501	166

Description

GTC ORF with score 239 to: (sr:human) (db:genpept-pri2) (de:homo sapiens dna sequence from pac 337o18 on chromosome 20q12-13.1.contains the plpt gene coding for phospholipid transfer protein,the ppgb gene coding for lysosomal protective protein ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804025	5030	27186	786	262

Description

5000689225 hypothetical protein:hypothetical 48.8 kd gtp-binding protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphC yphC Bacillus subtilis 1423 -11531314 115591 yphc (de:region) (db:swissprot) YPHC_BACSU P50743 BACILLUS SUBTILIS 1423 -11531314 7000688222 yphc conserved hypothetical protein yphc (cl:mycobacterium leprae probable gtp-binding protein:translation elongation factor tu homology) (db:pir2.dat) A69936 A69936 Bacillus subtilis 1423 -11531314 7500952211 yphc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:193903) (re:195213) (di:complement) BSUB0012 Z99115 g2634702 Bacillus subtilis 1423 -11531314 216725 yphc (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146219 Bacillus subtilis 1423 -11531314 7502851706 yphc (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146219 Bacillus subtilis 1423 -11531314 6500727456 hypothetical protein:hypothetical 48.8 kd gtp-binding protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphC yphC Bacillus subtilis 1423 -11531314

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804042	5031	27187	846	281

Description

5000689224 hypothetical protein:hypothetical 32.9 kd protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphB yphB Bacillus subtilis 1423 -11531315 115590 yphb (de:hypothetical 32.9 kd protein in cmk-gpsa intergenic region) (db:swissprot) YPHB_BACSU P50742 BACILLUS SUBTILIS 1423 -11531315 7000688221 yphb hypothetical protein yphb (db:pir2.dat) H69935 H69935 Bacillus subtilis 1423 -11531315 7500952207 yphb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:195558) (re:196451) (di:complement) BSUB0012 Z99115 g2634703 Bacillus subtilis 1423 -11531315 216724 yphb (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146218 Bacillus subtilis 1423 -11531315 7502851707 yphb (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146218 Bacillus subtilis 1423 -11531315 6500727457 hypothetical protein:hypothetical 32.9 kd protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphB yphB Bacillus subtilis 1423 -11531315

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804046	5032	27188	192	63

Description

5000689223 hypothetical protein:hypothetical 23.0 kd protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphA yphA Bacillus subtilis 1423 -11531316 115589 ypha (de:hypothetical 23.0 kd protein in cmk-gpsa intergenic region) (db:swissprot) YPHA_BACSU P50741 BACILLUS SUBTILIS 1423 -11531316 7000688220 ypha hypothetical protein ypha (db:pir2.dat) G69935 G69935 Bacillus subtilis 1423 -11531316 7500952202 ypha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:196448) (re:197047) (di:complement) BSUB0012 Z99115 g2634704 Bacillus subtilis 1423 -11531316 216723 ypha (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146217 Bacillus subtilis 1423 -11531316 7502851708 ypha (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146217 Bacillus subtilis 1423 -11531316 6500727458 hypothetical protein:hypothetical 23.0 kd protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yphA yphA Bacillus subtilis 1423 -11531316

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804058	5033	27189	663	220

Description

5000689220 hypothetical protein:hypothetical 22.6 kd protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypgA ypgA Bacillus subtilis 1423 -11531317 115573 ypga (de:hypothetical 22.6 kd protein in cmk-gpsa intergenic region) (db:swissprot) YPGA_BACSU P50740 BACILLUS SUBTILIS 1423 -11531317 7000688217 ypga conserved hypothetical protein ypga (db:pir2.dat) D69935 D69935 Bacillus subtilis 1423 -11531317 7500952199 ypga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:197299) (re:197937) (di:complement) BSUB0012 Z99115 g2634705 Bacillus subtilis 1423 -11531317 216722 ypga (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146216 Bacillus subtilis 1423 -11531317 7502851709 ypga (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146216 Bacillus subtilis 1423 -11531317 6500727459 hypothetical protein:hypothetical 22.6 kd protein in cmk-gpsa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypgA ypgA Bacillus subtilis 1423 -11531317

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804061	5034	27190	474	157

Description

6500727460 jofd:ypfd hypothetical protein:30s ribosomal protein s1 homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypfD ypfD Bacillus subtilis 1423 -11531318 97135 ypfd:jofd (de:30s ribosomal protein s1 homolog) (db:swissprot) RS1H_BACSU P38494 BACILLUS SUBTILIS 1423 -11531318 7000686496 ypfd ribosomal protein s1 homolog homolog ypfd (cl:synechocystis ribosomal protein s1) (db:pir2.dat) B69935 B69935 Bacillus subtilis 1423 -11531318 219798 jofd unknown (db:genpept-bct1) (de:bacillus subtilis 168 jofa, jofb, mssa homolog (jofc) and ribosomalprotein s1 homolog (jofd) genes, complete cds, and joeb gene,partial cds.) (nt:similar to the escherichia coli s1 ribosomal) (le:2651) (re:3799) (di:direct) BSU11687 U11687 g533106 Bacillus subtilis 1423 -11531318 7500890982 ypfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jofd; similar to ribosomal) (le:198361) (re:199509) (di:complement) BSUB0012 Z99115 g2634706 Bacillus subtilis 1423 -11531318 216721 ypfd (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146215 Bacillus subtilis 1423 -11531318 5000688622 ypfd (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146215 Bacillus subtilis 1423 -11531318

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804064	5035	27191	726	241

Description

6500727461 jofb:ypfb hypothetical protein:hypothetical 7.1 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypfB ypfB Bacillus subtilis 1423 -11531319 115565 ypfb:jofb (de:hypothetical 7.1 kd protein in recq-cmk intergenic region) (db:swissprot) YPFB_BACSU P38492 BACILLUS SUBTILIS 1423 -11531319 7000688213 ypfb hypothetical protein ypfb (db:pir2.dat) A69935 A69935 Bacillus subtilis 1423 -11531319 219796 jofb unknown (db:genpept-bct1) (de:bacillus subtilis 168 jofa, jofb, mssa homolog (jofc) and ribosomalprotein s1 homolog (jofd) genes, complete cds, and joeb gene,partial cds.) (le:1489) (re:1665) (di:direct) BSU11687 U11687 g533104 Bacillus subtilis 1423 -11531319 6000685541 ypfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jofb) (le:200495) (re:200671) (di:complement) BSUB0012 Z99115 g2634708 Bacillus subtilis 1423 -11531319 7500952191 ypfb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: jofb) (le:775) (re:951) (di:complement) BSUB0013 Z99116 g2634725 Bacillus subtilis 1423 -11531319 216719 ypfb (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146213 Bacillus subtilis 1423 -11531319 5000689605 ypfb (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146213 Bacillus subtilis 1423 -11531319

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804065	5036	27192	264	87

Description

6500727462 jofa:ypfa hypothetical protein:hypothetical 25.1 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypfA ypfA Bacillus subtilis 1423 -11531320 115564 ypfa:jofa (de:hypothetical 25.1 kd protein in recq-cmk intergenic region) (db:swissprot) YPFA_BACSU P38491 BACILLUS SUBTILIS 1423 -11531320 7000688212 ypfa hypothetical protein ypfa (db:pir2.dat) H69934 H69934 Bacillus subtilis 1423 -11531320 219795 jofa unknown (db:genpept-bct1) (de:bacillus subtilis 168 jofa, jofb, mssa homolog (jofc) and ribosomalprotein s1 homolog (jofd) genes, complete cds, and joeb gene,partial cds.) (le:791) (re:1444) (di:direct) BSU11687 U11687 g533103 Bacillus subtilis 1423 -11531320 6000685539 ypfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: jofa) (le:200716) (re:201369) (di:complement) BSUB0012 Z99115 g2634709 Bacillus subtilis 1423 -11531320 7500952190 ypfa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: jofa) (le:996) (re:1649) (di:complement) BSUB0013 Z99116 g2634726 Bacillus subtilis 1423 -11531320 216718 ypfa (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146212 Bacillus subtilis 1423 -11531320 5000689604 ypfa (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146212 Bacillus subtilis 1423 -11531320

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804067	5037	27193	471	156

Description

6500727463 joeb:yzua:ypeb hypothetical protein:hypothetical 51.2 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypeB ypeB Bacillus subtilis 1423 -11531321 115554 ypeb:joeb (de:hypothetical 51.2 kd protein in recq-cmk intergenic region) (db:swissprot) YPEB_BACSU P38490 BACILLUS SUBTILIS 1423 -11531321 7000688209 ypeb conserved hypothetical protein ypeb (db:pir2.dat) E69934 E69934 Bacillus subtilis 1423 -11531321 6000685535 ypeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:alternate gene name: joeb, yzua; similar to) (le:201462) (re:202814) (di:complement) BSUB0012 Z99115 g2634710 Bacillus subtilis 1423 -11531321 7500952185 ypeb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: joeb, yzua; similar to) (le:1742) (re:3094) (di:complement) BSUB0013 Z99116 g2634727 Bacillus subtilis 1423 -11531321 216717 ypeb (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146211 Bacillus subtilis 1423 -11531321 5000689603 ypeb (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146211 Bacillus subtilis 1423 -11531321

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804068	5038	27194	720	239

Description

5000689213 hypothetical protein:hypothetical 24.7 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdC ypdC Bacillus subtilis 1423 -11531322 115539 ypdc (de:hypothetical 24.7 kd protein in recq-cmk intergenic region) (db:swissprot) YPDC_BACSU P50738 BACILLUS SUBTILIS 1423 -11531322 7000688206 ypdc conserved hypothetical protein ypdc (db:pir2.dat) B69934 B69934 Bacillus subtilis 1423 -11531322 6000685529 ypdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:203905) (re:204561) (di:complement) BSUB0012 Z99115 g2634712 Bacillus subtilis 1423 -11531322 7500952182 ypdc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:4185) (re:4841) (di:complement) BSUB0013 Z99116 g2634729 Bacillus subtilis 1423 -11531322 216715 ypdc (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146209 Bacillus subtilis 1423 -11531322 7502851710 ypdc (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146209 Bacillus subtilis 1423 -11531322 6500727464 hypothetical protein:hypothetical 24.7 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdC ypdC Bacillus subtilis 1423 -11531322

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804085	5039	27195	687	228

Description

GTC ORF with score 106 to: (fn:lps core biosynthesis) (db:genpept-bct2) (de:dichelobacter nodosus a198 lpsa (lpsa), putative peptide releasefactor 3 (prfc), and putative amino acid binding protein (aaba)genes, complete cds.) (le:105) (re:1061) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804089	5040	27196	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804098	5041	27197	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804100	5042	27198	630	209

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804119	5043	27199	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804139	5044	27200	1488	495

Description

5000689211 hypothetical protein:hypothetical 36.3 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdA ypdA Bacillus subtilis 1423 -11531323 115537 ypda (de:hypothetical 36.3 kd protein in recq-cmk intergenic region) (db:swissprot) YPDA_BACSU P50736 BACILLUS SUBTILIS 1423 -11531323 7000688205 ypda thioredoxin reductase homolog ypda (db:pir2.dat) A69934 A69934 Bacillus subtilis 1423 -11531323 6000685527 ypda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to thioredoxin reductase) (le:204681) (re:205655) (di:complement) BSUB0012 Z99115 g2634713 Bacillus subtilis 1423 -11531323 7500952181 ypda (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to thioredoxin reductase) (le:4961) (re:5935) (di:complement) BSUB0013 Z99116 g2634730 Bacillus subtilis 1423 -11531323 216713 ypda (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146207 Bacillus subtilis 1423 -11531323 7502851711 ypda (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146207 Bacillus subtilis 1423 -11531323 6500727465 hypothetical protein:hypothetical 36.3 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypdA ypdA Bacillus subtilis 1423 -11531323

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804140	5045	27201	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804154	5046	27202	1320	440

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804158	5047	27203	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804170	5048	27204	1035	344

Description

5000689207 hypothetical protein:hypothetical 22.2 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbH ypbH Bacillus subtilis 1423 -11531324 115515 ypbh (de:hypothetical 22.2 kd protein in recq-cmk intergenic region) (db:swissprot) YPBH_BACSU P50734 BACILLUS SUBTILIS 1423 -11531324 7000688200 ypbh negative regulation of competence meca hom homolog ypbh (db:pir2.dat) C69933 C69933 Bacillus subtilis 1423 -11531324 6000685520 ypbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to negative regulation of competence meca) (le:207200) (re:207784) (di:complement) BSUB0012 Z99115 g2634715 Bacillus subtilis 1423 -11531324 7500952175 ypbh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to negative regulation of competence meca) (le:7480) (re:8064) (di:complement) BSUB0013 Z99116 g2634732 Bacillus subtilis 1423 -11531324 216711 ypbh (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146205 Bacillus subtilis 1423 -11531324 7502851712 ypbh (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146205 Bacillus subtilis 1423 -11531324 6500727466 hypothetical protein:hypothetical 22.2 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbH ypbH Bacillus subtilis 1423 -11531324

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804176	5049	27205	285	95

Description

5000689206 hypothetical protein:hypothetical 28.6 kd protein in recq-cmk intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbG ypbG Bacillus subtilis 1423 -11531325 115514 ypbg (de:hypothetical 28.6 kd protein in recq-cmk intergenic region precursor) (db:swissprot) YPBG_BACSU P50733 BACILLUS SUBTILIS 1423 -11531325 7000688199 ypbg conserved hypothetical protein ypbg (cl:probable phosphoesterase yaei:phosphoesterase core homology) (db:pir2.dat) B69933 B69933 Bacillus subtilis 1423 -11531325 6000685518 ypbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (nt:similar to hypothetical proteins) (le:207943) (re:208722) (di:complement) BSUB0012 Z99115 g2634716 Bacillus subtilis 1423 -11531325 7500952174 ypbg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:8223) (re:9002) (di:complement) BSUB0013 Z99116 g2634733 Bacillus subtilis 1423 -11531325 216710 ypbg (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146204 Bacillus subtilis 1423 -11531325 7502851713 ypbg (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146204 Bacillus subtilis 1423 -11531325 6500727467 hypothetical protein:hypothetical 28.6 kd protein in recq-cmk intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbG ypbG Bacillus subtilis 1423 -11531325

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804182	5050	27206	276	91

Description

5000689205 hypothetical protein:hypothetical 17.9 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbF ypbF Bacillus subtilis 1423 -11531326 115513 ypbf (de:hypothetical 17.9 kd protein in recq-cmk intergenic region) (db:swissprot) YPBF_BACSU P50732 BACILLUS SUBTILIS 1423 -11531326 7000688198 ypbf hypothetical protein ypbf (db:pir2.dat) A69933 A69933 Bacillus subtilis 1423 -11531326 6000685516 ypbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:208808) (re:209251) (di:complement) BSUB0012 Z99115 g2634717 Bacillus subtilis 1423 -11531326 7500952173 ypbf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:9088) (re:9531) (di:complement) BSUB0013 Z99116 g2634734 Bacillus subtilis 1423 -11531326 216709 ypbf (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146203 Bacillus subtilis 1423 -11531326 7502851714 ypbf (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146203 Bacillus subtilis 1423 -11531326 6500727468 hypothetical protein:hypothetical 17.9 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbF ypbF Bacillus subtilis 1423 -11531326

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804183	5051	27207	1020	339

Description

5000689204 hypothetical protein:hypothetical 27.3 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbE ypbE Bacillus subtilis 1423 -11531327 115512 ypbe (de:hypothetical 27.3 kd protein in recq-cmk intergenic region) (db:swissprot) YPBE_BACSU P50731 BACILLUS SUBTILIS 1423 -11531327 7000688197 ypbe hypothetical protein ypbe (db:pir2.dat) H69932 H69932 Bacillus subtilis 1423 -11531327 6000685514 ypbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:209314) (re:210036) (di:complement) BSUB0012 Z99115 g2634718 Bacillus subtilis 1423 -11531327 7500952172 ypbe (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:9594) (re:10316) (di:complement) BSUB0013 Z99116 g2634735 Bacillus subtilis 1423 -11531327 216708 ypbe (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146202 Bacillus subtilis 1423 -11531327 7502851715 ypbe (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146202 Bacillus subtilis 1423 -11531327 6500727469 hypothetical protein:hypothetical 27.3 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbE ypbE Bacillus subtilis 1423 -11531327

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804190	5052	27208	432	143

Description

5000689203 hypothetical protein:hypothetical 22.0 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbD ypbD Bacillus subtilis 1423 -11531328 115511 ypbd (de:hypothetical 22.0 kd protein in recq-cmk intergenic region) (db:swissprot) YPBD_BACSU P50730 BACILLUS SUBTILIS 1423 -11531328 7000688196 ypbd hypothetical protein ypbd (db:pir2.dat) G69932 G69932 Bacillus subtilis 1423 -11531328 6000685512 ypbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:209987) (re:210556) (di:complement) BSUB0012 Z99115 g2634719 Bacillus subtilis 1423 -11531328 7500952171 ypbd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:10267) (re:10836) (di:complement) BSUB0013 Z99116 g2634736 Bacillus subtilis 1423 -11531328 216707 ypbd (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146201 Bacillus subtilis 1423 -11531328 7502851716 ypbd (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146201 Bacillus subtilis 1423 -11531328 6500727470 hypothetical protein:hypothetical 22.0 kd protein in recq-cmk intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbD ypbD Bacillus subtilis 1423 -11531328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804193	5053	27209	339	112

Description

5000689202 hypothetical protein:hypothetical 40.7 kd protein in fer-recq intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbB ypbB Bacillus subtilis 1423 -11531329 115510 ypbb (de:hypothetical 40.7 kd protein in fer-recq intergenic region) (db:swissprot) YPBB_BACSU P50728 BACILLUS SUBTILIS 1423 -11531329 7000688195 ypbb hypothetical protein ypbb (db:pir2.dat) F69932 F69932 Bacillus subtilis 1423 -11531329 6000685510 ypbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.) (le:212099) (re:213157) (di:complement) BSUB0012 Z99115 g2634721 Bacillus subtilis 1423 -11531329 7500952170 ypbb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:12379) (re:13437) (di:complement) BSUB0013 Z99116 g2634738 Bacillus subtilis 1423 -11531329 216705 ypbb (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146199 Bacillus subtilis 1423 -11531329 7502851717 ypbb (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146199 Bacillus subtilis 1423 -11531329 6500727471 hypothetical protein:hypothetical 40.7 kd protein in fer-recq intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypbB ypbB Bacillus subtilis 1423 -11531329

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804198	5054	27210	1395	464

Description

5000689201 hypothetical protein:hypothetical 20.5 kd protein in sera-fer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypaA ypaA Bacillus subtilis 1423 -11531330 115500 ypaa (de:hypothetical 20.5 kd protein in sera-fer intergenic region) (db:swissprot) YPAA_BACSU P50726 BACILLUS SUBTILIS 1423 -11531330 7000688194 ypaa hypothetical protein ypaa (db:pir2.dat) E69932 E69932 Bacillus subtilis 1423 -11531330 7500952169 ypaa (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:13991) (re:14563) (di:complement) BSUB0013 Z99116 g2634740 Bacillus subtilis 1423 -11531330 216703 ypaa (db:genpept-bct2) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine... BACSERA L47648 g1146197 Bacillus subtilis 1423 -11531330 7502851718 ypaa (db:genpept) (de:bacillus subtilis phosphoglycerate dehydrogenase (sera), ypaa,ferredoxin (fer), ypbb, recs, ypbd, ypbe, ypbf, ypbg, ypbh,glutamate dehydrogenase (ypca), ypda, ypdb, ypdc, spore cortexlytic enzyme (sleb), ypeb, ypfa, ypfb, cytidine mono... BACSERA L47648 g1146197 Bacillus subtilis 1423 -11531330 6500727472 hypothetical protein:hypothetical 20.5 kd protein in sera-fer intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypaA ypaA Bacillus subtilis 1423 -11531330

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804200	5055	27211	1110	369

Description

6500727473 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypzE ypzE Bacillus subtilis 1423 -11531331 7000693844 ypze hypothetical protein ypze (db:pir2.dat) H69943 H69943 Bacillus subtilis 1423 -11531331 7500964657 ypze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:14669) (re:14833) (di:complement) BSUB0013 Z99116 g2634741 Bacillus subtilis 1423 -11531331

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804221	5056	27212	279	92

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804222	5057	27213	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804223	5058	27214	927	308

Description

5000689625 hypothetical protein:hypothetical 41.3 kd protein in dacb-aroc intergenic region:orfx21 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuN ypuN Bacillus subtilis 1423 -11531332 115760 ypun (de:hypothetical 41.3 kd protein in dacb-aroc intergenic region (orfx21)) (db:swissprot) YPUN_BACSU P35166 BACILLUS SUBTILIS 1423 -11531332 7000688279 ypun hypothetical protein ypun (db:pir2.dat) S45562 S45562 Bacillus subtilis 1423 -11531332 7500952312 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx21) (le:24918) (re:26024) (di:direct) BACDIA L09228 g410144 Bacillus subtilis 1423 -11531332 215523 ypun (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to negative regulator of sigma-x activity) (le:17559) (re:18665) (di:complement) BSUB0013 Z99116 g2634744 Bacillus subtilis 1423 -11531332 170277 ypun hypothetical protein ypun (db:pir) S45562 S45562 Bacillus subtilis 1423 -11531332 6500727474 hypothetical protein:hypothetical 41.3 kd protein in dacb-aroc intergenic region:orfx21 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuN ypuN Bacillus subtilis 1423 -11531332

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804225	5059	27215	717	238

Description

5000689624 hypothetical protein:hypothetical 26.0 kd protein in spmb-aroc intergenic region:orfx13 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuL ypuL Bacillus subtilis 1423 -11531333 115758 rlub (ec:4.2.1.70) (de:(pseudouridylate synthase) (uracil hydrolyase)) (db:swissprot) RLUB_BACSU P35159 BACILLUS SUBTILIS 1423 -11531333 7000688278 ypul conserved hypothetical protein ypul (cl:conserved hypothetical protein hi1243) (db:pir2.dat) S45555 S45555 Bacillus subtilis 1423 -11531333 7500952311 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx13) (le:17440) (re:18129) (di:direct) BACDIA L09228 g410137 Bacillus subtilis 1423 -11531333 215516 ypul (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:25454) (re:26143) (di:complement) BSUB0013 Z99116 g2634751 Bacillus subtilis 1423 -11531333 170268 ypul conserved hypothetical protein ypul (db:pir) S45555 S45555 Bacillus subtilis 1423 -11531333 6500727475 hypothetical protein:hypothetical 26.0 kd protein in spmb-aroc intergenic region:orfx13 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuL ypuL Bacillus subtilis 1423 -11531333

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804228	5060	27216	366	121

Description

5000689623 hypothetical protein:hypothetical 20.4 kd protein in ribt-dacb intergenic region:orfx9 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuI ypuI Bacillus subtilis 1423 -11531334 115757 ypui (de:hypothetical 20.4 kd protein in ribt-dacb intergenic region (orfx9)) (db:swissprot) YPUI_BACSU P35156 BACILLUS SUBTILIS 1423 -11531334 7000688277 ypui conserved hypothetical protein ypui:dacb 5-region hypothetical protein:hypothetical protein x9 (db:pir2.dat) S45551 S45551 Bacillus subtilis 1423 -11531334 7500952310 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx9) (le:14416) (re:14955) (di:direct) BACDIA L09228 g410133 Bacillus subtilis 1423 -11531334 215512 ypui (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:28628) (re:29167) (di:complement) BSUB0013 Z99116 g2634755 Bacillus subtilis 1423 -11531334 169950 ypui conserved hypothetical protein ypui:dacb 5-region hypothetical protein:hypothetical protein x9 (db:pir) S45551 S45551 Bacillus subtilis 1423 -11531334 6500727476 hypothetical protein:hypothetical 20.4 kd protein in ribt-dacb intergenic region:orfx9 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuI ypuI Bacillus subtilis 1423 -11531334

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804237	5061	27217	195	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804241	5062	27218	660	219

Description

5000689622 hypothetical protein:hypothetical 22.0 kd protein in ribt-dacb intergenic region:orfx8 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuH ypuH Bacillus subtilis 1423 -11531335 115756 ypuh (de:hypothetical 22.0 kd protein in ribt-dacb intergenic region (orfx8)) (db:swissprot) YPUH_BACSU P35155 BACILLUS SUBTILIS 1423 -11531335 7000688276 ypuh conserved hypothetical protein ypuh (db:pir2.dat) S45550 S45550 Bacillus subtilis 1423 -11531335 7500952309 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx8) (le:13768) (re:14361) (di:direct) BACDIA L09228 g410132 Bacillus subtilis 1423 -11531335 215511 ypuh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:29222) (re:29815) (di:complement) BSUB0013 Z99116 g2634756 Bacillus subtilis 1423 -11531335 170280 ypuh conserved hypothetical protein ypuh (db:pir) S45550 S45550 Bacillus subtilis 1423 -11531335 6500727477 hypothetical protein:hypothetical 22.0 kd protein in ribt-dacb intergenic region:orfx8 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuH ypuH Bacillus subtilis 1423 -11531335

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804265	5063	27219	831	276

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804272	5064	27220	315	104

Description

5000689621 hypothetical protein:hypothetical 29.6 kd protein in ribt-dacb intergenic region:orfx7 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuG ypuG Bacillus subtilis 1423 -11531336 115755 ypug (de:hypothetical 29.6 kd protein in ribt-dacb intergenic region (orfx7)) (db:swissprot) YPUG_BACSU P35154 BACILLUS SUBTILIS 1423 -11531336 7000688275 ypug conserved hypothetical protein ypug (db:pir2.dat) S45549 S45549 Bacillus subtilis 1423 -11531336 7500952308 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx7) (le:13023) (re:13778) (di:direct) BACDIA L09228 g410131 Bacillus subtilis 1423 -11531336 215510 ypug (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:29805) (re:30560) (di:complement) BSUB0013 Z99116 g2634757 Bacillus subtilis 1423 -11531336 170279 ypug conserved hypothetical protein ypug (db:pir) S45549 S45549 Bacillus subtilis 1423 -11531336 6500727478 hypothetical protein:hypothetical 29.6 kd protein in ribt-dacb intergenic region:orfx7 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuG ypuG Bacillus subtilis 1423 -11531336

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804292	5065	27221	1152	384

Description

5000689620 hypothetical protein:hypothetical 21.0 kd protein in ribt-dacb intergenic region:orfx6 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuF ypuF Bacillus subtilis 1423 -11531337 215509 ypuf (de:hypothetical 21.0 kd protein in ribt-dacb intergenic region (orfx6)) (db:swissprot) YPUF_BACSU P17617 BACILLUS SUBTILIS 1423 -11531337 7000688274 ypuf hypothetical protein ypuf (db:pir2.dat) S45548 S45548 Bacillus subtilis 1423 -11531337 7500952307 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx6) (le:12218) (re:12742) (di:complement) BACDIA L09228 g410130 Bacillus subtilis 1423 -11531337 219582 (db:genpept-bct1) (de:b.subtilis riboflavin biosynthesis operon ribg, ribb, riba, ribh,and ribt genes.) (nt:orf y (aa 1-174)) (le:5164) (re:5688) (di:complement) BSRIB X51510 g580916 Bacillus subtilis 1423 -11531337 7502851719 ypuf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:30841) (re:31365) (di:direct) BSUB0013 Z99116 g2634758 Bacillus subtilis 1423 -11531337 115754 ypuf (de:hypothetical 21.0 kd protein in ribt-dacb intergenic region (orfx6)) (db:swissprot) YPUF_BACSU P17617 BACILLUS SUBTILIS 1423 -11531337 170278 ypuf hypothetical protein ypuf (db:pir) S45548 S45548 Bacillus subtilis 1423 -11531337 6500727479 hypothetical protein:hypothetical 21.0 kd protein in ribt-dacb intergenic region:orfx6 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuF ypuF Bacillus subtilis 1423 -11531337

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804296	5066	27222	1050	349

Description

5000689619 hypothetical protein:hypothetical 6.0 kd protein in sips-ribg intergenic region:orfx5 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuE ypuE Bacillus subtilis 1423 -11531338 115751 ypue (de:hypothetical 6.0 kd protein in sips-ribg intergenic region (orfx5)) (db:swissprot) YPUE_BACSU P35153 BACILLUS SUBTILIS 1423 -11531338 7000688273 ypue hypothetical protein ypue:hypothetical 6k protein ribo region:hypothetical protein x5 (db:pir2.dat) PN0101 PN0101 Bacillus subtilis 1423 -11531338 7500952306 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx5) (le:8132) (re:8284) (di:direct) BACDIA L09228 g410124 Bacillus subtilis 1423 -11531338 215503 ypue (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:35299) (re:35451) (di:complement) BSUB0013 Z99116 g2634764 Bacillus subtilis 1423 -11531338 170049 ypue hypothetical protein ypue:hypothetical 6k protein ribo region:hypothetical protein x5 (db:pir) PN0101 PN0101 Bacillus subtilis 1423 -11531338 6500727480 hypothetical protein:hypothetical 6.0 kd protein in sips-ribg intergenic region:orfx5 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuE ypuE Bacillus subtilis 1423 -11531338

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804298	5067	27223	1341	446

Description

5000689618 hypothetical protein:hypothetical 12.8 kd protein in sips-ribg intergenic region:orfx4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuD ypuD Bacillus subtilis 1423 -11531339 215502 ypud (de:hypothetical 12.8 kd protein in sips-ribg intergenic region (orfx4)) (db:swissprot) YPUD_BACSU P17616 BACILLUS SUBTILIS 1423 -11531339 7000688272 ypud hypothetical protein ypud (db:pir2.dat) S45541 S45541 Bacillus subtilis 1423 -11531339 7500952305 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx4) (le:7529) (re:7873) (di:direct) BACDIA L09228 g410123 Bacillus subtilis 1423 -11531339 219576 (db:genpept-bct1) (de:b.subtilis riboflavin biosynthesis operon ribg, ribb, riba, ribh,and ribt genes.) (nt:orf x (aa 1-114)) (le:475) (re:819) (di:direct) BSRIB X51510 g40084 Bacillus subtilis 1423 -11531339 7502851720 ypud (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:35710) (re:36054) (di:complement) BSUB0013 Z99116 g2634765 Bacillus subtilis 1423 -11531339 115750 ypud (de:hypothetical 12.8 kd protein in sips-ribg intergenic region (orfx4)) (db:swissprot) YPUD_BACSU P17616 BACILLUS SUBTILIS 1423 -11531339 170171 ypud hypothetical protein ypud (db:pir) S45541 S45541 Bacillus subtilis 1423 -11531339 6500727481 hypothetical protein:hypothetical 12.8 kd protein in sips-ribg intergenic region:orfx4 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuD ypuD Bacillus subtilis 1423 -11531339

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804326	5068	27224	1155	385

Description

6500727482 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypzC ypzC Bacillus subtilis 1423 -11531340 7000693843 ypzc hypothetical protein ypzc (db:pir2.dat) F69943 F69943 Bacillus subtilis 1423 -11531340 7500964656 ypzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:37110) (re:37346) (di:direct) BSUB0013 Z99116 g2634767 Bacillus subtilis 1423 -11531340

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804330	5069	27225	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804331	5070	27226	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804332	5071	27227	432	143

Description

5000689617 hypothetical protein:hypothetical 14.8 kd protein in ppib-sips intergenic region:orfx2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuC ypuC Bacillus subtilis 1423 -11531341 115749 ypuc (de:hypothetical 14.8 kd protein in ppib-sips intergenic region (orfx2)) (db:swissprot) YPUC_BACSU P35152 BACILLUS SUBTILIS 1423 -11531341 7000688271 ypuc hypothetical protein ypuc (db:pir2.dat) S45539 S45539 Bacillus subtilis 1423 -11531341 7500952304 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx2) (le:5445) (re:5834) (di:direct) BACDIA L09228 g410121 Bacillus subtilis 1423 -11531341 215500 ypuc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:37749) (re:38138) (di:complement) BSUB0013 Z99116 g2634768 Bacillus subtilis 1423 -11531341 170275 ypuc hypothetical protein ypuc (db:pir) S45539 S45539 Bacillus subtilis 1423 -11531341 6500727483 hypothetical protein:hypothetical 14.8 kd protein in ppib-sips intergenic region:orfx2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuC ypuC Bacillus subtilis 1423 -11531341

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804334	5072	27228	684	228

Description

5000689616 hypothetical protein:hypothetical 7.2 kd protein in ppib-sips intergenic region:orfx1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuB ypuB Bacillus subtilis 1423 -11531342 115746 ypub (de:hypothetical 7.2 kd protein in ppib-sips intergenic region (orfx1)) (db:swissprot) YPUB_BACSU P35151 BACILLUS SUBTILIS 1423 -11531342 7000688270 ypub hypothetical protein ypub (db:pir2.dat) S45538 S45538 Bacillus subtilis 1423 -11531342 7500952303 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx1) (le:5264) (re:5467) (di:direct) BACDIA L09228 g410120 Bacillus subtilis 1423 -11531342 215499 ypub (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:38116) (re:38319) (di:complement) BSUB0013 Z99116 g2634769 Bacillus subtilis 1423 -11531342 170266 ypub hypothetical protein ypub (db:pir) S45538 S45538 Bacillus subtilis 1423 -11531342 6500727484 hypothetical protein:hypothetical 7.2 kd protein in ppib-sips intergenic region:orfx1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuB ypuB Bacillus subtilis 1423 -11531342

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804338	5073	27229	504	167

Description

6500727485 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypzD ypzD Bacillus subtilis 1423 -11531343 7000692712 ypzd conserved hypothetical protein ypzd (db:pir2.dat) G69943 G69943 Bacillus subtilis 1423 -11531343 7500963797 ypzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:38985) (re:39197) (di:direct) BSUB0013 Z99116 g2634770 Bacillus subtilis 1423 -11531343

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804341	5074	27230	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804351	5075	27231	510	169

Description

GTC ORF with score 93 to: (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae multicopy suppressor of mrtg2-5 (zds1)gene, nuclear gene encoding mitochondrial protein, complete cds.) (nt:gene also called rtg2s1, ces1, nrc1; highly charged)...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804360	5076	27232	342	113

Description

5000689615 hypothetical protein:hypothetical 31.3 kd protein in lysa-ppib intergenic region:orfx19 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuA ypuA Bacillus subtilis 1423 -11531344 115745 ypua (de:hypothetical 31.3 kd protein in lysa-ppib intergenic region (orfx19)) (db:swissprot) YPUA_BACSU P31847 BACILLUS SUBTILIS 1423 -11531344 170274 ypua ypua protein (db:pir2.dat) JU0473 S45536 Bacillus subtilis 1423 -11531344 7500952302 (sr:bacillus subtilis (strain 168, sub_species marburg) dna) (db:genpept-bct1) (de:bacillus subtilis spova to sera region.) (nt:orfx19) (le:2693) (re:3565) (di:complement) BACDIA L09228 g410118 Bacillus subtilis 1423 -11531344 215497 ypua (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:40018) (re:40890) (di:direct) BSUB0013 Z99116 g2634772 Bacillus subtilis 1423 -11531344 7000688269 ypua ypua protein (db:pir) JU0473 JU0473 Bacillus subtilis 1423 -11531344 6500727486 hypothetical protein:hypothetical 31.3 kd protein in lysa-ppib intergenic region:orfx19 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) ypuA ypuA Bacillus subtilis 1423 -11531344

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804384	5077	27233	387	128

Description

5000689384 hypothetical protein:ferric uptake regulation protein homolog 2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkL yqkL Bacillus subtilis 1423 -11531345 72534 yqkl (de:ferric uptake regulation protein homolog 2) (db:swissprot) FUR2_BACSU P54574 BACILLUS SUBTILIS 1423 -11531345 7000685334 yqkl transcription regulator fur family homolog yqkl (cl:ferric uptake regulator) (db:pir2.dat) E69967 E69967 Bacillus subtilis 1423 -11531345 216237 yqkl (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:269361) (re:269810) (di:direct) BACJH642 D84432 g1303993 Bacillus subtilis 1423 -11531345 7500881917 yqkl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to transcriptional regulator (fur family)) (le:53809) (re:54258) (di:complement) BSUB0013 Z99116 g2634787 Bacillus subtilis 1423 -11531345 6500727487 hypothetical protein:ferric uptake regulation protein homolog 2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkL yqkL Bacillus subtilis 1423 -11531345

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804385	5078	27234	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804390	5079	27235	888	295

Description

5000689383 hypothetical protein:hypothetical 8.1 kd protein in ansb-spoiim intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkK yqkK Bacillus subtilis 1423 -11531346 116006 yqkk (de:hypothetical 8.1 kd protein in ansb-spoiim intergenic region) (db:swissprot) YQKK_BACSU P54573 BACILLUS SUBTILIS 1423 -11531346 7000688491 yqkk hypothetical protein yqkk (db:pir2.dat) D69967 D69967 Bacillus subtilis 1423 -11531346 216235 yqkk (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:268288) (re:268503) (di:direct) BACJH642 D84432 g1303991 Bacillus subtilis 1423 -11531346 7500952564 yqkk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:55116) (re:55331) (di:complement) BSUB0013 Z99116 g2634789 Bacillus subtilis 1423 -11531346 6500727488 hypothetical protein:hypothetical 8.1 kd protein in ansb-spoiim intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkK yqkK Bacillus subtilis 1423 -11531346

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804403	5080	27236	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804414	5081	27237	309	102

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804432	5082	27238	183	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804438	5083	27239	828	275

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804444	5084	27240	1560	520

Description

5000689382 hypothetical protein:hypothetical na+/h+ antiporter in ansb-spoiim intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkI yqkI Bacillus subtilis 1423 -11531347 116005 yqki (de:hypothetical na+/h+ antiporter in ansb-spoiim intergenic region) (db:swissprot) YQKI_BACSU P54571 BACILLUS SUBTILIS 1423 -11531347 7000688490 yqki na+/h+ antiporter homolog yqki (cl:na+/h+-exchanging protein) (db:pir2.dat) B69967 B69967 Bacillus subtilis 1423 -11531347 216233 yqki (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:265445) (re:266851) (di:direct) BACJH642 D84432 g1303989 Bacillus subtilis 1423 -11531347 7500952563 yqki (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to na+/h+ antiporter) (le:56768) (re:58174) (di:complement) BSUB0013 Z99116 g2634791 Bacillus subtilis 1423 -11531347 6500727489 hypothetical protein:hypothetical na+/h+ antiporter in ansb-spoiim intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkI yqkI Bacillus subtilis 1423 -11531347

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804485	5085	27241	1338	445

Description

6500727490 yqkh:yqxk hypothetical protein:hypothetical 32.2 kd protein in bmru-ansr intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxK yqxK Bacillus subtilis 1423 -11531348 116034 yqxk:yqkh (de:hypothetical 32.2 kd protein in bmru-ansr intergenic region (orf2)) (db:swissprot) YQXK_BACSU P38423 BACILLUS SUBTILIS 1423 -11531348 7000688499 yqxk conserved hypothetical protein yqxk:orf2 5 of ansr (db:pir2.dat) E69968 E69968 Bacillus subtilis 1423 -11531348 216229 yqkh (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:261418) (re:262302) (di:direct) BACJH642 D84432 g1303985 Bacillus subtilis 1423 -11531348 7500952576 yqxk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqkh; similar to hypothetical) (le:61317) (re:62201) (di:complement) BSUB0013 Z99116 g2634795 Bacillus subtilis 1423 -11531348 5000689683 (de:(yqxk) (pn:hypothetical 32:hypothetical protein in ansr 5"region:orf2:fragment) (gn:yqkh) (gtcfc:13.07) (ec:) (yqxk_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxK yqxK Bacillus subtilis 1423 10057760

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804495	5086	27242	294	98

Description

5000689381 hypothetical protein:hypothetical 21.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkG yqkG Bacillus subtilis 1423 -11531349 116004 yqkg (de:hypothetical 21.0 kd protein in glnq-ansr intergenic region) (db:swissprot) YQKG_BACSU P54570 BACILLUS SUBTILIS 1423 -11531349 7000688489 yqkg conserved hypothetical protein yqkg (cl:yffh protein:mutt domain homology) (db:pir2.dat) A69967 A69967 Bacillus subtilis 1423 -11531349 216228 yqkg (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:260584) (re:261141) (di:direct) BACJH642 D84432 g1303984 Bacillus subtilis 1423 -11531349 7500952562 yqkg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:62478) (re:63035) (di:complement) BSUB0013 Z99116 g2634796 Bacillus subtilis 1423 -11531349 6500727491 hypothetical protein:hypothetical 21.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkG yqkG Bacillus subtilis 1423 -11531349

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804498	5087	27243	396	131

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804499	5088	27244	324	107

Description

5000689380 hypothetical protein:hypothetical oxidoreductase in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkF yqkF Bacillus subtilis 1423 -11531350 116003 yqkf (de:hypothetical oxidoreductase in ansr-bmru intergenic region) (db:swissprot) YQKF_BACSU P54569 BACILLUS SUBTILIS 1423 -11531350 7000688488 yqkf conserved hypothetical protein yqkf (db:pir2.dat) H69966 H69966 Bacillus subtilis 1423 -11531350 216227 yqkf (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:259404) (re:260324) (di:complement) BACJH642 D84432 g1303983 Bacillus subtilis 1423 -11531350 7500952561 yqkf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:63295) (re:64215) (di:direct) BSUB0013 Z99116 g2634797 Bacillus subtilis 1423 -11531350 6500727492 hypothetical protein:hypothetical oxidoreductase in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkF yqkF Bacillus subtilis 1423 -11531350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804501	5089	27245	255	84

Description

5000689379 hypothetical protein:hypothetical 9.1 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkE yqkE Bacillus subtilis 1423 -11531351 116002 yqke (de:hypothetical 9.1 kd protein in glnq-ansr intergenic region) (db:swissprot) YQKE_BACSU P54568 BACILLUS SUBTILIS 1423 -11531351 7000688487 yqke hypothetical protein yqke (db:pir2.dat) G69966 G69966 Bacillus subtilis 1423 -11531351 216226 yqke (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:259148) (re:259372) (di:direct) BACJH642 D84432 g1303982 Bacillus subtilis 1423 -11531351 7500952560 yqke (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:64247) (re:64471) (di:complement) BSUB0013 Z99116 g2634798 Bacillus subtilis 1423 -11531351 6500727493 hypothetical protein:hypothetical 9.1 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkE yqkE Bacillus subtilis 1423 -11531351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804517	5090	27246	639	212

Description

GTC ORF with score 328 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.).) (nt:orf_id:o332#10; similar to (swissprot accession) (le:10741) (re:11985) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804518	5091	27247	432	143

Description

5000689378 hypothetical protein:hypothetical 34.6 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkD yqkD Bacillus subtilis 1423 -11531352 116001 yqkd (de:hypothetical 34.6 kd protein in glnq-ansr intergenic region) (db:swissprot) YQKD_BACSU P54567 BACILLUS SUBTILIS 1423 -11531352 7000688486 yqkd hypothetical protein yqkd (db:pir2.dat) F69966 F69966 Bacillus subtilis 1423 -11531352 216225 yqkd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:258069) (re:258986) (di:complement) BACJH642 D84432 g1303981 Bacillus subtilis 1423 -11531352 7500952559 yqkd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:64633) (re:65550) (di:direct) BSUB0013 Z99116 g2634799 Bacillus subtilis 1423 -11531352 6500727494 hypothetical protein:hypothetical 34.6 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkD yqkD Bacillus subtilis 1423 -11531352

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804532	5092	27248	1029	342

Description

5000689377 hypothetical protein:hypothetical 9.3 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkC yqkC Bacillus subtilis 1423 -11531353 116000 yqkc (de:hypothetical 9.3 kd protein in glnq-ansr intergenic region) (db:swissprot) YQKC_BACSU P54566 BACILLUS SUBTILIS 1423 -11531353 7000688485 yqkc hypothetical protein yqkc (db:pir2.dat) E69966 E69966 Bacillus subtilis 1423 -11531353 216224 yqkc (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:257790) (re:258029) (di:direct) BACJH642 D84432 g1303980 Bacillus subtilis 1423 -11531353 7500952558 yqkc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:65590) (re:65829) (di:complement) BSUB0013 Z99116 g2634800 Bacillus subtilis 1423 -11531353 6500727495 hypothetical protein:hypothetical 9.3 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkC yqkC Bacillus subtilis 1423 -11531353

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804533	5093	27249	546	181

Description

5000689376 hypothetical protein:hypothetical 11.8 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkB yqkB Bacillus subtilis 1423 -11531354 115999 yqkb (de:hypothetical 11.8 kd protein in glnq-ansr intergenic region) (db:swissprot) YQKB_BACSU P54565 BACILLUS SUBTILIS 1423 -11531354 7000688484 yqkb hypothetical protein yqkb (db:pir2.dat) D69966 D69966 Bacillus subtilis 1423 -11531354 216223 yqkb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:257454) (re:257777) (di:direct) BACJH642 D84432 g1303979 Bacillus subtilis 1423 -11531354 7500952557 yqkb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:65842) (re:66165) (di:complement) BSUB0013 Z99116 g2634801 Bacillus subtilis 1423 -11531354 6500727496 hypothetical protein:hypothetical 11.8 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkB yqkB Bacillus subtilis 1423 -11531354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804544	5094	27250	1233	410

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804551	5095	27251	504	167

Description

5000689375 hypothetical protein:hypothetical 39.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkA yqkA Bacillus subtilis 1423 -11531355 115998 yqka (de:hypothetical 39.0 kd protein in glnq-ansr intergenic region) (db:swissprot) YQKA_BACSU P54564 BACILLUS SUBTILIS 1423 -11531355 7000688483 yqka hypothetical protein yqka (db:pir2.dat) C69966 C69966 Bacillus subtilis 1423 -11531355 216222 yqka (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:256426) (re:257457) (di:direct) BACJH642 D84432 g1303978 Bacillus subtilis 1423 -11531355 7500952556 yqka (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:66162) (re:67193) (di:complement) BSUB0013 Z99116 g2634802 Bacillus subtilis 1423 -11531355 6500727497 hypothetical protein:hypothetical 39.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqkA yqkA Bacillus subtilis 1423 -11531355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804556	5096	27252	759	252

Description

5000689374 hypothetical protein:hypothetical 13.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjZ yqjZ Bacillus subtilis 1423 -11531356 115997 yqjz (de:hypothetical 13.0 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJZ_BACSU P54563 BACILLUS SUBTILIS 1423 -11531356 7000688482 yqjz hypothetical protein yqjz (db:pir2.dat) B69966 B69966 Bacillus subtilis 1423 -11531356 216221 yqjz (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:256089) (re:256433) (di:direct) BACJH642 D84432 g1303977 Bacillus subtilis 1423 -11531356 7500952555 yqjz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:67186) (re:67530) (di:complement) BSUB0013 Z99116 g2634803 Bacillus subtilis 1423 -11531356 6500727498 hypothetical protein:hypothetical 13.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjZ yqjZ Bacillus subtilis 1423 -11531356

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804574	5097	27253	1251	416

Description

5000689373 hypothetical protein:hypothetical 17.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjY yqjY Bacillus subtilis 1423 -11531357 115996 yqjy (de:hypothetical 17.9 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJY_BACSU P54562 BACILLUS SUBTILIS 1423 -11531357 7000688481 yqjy hypothetical protein yqjy (db:pir2.dat) A69966 A69966 Bacillus subtilis 1423 -11531357 216220 yqjy (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:255609) (re:256079) (di:direct) BACJH642 D84432 g1303976 Bacillus subtilis 1423 -11531357 7500952554 yqjy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:67540) (re:68010) (di:complement) BSUB0013 Z99116 g2634804 Bacillus subtilis 1423 -11531357 6500727499 hypothetical protein:hypothetical 17.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjY yqjY Bacillus subtilis 1423 -11531357

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804586	5098	27254	201	66

Description

5000689372 hypothetical protein:hypothetical 13.2 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjX yqjX Bacillus subtilis 1423 -11531358 115995 yqjx (de:hypothetical 13.2 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJX_BACSU P54561 BACILLUS SUBTILIS 1423 -11531358 7000688480 yqjx conserved hypothetical protein yqjx (db:pir2.dat) H69965 H69965 Bacillus subtilis 1423 -11531358 216219 yqjx (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:255085) (re:255423) (di:direct) BACJH642 D84432 g1303975 Bacillus subtilis 1423 -11531358 7500952553 yqjx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:68196) (re:68534) (di:complement) BSUB0013 Z99116 g2634805 Bacillus subtilis 1423 -11531358 6500727500 hypothetical protein:hypothetical 13.2 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjX yqjX Bacillus subtilis 1423 -11531358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804592	5099	27255	558	185

Description

5000689371 hypothetical protein:hypothetical 45.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjW yqjW Bacillus subtilis 1423 -11531359 115994 yqjw (de:hypothetical 45.9 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJW_BACSU P54560 BACILLUS SUBTILIS 1423 -11531359 7000688479 yqjw atp/gtp-binding protein homolog yqjw (cl:umuc protein) (db:pir2.dat) G69965 G69965 Bacillus subtilis 1423 -11531359 216218 yqjw (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:253850) (re:255088) (di:direct) BACJH642 D84432 g1303974 Bacillus subtilis 1423 -11531359 7500952552 yqjw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to atp/gtp-binding protein) (le:68531) (re:69769) (di:complement) BSUB0013 Z99116 g2634806 Bacillus subtilis 1423 -11531359 6500727501 hypothetical protein:hypothetical 45.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjW yqjW Bacillus subtilis 1423 -11531359

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804598	5100	27256	321	106

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804612	5101	27257	468	155

Description

6500727502 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzH yqzH Bacillus subtilis 1423 -11531360 7000693850 yqzh hypothetical protein yqzh (db:pir2.dat) G69969 G69969 Bacillus subtilis 1423 -11531360 7500964663 yqzh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:69935) (re:70141) (di:direct) BSUB0013 Z99116 g2634807 Bacillus subtilis 1423 -11531360

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804621	5102	27258	237	78

Description

5000689370 hypothetical protein:hypothetical 44.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjV yqjV Bacillus subtilis 1423 -11531361 115993 yqjv (de:hypothetical 44.7 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJV_BACSU P54559 BACILLUS SUBTILIS 1423 -11531361 7000688478 yqjv multidrug resistance protein homolog yqjv (db:pir2.dat) F69965 F69965 Bacillus subtilis 1423 -11531361 216217 yqjv (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:251697) (re:252929) (di:complement) BACJH642 D84432 g1303973 Bacillus subtilis 1423 -11531361 7500952551 yqjv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to multidrug resistance protein) (le:70690) (re:71922) (di:direct) BSUB0013 Z99116 g2634808 Bacillus subtilis 1423 -11531361 6500727503 hypothetical protein:hypothetical 44.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjV yqjV Bacillus subtilis 1423 -11531361

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804624	5103	27259	495	164

Description

6500727504 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjU yqjU Bacillus subtilis 1423 -11531362 7000693845 yqju hypothetical protein yqju (db:pir2.dat) E69965 E69965 Bacillus subtilis 1423 -11531362 7500964658 yqju (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:71940) (re:72131) (di:direct) BSUB0013 Z99116 g2634809 Bacillus subtilis 1423 -11531362

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804629	5104	27260	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804630	5105	27261	759	252

Description

GTC ORF with score 115 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus long unique region, 80putative orf's and kaposin gene, complete cds.) (nt:orf 73; extensive ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804640	5106	27262	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804642	5107	27263	1395	464

Description

5000689368 hypothetical protein:hypothetical 15.2 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjT yqjT Bacillus subtilis 1423 -11531363 115991 yqjt (de:hypothetical 15.2 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJT_BACSU P54557 BACILLUS SUBTILIS 1423 -11531363 7000688477 yqjt hypothetical protein yqjt (db:pir2.dat) D69965 D69965 Bacillus subtilis 1423 -11531363 216215 yqjt (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:251105) (re:251491) (di:direct) BACJH642 D84432 g1303971 Bacillus subtilis 1423 -11531363 7500952550 yqjt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:72128) (re:72514) (di:complement) BSUB0013 Z99116 g2634810 Bacillus subtilis 1423 -11531363 6500727505 hypothetical protein:hypothetical 15.2 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjT yqjT Bacillus subtilis 1423 -11531363

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804648	5108	27264	414	137

Description

5000689367 hypothetical protein:hypothetical 33.6 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjS yqjS Bacillus subtilis 1423 -11531364 115990 yqjs (de:hypothetical 33.6 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJS_BACSU P54556 BACILLUS SUBTILIS 1423 -11531364 7000688476 yqjs pantothenate kinase homolog yqjs (cl:pantothenate kinase) (db:pir2.dat) C69965 C69965 Bacillus subtilis 1423 -11531364 216214 yqjs (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:250220) (re:251101) (di:direct) BACJH642 D84432 g1303970 Bacillus subtilis 1423 -11531364 7500952549 yqjs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to pantothenate kinase) (le:72518) (re:73399) (di:complement) BSUB0013 Z99116 g2634811 Bacillus subtilis 1423 -11531364 6500727506 hypothetical protein:hypothetical 33.6 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjS yqjS Bacillus subtilis 1423 -11531364

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804659	5109	27265	648	216

Description

6500727507 hypothetical protein:hypothetical oxidoreductase in glnq-ansr intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjQ yqjQ Bacillus subtilis 1423 -11531365 115989 yqjq (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YQJQ_BACSU P54554 BACILLUS SUBTILIS 1423 -11531365 7000688475 yqjq ketoacyl reductase homolog yqjq (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) A69965 A69965 Bacillus subtilis 1423 -11531365 216212 yqjq (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:247869) (re:248648) (di:direct) BACJH642 D84432 g1303968 Bacillus subtilis 1423 -11531365 7500952546 yqjq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to ketoacyl reductase) (le:74971) (re:75750) (di:complement) BSUB0013 Z99116 g2634813 Bacillus subtilis 1423 -11531365 5000689450 (de:(yqjq) (pn:hypothetical oxidoreductase in glnq-ansr intergenic region) (gtcfc:13.07) (ec:1.-.-.-) (yqjq_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yqjQ yqjQ Bacillus subtilis 1423 10057715

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804670	5110	27266	1380	459

Description

5000689366 hypothetical protein:hypothetical 35.8 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjP yqjP Bacillus subtilis 1423 -11531366 115988 yqjp (de:hypothetical 35.8 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJP_BACSU P54553 BACILLUS SUBTILIS 1423 -11531366 7000688474 yqjp hypothetical protein yqjp (db:pir2.dat) H69964 H69964 Bacillus subtilis 1423 -11531366 216211 yqjp (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:246904) (re:247863) (di:direct) BACJH642 D84432 g1303967 Bacillus subtilis 1423 -11531366 7500952545 yqjp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:75756) (re:76715) (di:complement) BSUB0013 Z99116 g2634814 Bacillus subtilis 1423 -11531366 6500727508 hypothetical protein:hypothetical 35.8 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjP yqjP Bacillus subtilis 1423 -11531366

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804671	5111	27267	474	157

Description

5000689365 hypothetical protein:pyrroline-5-carboxylate reductase homolog 2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjO yqjO Bacillus subtilis 1423 -11531367 91209 yqjo (de:pyrroline-5-carboxylate reductase homolog 2) (db:swissprot) PROI_BACSU P54552 BACILLUS SUBTILIS 1423 -11531367 7000686183 yqjo pyrroline-5-carboxylate reductase homolog yqjo (cl:pyrroline-5-carboxylate reductase) (db:pir2.dat) G69964 G69964 Bacillus subtilis 1423 -11531367 216210 yqjo (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:245663) (re:246499) (di:complement) BACJH642 D84432 g1303966 Bacillus subtilis 1423 -11531367 7500888557 yqjo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to pyrroline-5-carboxylate reductase) (le:77120) (re:77956) (di:direct) BSUB0013 Z99116 g2634815 Bacillus subtilis 1423 -11531367 6500727509 hypothetical protein:pyrroline-5-carboxylate reductase homolog 2 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjO yqjO Bacillus subtilis 1423 -11531367

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804677	5112	27268	810	269

Description

5000689364 hypothetical protein:hypothetical 61.8 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjN yqjN Bacillus subtilis 1423 -11531368 115987 yqjn (de:hypothetical 61.8 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJN_BACSU P54551 BACILLUS SUBTILIS 1423 -11531368 7000688473 yqjn amino acid degradation homolog yqjn (db:pir2.dat) F69964 F69964 Bacillus subtilis 1423 -11531368 216209 yqjn (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:243979) (re:245622) (di:direct) BACJH642 D84432 g1303965 Bacillus subtilis 1423 -11531368 7500952544 yqjn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to amino acid degradation) (le:77997) (re:79640) (di:complement) BSUB0013 Z99116 g2634816 Bacillus subtilis 1423 -11531368 6500727510 hypothetical protein:hypothetical 61.8 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjN yqjN Bacillus subtilis 1423 -11531368

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804690	5113	27269	465	154

Description

GTC ORF with score 119 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone t4l20 (essaiiproject).) (nt:similarity to daucus carota somatic embryogenesis) (le:2017:2609:2881:3449) (re:2554:2731:3360:3568) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804695	5114	27270	276	91

Description

6500727511 hypothetical protein:probable nadh-dependent flavin oxidoreductase yqjm (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjM yqjM Bacillus subtilis 1423 -11531369 115986 yqjm (ec:1.-.-.-) (de:probable nadh-dependent flavin oxidoreductase yqjm,) (db:swissprot) YQJM_BACSU P54550 BACILLUS SUBTILIS 1423 -11531369 7000688472 yqjm nadh-dependent flavin oxidoreductase homolog yqjm (db:pir2.dat) E69964 E69964 Bacillus subtilis 1423 -11531369 216208 yqjm (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:242791) (re:243807) (di:complement) BACJH642 D84432 g1303964 Bacillus subtilis 1423 -11531369 7500952543 yqjm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to nadh-dependent flavin oxidoreductase) (le:79812) (re:80828) (di:direct) BSUB0013 Z99116 g2634817 Bacillus subtilis 1423 -11531369 5000689449 (de:(yqjm) (pn:probable nadh-dependent flavin oxidoreductase yqjm) (gtcfc:13.07) (ec:1.-.-.-) (yqjm_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yqjM yqjM Bacillus subtilis 1423 10057712

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804697	5115	27271	204	68

Description

5000689363 hypothetical protein:hypothetical 28.2 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjL yqjL Bacillus subtilis 1423 -11531370 115985 yqjl (de:hypothetical 28.2 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJL_BACSU P54549 BACILLUS SUBTILIS 1423 -11531370 7000688471 yqjl conserved hypothetical protein yqjl (db:pir2.dat) D69964 D69964 Bacillus subtilis 1423 -11531370 216207 yqjl (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:241920) (re:242681) (di:complement) BACJH642 D84432 g1303963 Bacillus subtilis 1423 -11531370 7500952542 yqjl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:80938) (re:81699) (di:direct) BSUB0013 Z99116 g2634818 Bacillus subtilis 1423 -11531370 6500727512 hypothetical protein:hypothetical 28.2 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjL yqjL Bacillus subtilis 1423 -11531370

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804707	5116	27272	309	102

Description

5000689362 hypothetical protein:hypothetical 34.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjK yqjK Bacillus subtilis 1423 -11531371 115984 yqjk (de:hypothetical 34.0 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJK_BACSU P54548 BACILLUS SUBTILIS 1423 -11531371 7000688470 yqjk conserved hypothetical protein yqjk (cl:conserved hypothetical protein mj1502) (db:pir2.dat) C69964 C69964 Bacillus subtilis 1423 -11531371 216206 yqjk (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:240721) (re:241644) (di:direct) BACJH642 D84432 g1303962 Bacillus subtilis 1423 -11531371 7500952537 yqjk (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:81975) (re:82898) (di:complement) BSUB0013 Z99116 g2634819 Bacillus subtilis 1423 -11531371 6500727513 hypothetical protein:hypothetical 34.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjK yqjK Bacillus subtilis 1423 -11531371

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804710	5117	27273	486	161

Description

5000689361 hypothetical protein:hypothetical 44.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjI yqjI Bacillus subtilis 1423 -11531372 115983 yqji (de:hypothetical 44.9 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJI_BACSU P54546 BACILLUS SUBTILIS 1423 -11531372 7000688467 yqji 6-phosphogluconate dehydrogenase pentose homolog yqji (cl:phosphogluconate dehydrogenase (decarboxylating):3-hydroxyisobutyrate dehydrogenase homology) (db:pir2.dat) A69964 A69964 Bacillus subtilis 1423 -11531372 216204 yqji (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:237682) (re:238902) (di:direct) BACJH642 D84432 g1303960 Bacillus subtilis 1423 -11531372 7500952535 yqji (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to 6-phosphogluconate dehydrogenase) (le:84717) (re:85937) (di:complement) BSUB0013 Z99116 g2634821 Bacillus subtilis 1423 -11531372 6500727514 hypothetical protein:hypothetical 44.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjI yqjI Bacillus subtilis 1423 -11531372

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804711	5118	27274	453	150

Description

5000689360 hypothetical protein:hypothetical 47.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjH yqjH Bacillus subtilis 1423 -11531373 115982 yqjh (de:hypothetical 47.0 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJH_BACSU P54545 BACILLUS SUBTILIS 1423 -11531373 7000688464 yqjh dna-damage repair protein homolog yqjh (cl:umuc protein) (db:pir2.dat) H69963 H69963 Bacillus subtilis 1423 -11531373 216203 yqjh (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:236138) (re:237382) (di:direct) BACJH642 D84432 g1303959 Bacillus subtilis 1423 -11531373 7500952533 yqjh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to dna-damage repair protein) (le:86237) (re:87481) (di:complement) BSUB0013 Z99116 g2634822 Bacillus subtilis 1423 -11531373 6500727515 hypothetical protein:hypothetical 47.0 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjH yqjH Bacillus subtilis 1423 -11531373

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804725	5119	27275	528	175

Description

5000689359 hypothetical protein:hypothetical 30.7 kd lipoprotein in glnq-ansr intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjG yqjG Bacillus subtilis 1423 -11531374 115980 yqjg (de:precursor) (db:swissprot) YQJG_BACSU P54544 BACILLUS SUBTILIS 1423 -11531374 7000688462 yqjg lipoprotein spoiiij-like homolog yqjg (cl:stage iii sporulation protein:stage iii sporulation protein homology) (db:pir2.dat) G69963 G69963 Bacillus subtilis 1423 -11531374 216202 yqjg (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:234919) (re:235746) (di:complement) BACJH642 D84432 g1303958 Bacillus subtilis 1423 -11531374 7500952531 yqjg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to lipoprotein spoiiij-like) (le:87873) (re:88700) (di:direct) BSUB0013 Z99116 g2634823 Bacillus subtilis 1423 -11531374 6500727516 hypothetical protein:hypothetical 30.7 kd lipoprotein in glnq-ansr intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjG yqjG Bacillus subtilis 1423 -11531374

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804735	5120	27276	219	72

Description

5000689358 hypothetical protein:hypothetical 23.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjF yqjF Bacillus subtilis 1423 -11531375 115978 yqjf (de:hypothetical 23.9 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJF_BACSU P54543 BACILLUS SUBTILIS 1423 -11531375 7000688460 yqjf conserved hypothetical protein yqjf (db:pir2.dat) F69963 F69963 Bacillus subtilis 1423 -11531375 216201 yqjf (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:234110) (re:234739) (di:complement) BACJH642 D84432 g1303957 Bacillus subtilis 1423 -11531375 7500952529 yqjf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:88880) (re:89509) (di:direct) BSUB0013 Z99116 g2634824 Bacillus subtilis 1423 -11531375 6500727517 hypothetical protein:hypothetical 23.9 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjF yqjF Bacillus subtilis 1423 -11531375

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804738	5121	27277	246	81

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804747	5122	27278	189	62

Description

5000689357 hypothetical protein:hypothetical 39.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjE yqjE Bacillus subtilis 1423 -11531376 115976 yqje (de:hypothetical 39.7 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJE_BACSU P54542 BACILLUS SUBTILIS 1423 -11531376 7000688458 yqje tripeptidase homolog yqje (db:pir2.dat) E69963 E69963 Bacillus subtilis 1423 -11531376 216200 yqje (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:232856) (re:233971) (di:direct) BACJH642 D84432 g1303956 Bacillus subtilis 1423 -11531376 7500952527 yqje (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to tripeptidase) (le:89648) (re:90763) (di:complement) BSUB0013 Z99116 g2634825 Bacillus subtilis 1423 -11531376 6500727518 hypothetical protein:hypothetical 39.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjE yqjE Bacillus subtilis 1423 -11531376

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804749	5123	27279	672	223

Description

5000689356 hypothetical protein:hypothetical 15.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjC yqjC Bacillus subtilis 1423 -11531377 115973 yqjc (de:hypothetical 15.7 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJC_BACSU P54540 BACILLUS SUBTILIS 1423 -11531377 7000688456 yqjc conserved hypothetical protein yqjc (cl:hypothetical protein af2218) (db:pir2.dat) C69963 C69963 Bacillus subtilis 1423 -11531377 216198 yqjc (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:230899) (re:231321) (di:direct) BACJH642 D84432 g1303954 Bacillus subtilis 1423 -11531377 7500952522 yqjc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:92298) (re:92720) (di:complement) BSUB0013 Z99116 g2634827 Bacillus subtilis 1423 -11531377 6500727519 hypothetical protein:hypothetical 15.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjC yqjC Bacillus subtilis 1423 -11531377

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804754	5124	27280	192	64

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804761	5125	27281	255	84

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804775	5126	27282	1119	372

Description

GTC ORF with score 125 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vrl) (de:kaposi's sarcoma-associated herpesvirus long unique region, 80putative orf's and kaposin gene, complete cds.) (nt:orf 73; extensive ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804784	5127	27283	723	240

Description

GTC ORF with score 221 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to s.cerevisiae hypothetical 105.9 kd) (le:35939:36599) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804791	5128	27284	315	104

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804792	5129	27285	240	79

Description

5000689355 hypothetical protein:hypothetical 19.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjB yqjB Bacillus subtilis 1423 -11531378 115971 yqjb (de:hypothetical 19.7 kd protein in glnq-ansr intergenic region) (db:swissprot) YQJB_BACSU P54539 BACILLUS SUBTILIS 1423 -11531378 7000688454 yqjb conserved hypothetical protein yqjb (db:pir2.dat) B69963 B69963 Bacillus subtilis 1423 -11531378 216197 yqjb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:230167) (re:230697) (di:direct) BACJH642 D84432 g1303953 Bacillus subtilis 1423 -11531378 7500952520 yqjb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:92922) (re:93452) (di:complement) BSUB0013 Z99116 g2634828 Bacillus subtilis 1423 -11531378 6500727520 hypothetical protein:hypothetical 19.7 kd protein in glnq-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjB yqjB Bacillus subtilis 1423 -11531378

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804809	5130	27286	525	174

Description

5000689354 hypothetical protein:hypothetical 37.1 kd protein in bmru-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjA yqjA Bacillus subtilis 1423 -11531379 115969 yqja (de:hypothetical 37.1 kd protein in bmru-ansr intergenic region) (db:swissprot) YQJA_BACSU P54538 BACILLUS SUBTILIS 1423 -11531379 7000688452 yqja hypothetical protein yqja (db:pir2.dat) A69963 A69963 Bacillus subtilis 1423 -11531379 216196 yqja (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:229147) (re:230115) (di:direct) BACJH642 D84432 g1303952 Bacillus subtilis 1423 -11531379 7500952518 yqja (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:93504) (re:94472) (di:complement) BSUB0013 Z99116 g2634829 Bacillus subtilis 1423 -11531379 6500727521 hypothetical protein:hypothetical 37.1 kd protein in bmru-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqjA yqjA Bacillus subtilis 1423 -11531379

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804819	5131	27287	561	186

Description

GTC ORF with score 102 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c18h9.) (nt:similar to glycoprotein x; data from yk13h8.3 and) (le:87:1166:1363:1488:1606) (re:1121:1305:1440:1559:1810) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804828	5132	27288	618	205

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804838	5133	27289	504	168

Description

GTC ORF with score 249 to: (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae putative acyltransferase (slc1) gene andputative la homolog (yla1) gene, complete cds.) (nt:complements e.coli mutant defective in) (le:1430) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804845	5134	27290	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804848	5135	27291	270	89

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804859	5136	27292	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804861	5137	27293	219	72

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804868	5138	27294	951	316

Description

5000689350 hypothetical protein:hypothetical 16.2 kd protein in bmru-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiW yqiW Bacillus subtilis 1423 -11531380 115965 yqiw (de:hypothetical 16.2 kd protein in bmru-ansr intergenic region) (db:swissprot) YQIW_BACSU P54534 BACILLUS SUBTILIS 1423 -11531380 7000688448 yqiw conserved hypothetical protein yqiw (db:pir2.dat) E69962 E69962 Bacillus subtilis 1423 -11531380 216192 yqiw (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:226148) (re:226585) (di:direct) BACJH642 D84432 g1303948 Bacillus subtilis 1423 -11531380 7500952514 yqiw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:97034) (re:97471) (di:complement) BSUB0013 Z99116 g2634833 Bacillus subtilis 1423 -11531380 6500727522 hypothetical protein:hypothetical 16.2 kd protein in bmru-ansr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiW yqiW Bacillus subtilis 1423 -11531380

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804892	5139	27295	1380	459

Description

GTC ORF with score 247 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c14f5.) (nt:spbc14f5.07, unknown; integral membrane protein,) (le:17309:17437:17541:17665) (re:17382:17475:17614:21206) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804897	5140	27296	981	326

Description

6500727523 hypothetical protein:putative branched-chain-fatty-acid kinase (gtcfc:14.1) (ec:2.7.2.14) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiU yqiU Bacillus subtilis 1423 -11531381 61455 yqiu (ec:2.7.2.14) (de:putative branched-chain-fatty-acid kinase,) (db:swissprot) BCFK_BACSU P54532 BACILLUS SUBTILIS 1423 -11531381 7000684688 yqiu branched-chain fatty-acid kinase homolog yqiu (db:pir2.dat) C69962 C69962 Bacillus subtilis 1423 -11531381 216184 yqiu (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:217003) (re:218094) (di:direct) BACJH642 D84432 g1303940 Bacillus subtilis 1423 -11531381 7500877712 yqiu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to branched-chain fatty-acid kinase) (le:105525) (re:106616) (di:complement) BSUB0013 Z99116 g2634841 Bacillus subtilis 1423 -11531381 5000689448 (de:(yqiu) (pn:putative branched-chain-fatty-acid kinase) (gtcfc:13.07) (ec:2.7.2.14) (bcfk_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yqiU yqiU Bacillus subtilis 1423 10004164

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804908	5141	27297	435	144

Description

5000689349 hypothetical protein:putative sigma l-dependent transcriptional regulator in mmge-bfmbaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiR yqiR Bacillus subtilis 1423 -11531382 115964 yqir (de:intergenic region) (db:swissprot) YQIR_BACSU P54529 BACILLUS SUBTILIS 1423 -11531382 7000688447 yqir transcription regulator sigma-l-dependent homolog yqir (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) H69961 H69961 Bacillus subtilis 1423 -11531382 216181 yqir (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:212776) (re:214854) (di:direct) BACJH642 D84432 g1303937 Bacillus subtilis 1423 -11531382 7500952513 yqir (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to transcriptional regulator) (le:108765) (re:110843) (di:complement) BSUB0013 Z99116 g2634844 Bacillus subtilis 1423 -11531382 6500727524 hypothetical protein:putative sigma l-dependent transcriptional regulator in mmge-bfmbaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiR yqiR Bacillus subtilis 1423 -11531382

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804910	5142	27298	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804911	5143	27299	570	189

Description

GTC ORF with score 116 to: (db:genpept-inv) (de:litomosoides sigmodontis microfilarial sheath proteins shp3a(shp3a) and shp3 (shp3) genes, complete cds.) (nt:structural protein; similar to shp3 genes from) (le:7991:8260) (re:8047:9219) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804912	5144	27300	486	161

Description

6500727525 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzF yqzF Bacillus subtilis 1423 -11531383 7000693848 yqzf hypothetical protein yqzf (db:pir2.dat) E69969 E69969 Bacillus subtilis 1423 -11531383 7500964661 yqzf (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:110996) (re:111232) (di:direct) BSUB0013 Z99116 g2634845 Bacillus subtilis 1423 -11531383

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804917	5145	27301	234	77

Description

5000689348 hypothetical protein:hypothetical 33.1 kd protein in mmge-bfmbaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiQ yqiQ Bacillus subtilis 1423 -11531384 115963 yqiq (de:hypothetical 33.1 kd protein in mmge-bfmbaa intergenic region) (db:swissprot) YQIQ_BACSU P54528 BACILLUS SUBTILIS 1423 -11531384 7000688446 yqiq phosphoenolpyruvate mutase homolog yqiq (cl:carboxyphosphonoenolpyruvate phosphonomutase) (db:pir2.dat) G69961 G69961 Bacillus subtilis 1423 -11531384 216180 yqiq (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:211440) (re:212345) (di:direct) BACJH642 D84432 g1303936 Bacillus subtilis 1423 -11531384 7500952512 yqiq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to phosphoenolpyruvate mutase) (le:111274) (re:112179) (di:complement) BSUB0013 Z99116 g2634846 Bacillus subtilis 1423 -11531384 6500727526 hypothetical protein:hypothetical 33.1 kd protein in mmge-bfmbaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiQ yqiQ Bacillus subtilis 1423 -11531384

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804921	5146	27302	318	105

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804924	5147	27303	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804929	5148	27304	897	298

Description

5000689347 hypothetical protein:hypothetical 27.0 kd protein in spo0a-mmga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiK yqiK Bacillus subtilis 1423 -11531385 115962 yqik (de:hypothetical 27.0 kd protein in spo0a-mmga intergenic region) (db:swissprot) YQIK_BACSU P54527 BACILLUS SUBTILIS 1423 -11531385 7000688445 yqik glycerophosphodiester phosphodiesterase homolog yqik (db:pir2.dat) F69961 F69961 Bacillus subtilis 1423 -11531385 216174 yqik (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:204751) (re:205470) (di:direct) BACJH642 D84432 g1303930 Bacillus subtilis 1423 -11531385 7500952511 yqik (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to glycerophosphodiester phosphodiesterase) (le:118149) (re:118868) (di:complement) BSUB0013 Z99116 g2634852 Bacillus subtilis 1423 -11531385 6500727527 hypothetical protein:hypothetical 27.0 kd protein in spo0a-mmga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiK yqiK Bacillus subtilis 1423 -11531385

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804948	5149	27305	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501804979	5150	27306	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805005	5151	27307	249	82

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805006	5152	27308	336	111

Description

6500727528 yqii:yqii hypothetical protein:similar to n-acetylmuramoyl-l-alanine amidase (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiI yqiI Bacillus subtilis 1423 -11531386 7000694283 yqii n-acetylmuramoyl-l-alanine amidase homolog yqii (db:pir2.dat) E69961 E69961 Bacillus subtilis 1423 -11531386 7500964994 yqii (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqii; similar to) (le:118947) (re:119567) (di:complement) BSUB0013 Z99116 g2634853 Bacillus subtilis 1423 -11531386

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805007	5153	27309	216	71

Description

6500727529 yzpa:yqih hypothetical protein:hypothetical lipoprotein in spo0a-mmga intergenic region precursor:pspb9 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiH yqiH Bacillus subtilis 1423 -11531387 115959 yqih (de:(pspb9')) (db:swissprot) YQIH_BACSU P40770 BACILLUS SUBTILIS 1423 -11531387 7000688440 yqih lipoprotein homolog yqih (cl:bacillus subtilis major autolysin secretion protein lyta) (db:pir2.dat) D69961 D69961 Bacillus subtilis 1423 -11531387 216171 yqih (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:203746) (re:204039) (di:direct) BACJH642 D84432 g1303927 Bacillus subtilis 1423 -11531387 7500952508 yqih (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yzpa; similar to lipoprotein) (le:119582) (re:119875) (di:complement) BSUB0013 Z99116 g2634854 Bacillus subtilis 1423 -11531387 5000689344 (de:(yqih) (pn:hypothetical lipoprotein in spo0a-mmga intergenic region precursor:pspb9") (gtcfc:13.07) (ec:) (yqih_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqiH yqiH Bacillus subtilis 1423 10057685

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805026	5154	27310	1011	337

Description

GTC ORF with score 380 to: (fn:controls entry of the cell into the asexual) (db:genpept-pln2) (de:neurospora crassa protein kinase nrc-2 (nrc-2) gene, complete cds.) (nt:similar to kad5 from schizzosaccharomyces pombe;) (le:81:953:1322:1766) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805035	5155	27311	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805039	5156	27312	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805067	5157	27313	228	75

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805068	5158	27314	1794	597

Description

6500727530 hypothetical protein:probable nadh-dependent flavin oxidoreductase yqig (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiG yqiG Bacillus subtilis 1423 -11531388 115958 yqig (ec:1.-.-.-) (de:probable nadh-dependent flavin oxidoreductase yqig,) (db:swissprot) YQIG_BACSU P54524 BACILLUS SUBTILIS 1423 -11531388 7000688438 yqig nadh-dependent flavin oxidoreductase homolog yqig (db:pir2.dat) C69961 C69961 Bacillus subtilis 1423 -11531388 216170 yqig (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:202096) (re:203214) (di:complement) BACJH642 D84432 g1303926 Bacillus subtilis 1423 -11531388 7500952504 yqig (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to nadh-dependent flavin oxidoreductase) (le:120407) (re:121525) (di:direct) BSUB0013 Z99116 g2634855 Bacillus subtilis 1423 -11531388 5000689447 (de:(yqig) (pn:probable nadh-dependent flavin oxidoreductase yqig) (gtcfc:13.07) (ec:1.-.-.-) (yqig_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yqiG yqiG Bacillus subtilis 1423 10057684

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805073	5159	27315	594	197

Description

6500727531 yqif:yqxc hypothetical protein:hypothetical 29.7 kd protein in fold-ahrc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxC yqxC Bacillus subtilis 1423 -11531389 116027 yqxc:yqif (de:hypothetical 29.7 kd protein in fold-ahrc intergenic region) (db:swissprot) YQXC_BACSU P19672 BACILLUS SUBTILIS 1423 -11531389 7000688493 yqxc hemolysin homolog yqxc:hypothetical protein 65 ahrc 5 region (cl:hemolysin homolog yqxc) (db:pir2.dat) G69967 G69967 Bacillus subtilis 1423 -11531389 216165 yqif (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:195889) (re:196698) (di:direct) BACJH642 D84432 g1303921 Bacillus subtilis 1423 -11531389 7500952570 yqxc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqif; similar to) (le:126923) (re:127732) (di:complement) BSUB0013 Z99116 g2634860 Bacillus subtilis 1423 -11531389 5000689677 (de:(yqxc) (pn:hypothetical 29:hypothetical protein in ahrc 5"region:fragment) (gn:yqif) (gtcfc:13.07) (ec:) (yqxc_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxC yqxC Bacillus subtilis 1423 10057753

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805080	5160	27316	240	79

Description

5000689343 hypothetical protein:hypothetical 69.6 kd protein in fold-ahrc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiE yqiE Bacillus subtilis 1423 -11531390 115955 dxs (de:probable 1-deoxyxylulose-5-phosphate synthase (dxp synthase)) (db:swissprot) DXS_BACSU P54523 BACILLUS SUBTILIS 1423 -11531390 7000688436 yqie conserved hypothetical protein yqie (cl:hypothetical protein c2814) (db:pir2.dat) B69961 B69961 Bacillus subtilis 1423 -11531390 216164 yqie (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:193991) (re:195892) (di:direct) BACJH642 D84432 g1303920 Bacillus subtilis 1423 -11531390 7500880716 yqie (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:127729) (re:129630) (di:complement) BSUB0013 Z99116 g2634861 Bacillus subtilis 1423 -11531390 6500727532 hypothetical protein:hypothetical 69.6 kd protein in fold-ahrc intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiE yqiE Bacillus subtilis 1423 -11531390

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805104	5161	27317	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805128	5162	27318	1383	460

Description

6500727533 hypothetical protein:putative exodeoxyribonuclease small subunit:exonuclease vii small subunit (gtcfc:14.1) (ec:3.1.11.6) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiC yqiC Bacillus subtilis 1423 -11531391 70783 yqic (ec:3.1.11.6) (de:vii small subunit)) (db:swissprot) EX7S_BACSU P54522 BACILLUS SUBTILIS 1423 -11531391 7000685205 yqic exodeoxyribonuclease vii small subunit homolog yqic (cl:exodeoxyribonuclease vii small chain) (db:pir2.dat) H69960 H69960 Bacillus subtilis 1423 -11531391 216162 yqic (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:192772) (re:192936) (di:direct) BACJH642 D84432 g1303918 Bacillus subtilis 1423 -11531391 7500881227 yqic (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to exodeoxyribonuclease vii (small) (le:130685) (re:130849) (di:complement) BSUB0013 Z99116 g2634863 Bacillus subtilis 1423 -11531391 5000689446 (de:(yqic) (pn:putative exodeoxyribonuclease small subunit:exonuclease vii small subunit) (gtcfc:13.07) (ec:3.1.11.6) (ex7s_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yqiC yqiC Bacillus subtilis 1423 10013358

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805130	5163	27319	534	178

Description

6500727534 hypothetical protein:putative exodeoxyribonuclease large subunit:exonuclease vii large subunit (gtcfc:14.1) (ec:3.1.11.6) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqiB yqiB Bacillus subtilis 1423 -11531392 70780 yqib (ec:3.1.11.6) (de:vii large subunit)) (db:swissprot) EX7L_BACSU P54521 BACILLUS SUBTILIS 1423 -11531392 7000685203 yqib exodeoxyribonuclease vii large subunit homolog yqib (cl:exodeoxyribonuclease vii) (db:pir2.dat) G69960 G69960 Bacillus subtilis 1423 -11531392 216161 yqib (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:191340) (re:192686) (di:direct) BACJH642 D84432 g1303917 Bacillus subtilis 1423 -11531392 7500881224 yqib (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to exodeoxyribonuclease vii (large) (le:130935) (re:132281) (di:complement) BSUB0013 Z99116 g2634864 Bacillus subtilis 1423 -11531392 5000689445 (de:(yqib) (pn:putative exodeoxyribonuclease large subunit:exonuclease vii large subunit) (gtcfc:13.07) (ec:3.1.11.6) (ex7l_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yqiB yqiB Bacillus subtilis 1423 10013355

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805145	5164	27320	1656	552

Description

5000689342 hypothetical protein:n utilization substance protein b homolog:nusb protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhZ yqhZ Bacillus subtilis 1423 -11531393 87238 yqhz (de:n utilization substance protein b homolog (nusb protein)) (db:swissprot) NUSB_BACSU P54520 BACILLUS SUBTILIS 1423 -11531393 7000686020 yqhz transcription termination homolog yqhz (cl:nusb protein) (db:pir2.dat) F69960 F69960 Bacillus subtilis 1423 -11531393 216159 yqhz (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:189944) (re:190339) (di:direct) BACJH642 D84432 g1303915 Bacillus subtilis 1423 -11531393 7500887012 yqhz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to transcription termination) (le:133282) (re:133677) (di:complement) BSUB0013 Z99116 g2634866 Bacillus subtilis 1423 -11531393 6500727535 hypothetical protein:n utilization substance protein b homolog:nusb protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhZ yqhZ Bacillus subtilis 1423 -11531393

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805151	5165	27321	1017	338

Description

5000689341 hypothetical protein:hypothetical 14.7 kd protein in accc-fold intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhY yqhY Bacillus subtilis 1423 -11531394 115941 yqhy (de:hypothetical 14.7 kd protein in accc-fold intergenic region) (db:swissprot) YQHY_BACSU P54519 BACILLUS SUBTILIS 1423 -11531394 7000688433 yqhy conserved hypothetical protein yqhy (db:pir2.dat) E69960 E69960 Bacillus subtilis 1423 -11531394 216158 yqhy (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:189273) (re:189680) (di:direct) BACJH642 D84432 g1303914 Bacillus subtilis 1423 -11531394 7500952495 yqhy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:133941) (re:134348) (di:complement) BSUB0013 Z99116 g2634867 Bacillus subtilis 1423 -11531394 6500727536 hypothetical protein:hypothetical 14.7 kd protein in accc-fold intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhY yqhY Bacillus subtilis 1423 -11531394

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805152	5166	27322	192	63

Description

6500727537 yqge:yqhv hypothetical protein:hypothetical 9.9 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhV yqhV Bacillus subtilis 1423 -11531395 115940 yqhv:yqge (de:hypothetical 9.9 kd protein in gcvt-spoiiiaa intergenic region) (db:swissprot) YQHV_BACSU P49779 BACILLUS SUBTILIS 1423 -11531395 7000688432 yqhv hypothetical protein yqhv (db:pir2.dat) D69960 D69960 Bacillus subtilis 1423 -11531395 216147 yqhv (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:181635) (re:181916) (di:direct) BACJH642 D84432 g1303903 Bacillus subtilis 1423 -11531395 219973 (db:genpept-bct1) (de:bacillus subtilis spoiiia locus, complete cds.) (nt:orf; method: conceptual translation supplied by) (le:290) (re:571) (di:direct) BSU35252 U35252 g1000358 Bacillus subtilis 1423 -11531395 7500952494 yqhv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqge) (le:141705) (re:141986) (di:complement) BSUB0013 Z99116 g2634878 Bacillus subtilis 1423 -11531395 5000689340 (de:(yqhv) (pn:hypothetical 9) (gn:yqge) (gtcfc:13.07) (ec:) (yqhv_bacsu) (keggfc:11.2) (db:gtc-bacillus subtilis)) yqhV yqhV Bacillus subtilis 1423 10057666

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805154	5167	27323	354	117

Description

6500727538 hypothetical protein:putative peptidase in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (ec:3.4.-.-) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhT yqhT Bacillus subtilis 1423 -11531396 115939 yqht (ec:3.4.-.-) (de:putative peptidase in gcvt-spoiiiaa intergenic region,) (db:swissprot) YQHT_BACSU P54518 BACILLUS SUBTILIS 1423 -11531396 7000688431 yqht xaa-pro dipeptidase homolog yqht (cl:x-pro aminopeptidase) (db:pir2.dat) C69960 C69960 Bacillus subtilis 1423 -11531396 216145 yqht (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:179847) (re:180908) (di:direct) BACJH642 D84432 g1303901 Bacillus subtilis 1423 -11531396 7500952493 yqht (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to xaa-pro dipeptidase) (le:142713) (re:143774) (di:complement) BSUB0013 Z99116 g2634880 Bacillus subtilis 1423 -11531396

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805164	5168	27324	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805178	5169	27325	435	144

Description

5000689338 hypothetical protein:hypothetical 20.2 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhR yqhR Bacillus subtilis 1423 -11531397 115938 yqhr (de:hypothetical 20.2 kd protein in gcvt-spoiiiaa intergenic region) (db:swissprot) YQHR_BACSU P54516 BACILLUS SUBTILIS 1423 -11531397 7000688430 yqhr hypothetical protein yqhr (db:pir2.dat) A69960 A69960 Bacillus subtilis 1423 -11531397 216143 yqhr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:178781) (re:179317) (di:direct) BACJH642 D84432 g1303899 Bacillus subtilis 1423 -11531397 7500952492 yqhr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:144304) (re:144840) (di:complement) BSUB0013 Z99116 g2634882 Bacillus subtilis 1423 -11531397 6500727539 hypothetical protein:hypothetical 20.2 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhR yqhR Bacillus subtilis 1423 -11531397

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805180	5170	27326	822	273

Description

5000689337 hypothetical protein:hypothetical 36.0 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhQ yqhQ Bacillus subtilis 1423 -11531398 115937 yqhq (de:hypothetical 36.0 kd protein in gcvt-spoiiiaa intergenic region) (db:swissprot) YQHQ_BACSU P54515 BACILLUS SUBTILIS 1423 -11531398 7000688429 yqhq hypothetical protein yqhq (db:pir2.dat) H69959 H69959 Bacillus subtilis 1423 -11531398 216142 yqhq (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:177598) (re:178554) (di:complement) BACJH642 D84432 g1303898 Bacillus subtilis 1423 -11531398 7500952491 yqhq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:145067) (re:146023) (di:direct) BSUB0013 Z99116 g2634883 Bacillus subtilis 1423 -11531398 6500727540 hypothetical protein:hypothetical 36.0 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhQ yqhQ Bacillus subtilis 1423 -11531398

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805183	5171	27327	1443	481

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805192	5172	27328	279	92

Description

5000689336 hypothetical protein:hypothetical 14.6 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhP yqhP Bacillus subtilis 1423 -11531399 115936 yqhp (de:hypothetical 14.6 kd protein in gcvt-spoiiiaa intergenic region) (db:swissprot) YQHP_BACSU P54514 BACILLUS SUBTILIS 1423 -11531399 7000688428 yqhp hypothetical protein yqhp (db:pir2.dat) G69959 G69959 Bacillus subtilis 1423 -11531399 216141 yqhp (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:177163) (re:177558) (di:complement) BACJH642 D84432 g1303897 Bacillus subtilis 1423 -11531399 7500952490 yqhp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:146063) (re:146458) (di:direct) BSUB0013 Z99116 g2634884 Bacillus subtilis 1423 -11531399 6500727541 hypothetical protein:hypothetical 14.6 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhP yqhP Bacillus subtilis 1423 -11531399

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805198	5173	27329	522	173

Description

5000689335 hypothetical protein:hypothetical 32.9 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhO yqhO Bacillus subtilis 1423 -11531400 115935 yqho (de:hypothetical 32.9 kd protein in gcvt-spoiiiaa intergenic region) (db:swissprot) YQHO_BACSU P54513 BACILLUS SUBTILIS 1423 -11531400 7000688427 yqho hypothetical protein yqho (db:pir2.dat) F69959 F69959 Bacillus subtilis 1423 -11531400 216140 yqho (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:176291) (re:177166) (di:direct) BACJH642 D84432 g1303896 Bacillus subtilis 1423 -11531400 7500952489 yqho (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:146455) (re:147330) (di:complement) BSUB0013 Z99116 g2634885 Bacillus subtilis 1423 -11531400 6500727542 hypothetical protein:hypothetical 32.9 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhO yqhO Bacillus subtilis 1423 -11531400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805204	5174	27330	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805205	5175	27331	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805206	5176	27332	645	214

Description

5000689334 hypothetical protein:hypothetical 16.7 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhN yqhN Bacillus subtilis 1423 -11531401 115934 yqhn (de:hypothetical 16.7 kd protein in gcvt-spoiiiaa intergenic region) (db:swissprot) YQHN_BACSU P54512 BACILLUS SUBTILIS 1423 -11531401 7000688426 yqhn transcription regulator homolog yqhn (cl:conserved hypothetical protein mj0568) (db:pir2.dat) E69959 E69959 Bacillus subtilis 1423 -11531401 216139 yqhn (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:175737) (re:176165) (di:direct) BACJH642 D84432 g1303895 Bacillus subtilis 1423 -11531401 7500952488 yqhn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to transcriptional regulator) (le:147456) (re:147884) (di:complement) BSUB0013 Z99116 g2634886 Bacillus subtilis 1423 -11531401 6500727543 hypothetical protein:hypothetical 16.7 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhN yqhN Bacillus subtilis 1423 -11531401

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805222	5177	27333	333	110

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805226	5178	27334	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805231	5179	27335	579	192

Description

6500727544 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhM yqhM Bacillus subtilis 1423 -11531402 7000692714 yqhm conserved hypothetical protein yqhm (db:pir2.dat) D69959 D69959 Bacillus subtilis 1423 -11531402 7500963799 yqhm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:147984) (re:148820) (di:complement) BSUB0013 Z99116 g2634887 Bacillus subtilis 1423 -11531402

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805236	5180	27336	186	62

Description

5000689332 hypothetical protein:hypothetical 14.6 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhL yqhL Bacillus subtilis 1423 -11531403 115932 yqhl (de:hypothetical 14.6 kd protein in gcvt-spoiiiaa intergenic region) (db:swissprot) YQHL_BACSU P54510 BACILLUS SUBTILIS 1423 -11531403 7000688425 yqhl glpe protein homolog yqhl (cl:glpe protein) (db:pir2.dat) C69959 C69959 Bacillus subtilis 1423 -11531403 216137 yqhl (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:174230) (re:174610) (di:complement) BACJH642 D84432 g1303893 Bacillus subtilis 1423 -11531403 7500952487 yqhl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:149011) (re:149391) (di:direct) BSUB0013 Z99116 g2634888 Bacillus subtilis 1423 -11531403 6500727545 hypothetical protein:hypothetical 14.6 kd protein in gcvt-spoiiiaa intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhL yqhL Bacillus subtilis 1423 -11531403

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805243	5181	27337	555	184

Description

5000689331 hypothetical protein:hypothetical helicase in sini-gcvt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhH yqhH Bacillus subtilis 1423 -11531404 115931 yqhh (de:hypothetical helicase in sini-gcvt intergenic region) (db:swissprot) YQHH_BACSU P54509 BACILLUS SUBTILIS 1423 -11531404 7000688424 yqhh snf2 helicase homolog yqhh (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) G69958 G69958 Bacillus subtilis 1423 -11531404 216133 yqhh (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:168157) (re:169830) (di:complement) BACJH642 D84432 g1303889 Bacillus subtilis 1423 -11531404 7500952482 yqhh (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to snf2 helicase) (le:153791) (re:155464) (di:direct) BSUB0013 Z99116 g2634892 Bacillus subtilis 1423 -11531404 6500727546 hypothetical protein:hypothetical helicase in sini-gcvt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhH yqhH Bacillus subtilis 1423 -11531404

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805247	5182	27338	1383	461

Description

5000689330 hypothetical protein:hypothetical 30.8 kd protein in sini-gcvt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhG yqhG Bacillus subtilis 1423 -11531405 115930 yqhg (de:hypothetical 30.8 kd protein in sini-gcvt intergenic region) (db:swissprot) YQHG_BACSU P54508 BACILLUS SUBTILIS 1423 -11531405 7000688423 yqhg hypothetical protein yqhg (db:pir2.dat) F69958 F69958 Bacillus subtilis 1423 -11531405 216132 yqhg (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:167342) (re:168136) (di:complement) BACJH642 D84432 g1303888 Bacillus subtilis 1423 -11531405 7500952478 yqhg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:155485) (re:156279) (di:direct) BSUB0013 Z99116 g2634893 Bacillus subtilis 1423 -11531405 6500727547 hypothetical protein:hypothetical 30.8 kd protein in sini-gcvt intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhG yqhG Bacillus subtilis 1423 -11531405

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805248	5183	27339	1290	429

Description

6500727548 yqhd:yqxm hypothetical protein:hypothetical 29.1 kd protein in comgg-sinr intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxM yqxM Bacillus subtilis 1423 -11531406 116036 yqxm:yqhd (de:hypothetical 29.1 kd protein in comgg-sinr intergenic region) (db:swissprot) YQXM_BACSU P40949 BACILLUS SUBTILIS 1423 -11531406 7000688501 yqxm hypothetical protein yqxm (db:pir2.dat) G69968 G69968 Bacillus subtilis 1423 -11531406 216127 yqhd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:164358) (re:165119) (di:direct) BACJH642 D84432 g1303883 Bacillus subtilis 1423 -11531406 7500952578 yqxm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqhd) (le:158502) (re:159263) (di:complement) BSUB0013 Z99116 g2634898 Bacillus subtilis 1423 -11531406 5000689685 (de:(yqxm) (pn:hypothetical 29:hypothetical protein in comg 3"region:fragment) (gn:yqhd) (gtcfc:13.07) (ec:) (yqxm_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxM yqxM Bacillus subtilis 1423 10057762

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805257	5184	27340	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805265	5185	27341	411	137

Description

6500727549 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzG yqzG Bacillus subtilis 1423 -11531407 7000693849 yqzg hypothetical protein yqzg (db:pir2.dat) F69969 F69969 Bacillus subtilis 1423 -11531407 7500964662 yqzg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:159535) (re:159861) (di:direct) BSUB0013 Z99116 g2634899 Bacillus subtilis 1423 -11531407

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805269	5186	27342	1176	391

Description

6500727550 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzE yqzE Bacillus subtilis 1423 -11531408 7000693847 yqze hypothetical protein yqze (db:pir2.dat) D69969 D69969 Bacillus subtilis 1423 -11531408 7500964660 yqze (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:159844) (re:160083) (di:complement) BSUB0013 Z99116 g2634900 Bacillus subtilis 1423 -11531408

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805282	5187	27343	408	135

Description

6500727551 yqhc:yqxl hypothetical protein:hypothetical 37.7 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxL yqxL Bacillus subtilis 1423 -11531409 116035 yqxl:yqhc (de:hypothetical 37.7 kd protein in soda-comga intergenic region) (db:swissprot) YQXL_BACSU P40948 BACILLUS SUBTILIS 1423 -11531409 7000688500 yqxl conserved hypothetical protein yqxl:hypothetical protein comg 5 region (db:pir2.dat) F69968 F69968 Bacillus subtilis 1423 -11531409 216120 yqhc (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:158162) (re:159115) (di:direct) BACJH642 D84432 g1303876 Bacillus subtilis 1423 -11531409 7500952577 yqxl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqhc; similar to hypothetical) (le:164506) (re:165459) (di:complement) BSUB0013 Z99116 g2634908 Bacillus subtilis 1423 -11531409 5000689684 (de:(yqxl) (pn:hypothetical 37:hypothetical protein in comg 5"region:fragment) (gn:yqhc) (gtcfc:13.07) (ec:) (yqxl_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxL yqxL Bacillus subtilis 1423 10057761

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805283	5188	27344	1116	371

Description

5000689327 hypothetical protein:hypothetical 50.0 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhB yqhB Bacillus subtilis 1423 -11531410 115927 yqhb (de:hypothetical 50.0 kd protein in soda-comga intergenic region) (db:swissprot) YQHB_BACSU P54505 BACILLUS SUBTILIS 1423 -11531410 7000688420 yqhb conserved hypothetical protein yqhb (cl:hypothetical protein hi0107) (db:pir2.dat) E69958 E69958 Bacillus subtilis 1423 -11531410 216119 yqhb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:156691) (re:158019) (di:complement) BACJH642 D84432 g1303875 Bacillus subtilis 1423 -11531410 7500952468 yqhb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:165602) (re:166930) (di:direct) BSUB0013 Z99116 g2634909 Bacillus subtilis 1423 -11531410 6500727552 hypothetical protein:hypothetical 50.0 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhB yqhB Bacillus subtilis 1423 -11531410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805300	5189	27345	1257	419

Description

5000689326 hypothetical protein:hypothetical 31.8 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhA yqhA Bacillus subtilis 1423 -11531411 115924 yqha (de:hypothetical 31.8 kd protein in soda-comga intergenic region) (db:swissprot) YQHA_BACSU P54504 BACILLUS SUBTILIS 1423 -11531411 7000688418 yqha conserved hypothetical protein yqha (db:pir2.dat) D69958 D69958 Bacillus subtilis 1423 -11531411 216118 yqha (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:155802) (re:156638) (di:direct) BACJH642 D84432 g1303874 Bacillus subtilis 1423 -11531411 7500952465 yqha (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:166983) (re:167819) (di:complement) BSUB0013 Z99116 g2634910 Bacillus subtilis 1423 -11531411 6500727553 hypothetical protein:hypothetical 31.8 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqhA yqhA Bacillus subtilis 1423 -11531411

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805313	5190	27346	243	80

Description

5000689325 hypothetical protein:hypothetical 14.8 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgZ yqgZ Bacillus subtilis 1423 -11531412 115922 yqgz (de:hypothetical 14.8 kd protein in soda-comga intergenic region) (db:swissprot) YQGZ_BACSU P54503 BACILLUS SUBTILIS 1423 -11531412 7000688417 yqgz conserved hypothetical protein yqgz (cl:hypothetical protein yjbd) (db:pir2.dat) C69958 C69958 Bacillus subtilis 1423 -11531412 216117 yqgz (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:155198) (re:155578) (di:direct) BACJH642 D84432 g1303873 Bacillus subtilis 1423 -11531412 7500952464 yqgz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:168043) (re:168423) (di:complement) BSUB0013 Z99116 g2634911 Bacillus subtilis 1423 -11531412 6500727554 hypothetical protein:hypothetical 14.8 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgZ yqgZ Bacillus subtilis 1423 -11531412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805318	5191	27347	279	92

Description

5000689324 hypothetical protein:hypothetical 9.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgY yqgY Bacillus subtilis 1423 -11531413 115921 yqgy (de:hypothetical 9.4 kd protein in soda-comga intergenic region) (db:swissprot) YQGY_BACSU P54502 BACILLUS SUBTILIS 1423 -11531413 7000688416 yqgy hypothetical protein yqgy (db:pir2.dat) B69958 B69958 Bacillus subtilis 1423 -11531413 216116 yqgy (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:154721) (re:154966) (di:complement) BACJH642 D84432 g1303872 Bacillus subtilis 1423 -11531413 7500952463 yqgy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:168655) (re:168900) (di:direct) BSUB0013 Z99116 g2634912 Bacillus subtilis 1423 -11531413 6500727555 hypothetical protein:hypothetical 9.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgY yqgY Bacillus subtilis 1423 -11531413

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805323	5192	27348	819	272

Description

5000689323 hypothetical protein:hypothetical 23.2 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgX yqgX Bacillus subtilis 1423 -11531414 115920 yqgx (de:hypothetical 23.2 kd protein in soda-comga intergenic region) (db:swissprot) YQGX_BACSU P54501 BACILLUS SUBTILIS 1423 -11531414 7000688415 yqgx conserved hypothetical protein yqgx (cl:glyoxalase) (db:pir2.dat) A69958 A69958 Bacillus subtilis 1423 -11531414 216115 yqgx (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:154046) (re:154681) (di:direct) BACJH642 D84432 g1303871 Bacillus subtilis 1423 -11531414 7500952462 yqgx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:168940) (re:169575) (di:complement) BSUB0013 Z99116 g2634913 Bacillus subtilis 1423 -11531414 6500727556 hypothetical protein:hypothetical 23.2 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgX yqgX Bacillus subtilis 1423 -11531414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805345	5193	27349	744	248

Description

5000689322 hypothetical protein:hypothetical 6.3 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgW yqgW Bacillus subtilis 1423 -11531415 115919 yqgw (de:hypothetical 6.3 kd protein in soda-comga intergenic region) (db:swissprot) YQGW_BACSU P54500 BACILLUS SUBTILIS 1423 -11531415 7000688414 yqgw hypothetical protein yqgw (db:pir2.dat) H69957 H69957 Bacillus subtilis 1423 -11531415 216114 yqgw (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:153715) (re:153888) (di:complement) BACJH642 D84432 g1303870 Bacillus subtilis 1423 -11531415 7500952461 yqgw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:169733) (re:169906) (di:direct) BSUB0013 Z99116 g2634914 Bacillus subtilis 1423 -11531415 6500727557 hypothetical protein:hypothetical 6.3 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgW yqgW Bacillus subtilis 1423 -11531415

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805347	5194	27350	426	142

Description

5000689321 hypothetical protein:hypothetical 10.5 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgV yqgV Bacillus subtilis 1423 -11531416 115918 yqgv (de:hypothetical 10.5 kd protein in soda-comga intergenic region) (db:swissprot) YQGV_BACSU P54499 BACILLUS SUBTILIS 1423 -11531416 7000688413 yqgv conserved hypothetical protein yqgv (db:pir2.dat) G69957 G69957 Bacillus subtilis 1423 -11531416 216113 yqgv (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:153370) (re:153654) (di:direct) BACJH642 D84432 g1303869 Bacillus subtilis 1423 -11531416 7500952460 yqgv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:169967) (re:170251) (di:complement) BSUB0013 Z99116 g2634915 Bacillus subtilis 1423 -11531416 6500727558 hypothetical protein:hypothetical 10.5 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgV yqgV Bacillus subtilis 1423 -11531416

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805349	5195	27351	366	121

Description

5000689320 hypothetical protein:hypothetical 40.3 kd lipoprotein in soda-comga intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgU yqgU Bacillus subtilis 1423 -11531417 115917 yqgu (de:precursor) (db:swissprot) YQGU_BACSU P54498 BACILLUS SUBTILIS 1423 -11531417 7000688412 yqgu hypothetical protein yqgu (db:pir2.dat) F69957 F69957 Bacillus subtilis 1423 -11531417 216112 yqgu (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:152306) (re:153367) (di:direct) BACJH642 D84432 g1303868 Bacillus subtilis 1423 -11531417 7500952459 yqgu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:170254) (re:171315) (di:complement) BSUB0013 Z99116 g2634916 Bacillus subtilis 1423 -11531417 6500727559 hypothetical protein:hypothetical 40.3 kd lipoprotein in soda-comga intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgU yqgU Bacillus subtilis 1423 -11531417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805355	5196	27352	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805363	5197	27353	624	208

Description

5000689319 hypothetical protein:hypothetical 43.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgT yqgT Bacillus subtilis 1423 -11531418 115916 yqgt (de:hypothetical 43.4 kd protein in soda-comga intergenic region) (db:swissprot) YQGT_BACSU P54497 BACILLUS SUBTILIS 1423 -11531418 7000688411 yqgt gamma-d-glutamyl-l-diamino acid endopeptid homolog yqgt (cl:endopeptidase i) (db:pir2.dat) E69957 E69957 Bacillus subtilis 1423 -11531418 216111 yqgt (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:151114) (re:152244) (di:direct) BACJH642 D84432 g1303867 Bacillus subtilis 1423 -11531418 7500952458 yqgt (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to gamma-d-glutamyl-l-diamino acid) (le:171377) (re:172507) (di:complement) BSUB0013 Z99116 g2634917 Bacillus subtilis 1423 -11531418 6500727560 hypothetical protein:hypothetical 43.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgT yqgT Bacillus subtilis 1423 -11531418

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805376	5198	27354	258	85

Description

5000689318 hypothetical protein:hypothetical 73.2 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgS yqgS Bacillus subtilis 1423 -11531419 115915 yqgs (de:hypothetical 73.2 kd protein in soda-comga intergenic region) (db:swissprot) YQGS_BACSU P54496 BACILLUS SUBTILIS 1423 -11531419 7000688410 yqgs conserved hypothetical protein yqgs (db:pir2.dat) D69957 D69957 Bacillus subtilis 1423 -11531419 216110 yqgs (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:149115) (re:151031) (di:direct) BACJH642 D84432 g1303866 Bacillus subtilis 1423 -11531419 7500952457 yqgs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:172590) (re:174506) (di:complement) BSUB0013 Z99116 g2634918 Bacillus subtilis 1423 -11531419 6500727561 hypothetical protein:hypothetical 73.2 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgS yqgS Bacillus subtilis 1423 -11531419

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805400	5199	27355	231	76

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805419	5200	27356	900	299

Description

GTC ORF with score 131 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept) (de:kaposi's sarcoma-associated herpes-like virus membrane antigen p140homolog, g-protein coupled receptor homolog, and orf 73 unknownprotein ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805422	5201	27357	390	129

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805439	5202	27358	312	103

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805443	5203	27359	330	109

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805447	5204	27360	744	247

Description

5000689316 hypothetical protein:hypothetical 8.6 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgQ yqgQ Bacillus subtilis 1423 -11531420 115913 yqgq (de:hypothetical 8.6 kd protein in soda-comga intergenic region) (db:swissprot) YQGQ_BACSU P54494 BACILLUS SUBTILIS 1423 -11531420 7000688408 yqgq hypothetical protein yqgq (db:pir2.dat) C69957 C69957 Bacillus subtilis 1423 -11531420 216108 yqgq (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:147808) (re:148023) (di:direct) BACJH642 D84432 g1303864 Bacillus subtilis 1423 -11531420 7500952456 yqgq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:175598) (re:175813) (di:complement) BSUB0013 Z99116 g2634920 Bacillus subtilis 1423 -11531420 6500727562 hypothetical protein:hypothetical 8.6 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgQ yqgQ Bacillus subtilis 1423 -11531420

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805459	5205	27361	204	67

Description

5000689315 hypothetical protein:hypothetical 56.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgP yqgP Bacillus subtilis 1423 -11531421 115912 yqgp (de:hypothetical 56.4 kd protein in soda-comga intergenic region) (db:swissprot) YQGP_BACSU P54493 BACILLUS SUBTILIS 1423 -11531421 7000688407 yqgp conserved hypothetical protein yqgp (cl:tetratricopeptide repeat homology) (db:pir2.dat) B69957 B69957 Bacillus subtilis 1423 -11531421 216107 yqgp (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:146175) (re:147698) (di:direct) BACJH642 D84432 g1303863 Bacillus subtilis 1423 -11531421 7500952455 yqgp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:175923) (re:177446) (di:complement) BSUB0013 Z99116 g2634921 Bacillus subtilis 1423 -11531421 6500727563 hypothetical protein:hypothetical 56.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgP yqgP Bacillus subtilis 1423 -11531421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805460	5206	27362	240	79

Description

5000689314 hypothetical protein:hypothetical 6.9 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgO yqgO Bacillus subtilis 1423 -11531422 115911 yqgo (de:hypothetical 6.9 kd protein in soda-comga intergenic region) (db:swissprot) YQGO_BACSU P54492 BACILLUS SUBTILIS 1423 -11531422 7000688406 yqgo hypothetical protein yqgo (db:pir2.dat) A69957 A69957 Bacillus subtilis 1423 -11531422 216106 yqgo (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:145912) (re:146085) (di:direct) BACJH642 D84432 g1303862 Bacillus subtilis 1423 -11531422 7500952454 yqgo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:177536) (re:177709) (di:complement) BSUB0013 Z99116 g2634922 Bacillus subtilis 1423 -11531422 6500727564 hypothetical protein:hypothetical 6.9 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgO yqgO Bacillus subtilis 1423 -11531422

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805461	5207	27363	369	123

Description

5000689313 hypothetical protein:hypothetical 21.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgN yqgN Bacillus subtilis 1423 -11531423 115910 yqgn (de:hypothetical 21.4 kd protein in soda-comga intergenic region) (db:swissprot) YQGN_BACSU P54491 BACILLUS SUBTILIS 1423 -11531423 7000688405 yqgn 5-formyltetrahydrofolate cyclo-ligase homolog yqgn (db:pir2.dat) H69956 H69956 Bacillus subtilis 1423 -11531423 216105 yqgn (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:145282) (re:145845) (di:direct) BACJH642 D84432 g1303861 Bacillus subtilis 1423 -11531423 7500952453 yqgn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to 5-formyltetrahydrofolate cyclo-ligase) (le:177776) (re:178339) (di:complement) BSUB0013 Z99116 g2634923 Bacillus subtilis 1423 -11531423 6500727565 hypothetical protein:hypothetical 21.4 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgN yqgN Bacillus subtilis 1423 -11531423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805465	5208	27364	216	71

Description

5000689312 hypothetical protein:hypothetical 40.8 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgM yqgM Bacillus subtilis 1423 -11531424 115909 yqgm (de:hypothetical 40.8 kd protein in soda-comga intergenic region) (db:swissprot) YQGM_BACSU P54490 BACILLUS SUBTILIS 1423 -11531424 7000688404 yqgm conserved hypothetical protein yqgm (db:pir2.dat) G69956 G69956 Bacillus subtilis 1423 -11531424 216104 yqgm (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:143885) (re:144964) (di:direct) BACJH642 D84432 g1303860 Bacillus subtilis 1423 -11531424 7500952452 yqgm (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:178657) (re:179736) (di:complement) BSUB0013 Z99116 g2634924 Bacillus subtilis 1423 -11531424 6500727566 hypothetical protein:hypothetical 40.8 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgM yqgM Bacillus subtilis 1423 -11531424

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805474	5209	27365	1152	384

Description

5000689311 hypothetical protein:hypothetical 18.5 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgL yqgL Bacillus subtilis 1423 -11531425 115908 yqgl (de:hypothetical 18.5 kd protein in soda-comga intergenic region) (db:swissprot) YQGL_BACSU P54489 BACILLUS SUBTILIS 1423 -11531425 7000688403 yqgl hypothetical protein yqgl (db:pir2.dat) F69956 F69956 Bacillus subtilis 1423 -11531425 216103 yqgl (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:143418) (re:143888) (di:direct) BACJH642 D84432 g1303859 Bacillus subtilis 1423 -11531425 7500952451 yqgl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:179733) (re:180203) (di:complement) BSUB0013 Z99116 g2634925 Bacillus subtilis 1423 -11531425 6500727567 hypothetical protein:hypothetical 18.5 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgL yqgL Bacillus subtilis 1423 -11531425

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805490	5210	27366	966	321

Description

6500727568 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzD yqzD Bacillus subtilis 1423 -11531426 7000693846 yqzd hypothetical protein yqzd (db:pir2.dat) C69969 C69969 Bacillus subtilis 1423 -11531426 7500964659 yqzd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:180383) (re:180736) (di:direct) BSUB0013 Z99116 g2634926 Bacillus subtilis 1423 -11531426

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805491	5211	27367	222	73

Description

6500727569 hypothetical protein:similar to hypothetical proteins from b.subtilis (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzC yqzC Bacillus subtilis 1423 -11531427 7000692716 yqzc conserved hypothetical protein yqzc (db:pir2.dat) B69969 B69969 Bacillus subtilis 1423 -11531427 7500963801 yqzc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:180733) (re:181197) (di:direct) BSUB0013 Z99116 g2634927 Bacillus subtilis 1423 -11531427

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805492	5212	27368	519	173

Description

5000689304 hypothetical protein:hypothetical 48.2 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgE yqgE Bacillus subtilis 1423 -11531428 115897 yqge (de:hypothetical 48.2 kd protein in soda-comga intergenic region) (db:swissprot) YQGE_BACSU P54487 BACILLUS SUBTILIS 1423 -11531428 7000688395 yqge conserved hypothetical protein yqge (db:pir2.dat) H69955 H69955 Bacillus subtilis 1423 -11531428 216096 yqge (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:134278) (re:135570) (di:direct) BACJH642 D84432 g1303852 Bacillus subtilis 1423 -11531428 7500952441 yqge (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:188051) (re:189343) (di:complement) BSUB0013 Z99116 g2634934 Bacillus subtilis 1423 -11531428 6500727570 hypothetical protein:hypothetical 48.2 kd protein in soda-comga intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgE yqgE Bacillus subtilis 1423 -11531428

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805493	5213	27369	285	94

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805505	5214	27370	525	174

Description

5000689303 hypothetical protein:hypothetical 17.3 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgC yqgC Bacillus subtilis 1423 -11531429 115892 yqgc (de:hypothetical 17.3 kd protein in ccca-soda intergenic region) (db:swissprot) YQGC_BACSU P54486 BACILLUS SUBTILIS 1423 -11531429 7000688392 yqgc hypothetical protein yqgc (db:pir2.dat) G69955 G69955 Bacillus subtilis 1423 -11531429 216094 yqgc (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:132903) (re:133385) (di:direct) BACJH642 D84432 g1303850 Bacillus subtilis 1423 -11531429 7500952438 yqgc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:190236) (re:190718) (di:complement) BSUB0013 Z99116 g2634936 Bacillus subtilis 1423 -11531429 6500727571 hypothetical protein:hypothetical 17.3 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgC yqgC Bacillus subtilis 1423 -11531429

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805507	5215	27371	849	282

Description

5000689302 hypothetical protein:hypothetical 28.2 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgB yqgB Bacillus subtilis 1423 -11531430 115890 yqgb (de:hypothetical 28.2 kd protein in ccca-soda intergenic region) (db:swissprot) YQGB_BACSU P54485 BACILLUS SUBTILIS 1423 -11531430 7000688390 yqgb hypothetical protein yqgb (db:pir2.dat) F69955 F69955 Bacillus subtilis 1423 -11531430 216093 yqgb (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:132035) (re:132793) (di:complement) BACJH642 D84432 g1303849 Bacillus subtilis 1423 -11531430 7500952436 yqgb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:190828) (re:191586) (di:direct) BSUB0013 Z99116 g2634937 Bacillus subtilis 1423 -11531430 6500727572 hypothetical protein:hypothetical 28.2 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgB yqgB Bacillus subtilis 1423 -11531430

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805534	5216	27372	1677	558

Description

5000689301 hypothetical protein:hypothetical 15.3 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgA yqgA Bacillus subtilis 1423 -11531431 115889 yqga (de:hypothetical 15.3 kd protein in ccca-soda intergenic region) (db:swissprot) YQGA_BACSU P54484 BACILLUS SUBTILIS 1423 -11531431 7000688388 yqga hypothetical protein yqga (db:pir2.dat) E69955 E69955 Bacillus subtilis 1423 -11531431 216092 yqga (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:131181) (re:131609) (di:direct) BACJH642 D84432 g1303848 Bacillus subtilis 1423 -11531431 7500952434 yqga (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:192012) (re:192440) (di:complement) BSUB0013 Z99116 g2634938 Bacillus subtilis 1423 -11531431 6500727573 hypothetical protein:hypothetical 15.3 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqgA yqgA Bacillus subtilis 1423 -11531431

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805558	5217	27373	423	141

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805570	5218	27374	282	93

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805571	5219	27375	1725	574

Description

5000689300 hypothetical protein:hypothetical 10.8 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfZ yqfZ Bacillus subtilis 1423 -11531432 115887 yqfz (de:hypothetical 10.8 kd protein in ccca-soda intergenic region) (db:swissprot) YQFZ_BACSU P54483 BACILLUS SUBTILIS 1423 -11531432 7000688387 yqfz hypothetical protein yqfz (db:pir2.dat) D69955 D69955 Bacillus subtilis 1423 -11531432 216091 yqfz (sr:bacillus subtilis (strain:jh642(trpc2 pheal)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:130605) (re:130904) (di:complement) BACJH642 D84432 g1303847 Bacillus subtilis 1423 -11531432 7500952433 yqfz (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:192717) (re:193016) (di:direct) BSUB0013 Z99116 g2634939 Bacillus subtilis 1423 -11531432 6500727574 hypothetical protein:hypothetical 10.8 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfZ yqfZ Bacillus subtilis 1423 -11531432

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805584	5220	27376	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805587	5221	27377	213	70

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805599	5222	27378	771	256

Description

5000689299 hypothetical protein:gcpe protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfY yqfY Bacillus subtilis 1423 -11531433 73420 yqfy (de:gcpe protein homolog) (db:swissprot) GCPE_BACSU P54482 BACILLUS SUBTILIS 1423 -11531433 7000685375 yqfy peptidoglycan acetylation homolog yqfy (cl:gcpe protein) (db:pir2.dat) C69955 C69955 Bacillus subtilis 1423 -11531433 216090 yqfy (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:129349) (re:130482) (di:complement) BACJH642 D84432 g1303846 Bacillus subtilis 1423 -11531433 7500882259 yqfy (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to peptidoglycan acetylation) (le:193139) (re:194272) (di:direct) BSUB0013 Z99116 g2634940 Bacillus subtilis 1423 -11531433 6500727575 hypothetical protein:gcpe protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfY yqfY Bacillus subtilis 1423 -11531433

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805614	5223	27379	876	292

Description

5000689298 hypothetical protein:hypothetical 13.9 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfX yqfX Bacillus subtilis 1423 -11531434 115886 yqfx (de:hypothetical 13.9 kd protein in ccca-soda intergenic region) (db:swissprot) YQFX_BACSU P54481 BACILLUS SUBTILIS 1423 -11531434 7000688386 yqfx hypothetical protein yqfx (db:pir2.dat) B69955 B69955 Bacillus subtilis 1423 -11531434 216089 yqfx (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:128934) (re:129323) (di:direct) BACJH642 D84432 g1303845 Bacillus subtilis 1423 -11531434 7500952432 yqfx (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:194298) (re:194687) (di:complement) BSUB0013 Z99116 g2634941 Bacillus subtilis 1423 -11531434 6500727576 hypothetical protein:hypothetical 13.9 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfX yqfX Bacillus subtilis 1423 -11531434

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805617	5224	27380	285	95

Description

5000689297 hypothetical protein:hypothetical 22.7 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfW yqfW Bacillus subtilis 1423 -11531435 115885 yqfw (de:hypothetical 22.7 kd protein in ccca-soda intergenic region) (db:swissprot) YQFW_BACSU P54480 BACILLUS SUBTILIS 1423 -11531435 7000688385 yqfw hypothetical protein yqfw (db:pir2.dat) A69955 A69955 Bacillus subtilis 1423 -11531435 216088 yqfw (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:128220) (re:128801) (di:complement) BACJH642 D84432 g1303844 Bacillus subtilis 1423 -11531435 7500952431 yqfw (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:194820) (re:195401) (di:direct) BSUB0013 Z99116 g2634942 Bacillus subtilis 1423 -11531435 6500727577 hypothetical protein:hypothetical 22.7 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfW yqfW Bacillus subtilis 1423 -11531435

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805624	5225	27381	636	211

Description

5000689296 hypothetical protein:ferric uptake regulation protein homolog 1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfV yqfV Bacillus subtilis 1423 -11531436 72531 yqfv (de:ferric uptake regulation protein homolog 1) (db:swissprot) FUR1_BACSU P54479 BACILLUS SUBTILIS 1423 -11531436 7000685333 yqfv transcription regulator fur family homolog yqfv (cl:ferric uptake regulator) (db:pir2.dat) H69954 H69954 Bacillus subtilis 1423 -11531436 216087 yqfv (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:127740) (re:128177) (di:direct) BACJH642 D84432 g1303843 Bacillus subtilis 1423 -11531436 7500881916 yqfv (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to transcriptional regulator (fur family)) (le:195444) (re:195881) (di:complement) BSUB0013 Z99116 g2634943 Bacillus subtilis 1423 -11531436 6500727578 hypothetical protein:ferric uptake regulation protein homolog 1 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfV yqfV Bacillus subtilis 1423 -11531436

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805634	5226	27382	381	127

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805638	5227	27383	210	69

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805656	5228	27384	441	146

Description

5000689295 hypothetical protein:hypothetical 32.5 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfU yqfU Bacillus subtilis 1423 -11531437 115884 yqfu (de:hypothetical 32.5 kd protein in ccca-soda intergenic region) (db:swissprot) YQFU_BACSU P54478 BACILLUS SUBTILIS 1423 -11531437 7000688384 yqfu conserved hypothetical protein yqfu (cl:conserved hypothetical protein yitt) (db:pir2.dat) G69954 G69954 Bacillus subtilis 1423 -11531437 216086 yqfu (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:126721) (re:127602) (di:direct) BACJH642 D84432 g1303842 Bacillus subtilis 1423 -11531437 7500952430 yqfu (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins from b. subtilis) (le:196019) (re:196900) (di:complement) BSUB0013 Z99116 g2634944 Bacillus subtilis 1423 -11531437 6500727579 hypothetical protein:hypothetical 32.5 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfU yqfU Bacillus subtilis 1423 -11531437

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805659	5229	27385	378	125

Description

5000689294 hypothetical protein:hypothetical 9.7 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfT yqfT Bacillus subtilis 1423 -11531438 115883 yqft (de:hypothetical 9.7 kd protein in ccca-soda intergenic region) (db:swissprot) YQFT_BACSU P54477 BACILLUS SUBTILIS 1423 -11531438 7000688383 yqft hypothetical protein yqft (db:pir2.dat) F69954 F69954 Bacillus subtilis 1423 -11531438 216085 yqft (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:126351) (re:126605) (di:complement) BACJH642 D84432 g1303841 Bacillus subtilis 1423 -11531438 7500952429 yqft (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:197016) (re:197270) (di:direct) BSUB0013 Z99116 g2634945 Bacillus subtilis 1423 -11531438 6500727580 hypothetical protein:hypothetical 9.7 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfT yqfT Bacillus subtilis 1423 -11531438

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805662	5230	27386	207	68

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805664	5231	27387	624	207

Description

6500727581 hypothetical protein:probable endonuclease iv:endodeoxyribonuclease iv (gtcfc:14.1) (ec:3.1.21.2) (keggfc:14.1) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfS yqfS Bacillus subtilis 1423 -11531439 70157 yqfs (ec:3.1.21.2) (de:probable endonuclease iv, (endodeoxyribonuclease iv)) (db:swissprot) END4_BACSU P54476 BACILLUS SUBTILIS 1423 -11531439 7000685158 yqfs endonuclease iv homolog yqfs (cl:deoxyribonuclease iv (phage t4-induced)) (db:pir2.dat) E69954 E69954 Bacillus subtilis 1423 -11531439 216084 yqfs (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:125431) (re:126324) (di:direct) BACJH642 D84432 g1303840 Bacillus subtilis 1423 -11531439 7500881023 yqfs (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to endonuclease iv) (le:197297) (re:198190) (di:complement) BSUB0013 Z99116 g2634946 Bacillus subtilis 1423 -11531439 5000689444 (de:(yqfs) (pn:probable endonuclease iv:endodeoxyribonuclease iv) (gtcfc:13.07) (ec:3.1.21.2) (end4_bacsu) (keggfc:11.1) (db:gtc-bacillus subtilis)) yqfS yqfS Bacillus subtilis 1423 10012735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805665	5232	27388	2082	693

Description

5000689293 hypothetical protein:probable rna helicase in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfR yqfR Bacillus subtilis 1423 -11531440 115882 yqfr (de:probable rna helicase in ccca-soda intergenic region) (db:swissprot) YQFR_BACSU P54475 BACILLUS SUBTILIS 1423 -11531440 7000688382 yqfr atp-dependent rna helicase homolog yqfr (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) D69954 D69954 Bacillus subtilis 1423 -11531440 216083 yqfr (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:124105) (re:125421) (di:direct) BACJH642 D84432 g1303839 Bacillus subtilis 1423 -11531440 7500952428 yqfr (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to atp-dependent rna helicase) (le:198200) (re:199516) (di:complement) BSUB0013 Z99116 g2634947 Bacillus subtilis 1423 -11531440 6500727582 hypothetical protein:probable rna helicase in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfR yqfR Bacillus subtilis 1423 -11531440

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805692	5233	27389	723	240

Description

5000689292 hypothetical protein:hypothetical 25.9 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfQ yqfQ Bacillus subtilis 1423 -11531441 115881 yqfq (de:hypothetical 25.9 kd protein in ccca-soda intergenic region) (db:swissprot) YQFQ_BACSU P54474 BACILLUS SUBTILIS 1423 -11531441 7000688381 yqfq hypothetical protein yqfq (db:pir2.dat) C69954 C69954 Bacillus subtilis 1423 -11531441 216082 yqfq (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:123193) (re:123936) (di:complement) BACJH642 D84432 g1303838 Bacillus subtilis 1423 -11531441 7500952427 yqfq (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:199685) (re:200428) (di:direct) BSUB0013 Z99116 g2634948 Bacillus subtilis 1423 -11531441 6500727583 hypothetical protein:hypothetical 25.9 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfQ yqfQ Bacillus subtilis 1423 -11531441

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805700	5234	27390	429	142

Description

6500727584 hypothetical protein:lytb protein homolog (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfP yqfP Bacillus subtilis 1423 -11531442 115880 yqfp (de:lytb protein homolog) (db:swissprot) YQFP_BACSU P54473 BACILLUS SUBTILIS 1423 -11531442 7000688380 yqfp penicillin tolerance homolog yqfp (cl:penicillin tolerance protein) (db:pir2.dat) B69954 B69954 Bacillus subtilis 1423 -11531442 216081 yqfp (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:122126) (re:123070) (di:complement) BACJH642 D84432 g1303837 Bacillus subtilis 1423 -11531442 7500952426 yqfp (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to penicillin tolerance) (le:200551) (re:201495) (di:direct) BSUB0013 Z99116 g2634949 Bacillus subtilis 1423 -11531442

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805713	5235	27391	546	181

Description

6500727585 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfO yqfO Bacillus subtilis 1423 -11531443 7000692713 yqfo conserved hypothetical protein yqfo (db:pir2.dat) A69954 A69954 Bacillus subtilis 1423 -11531443 7500963798 yqfo (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:201518) (re:202639) (di:complement) BSUB0013 Z99116 g2634950 Bacillus subtilis 1423 -11531443

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805714	5236	27392	222	73

Description

5000689290 hypothetical protein:hypothetical 23.7 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfN yqfN Bacillus subtilis 1423 -11531444 115878 yqfn (de:hypothetical 23.7 kd protein in ccca-soda intergenic region) (db:swissprot) YQFN_BACSU P54471 BACILLUS SUBTILIS 1423 -11531444 7000688379 yqfn conserved hypothetical protein yqfn (db:pir2.dat) H69953 H69953 Bacillus subtilis 1423 -11531444 216079 yqfn (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:120338) (re:120988) (di:direct) BACJH642 D84432 g1303835 Bacillus subtilis 1423 -11531444 7500952425 yqfn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:202632) (re:203282) (di:complement) BSUB0013 Z99116 g2634951 Bacillus subtilis 1423 -11531444 6500727586 hypothetical protein:hypothetical 23.7 kd protein in ccca-soda intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfN yqfN Bacillus subtilis 1423 -11531444

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805716	5237	27393	309	103

Description

6500727587 yqfm:yqxd hypothetical protein:hypothetical 22.5 kd protein in glys-dnag/dnae intergenic region:p23 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxD yqxD Bacillus subtilis 1423 -11531445 216075 yqxd:yqfm (de:(p23)) (db:swissprot) YQXD_BACSU P17868 BACILLUS SUBTILIS 1423 -11531445 7000688494 yqxd conserved hypothetical protein yqxd:hypothetical p23 protein dnae 5 region (db:pir2.dat) A29279 A29279 Bacillus subtilis 1423 -11531445 7500952571 yqfm (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:115641) (re:116231) (di:direct) BACJH642 D84432 g1303831 Bacillus subtilis 1423 -11531445 5000689678 (db:genpept-bct1) (de:bacillus subtilis sigma 43 operon with p23-dnae-rpod genes (dnaefor dna primase, rpod for rna polymerase).) (nt:p23 (aa 1-196); unidentified reading frame) (le:855) (re:1445) (di:direct) BSSIG43 X03897 g40141 Bacillus subtilis 1423 -11531445 219622 yqxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqfm; similar to hypothetical) (le:207389) (re:207979) (di:complement) BSUB0013 Z99116 g2634955 Bacillus subtilis 1423 -11531445 6000685780 yqxd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqfm; similar to hypothetical) (le:3199) (re:3789) (di:complement) BSUB0014 Z99117 g2634969 Bacillus subtilis 1423 -11531445 116028 yqxd:yqfm (de:(p23)) (db:swissprot) YQXD_BACSU P17868 BACILLUS SUBTILIS 1423 -11531445 170060 yqxd conserved hypothetical protein yqxd:hypothetical p23 protein dnae 5 region (db:pir) A29279 A29279 Bacillus subtilis 1423 -11531445

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805717	5238	27394	279	92

Description

5000689289 hypothetical protein:hypothetical 30.3 kd protein in glys-dnag/dnae intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfL yqfL Bacillus subtilis 1423 -11531446 115877 yqfl (de:hypothetical 30.3 kd protein in glys-dnag/dnae intergenic region) (db:swissprot) YQFL_BACSU P54470 BACILLUS SUBTILIS 1423 -11531446 7000688378 yqfl conserved hypothetical protein yqfl (db:pir2.dat) G69953 G69953 Bacillus subtilis 1423 -11531446 216074 yqfl (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:114671) (re:115483) (di:direct) BACJH642 D84432 g1303830 Bacillus subtilis 1423 -11531446 6000685687 yqfl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:208137) (re:208949) (di:complement) BSUB0013 Z99116 g2634956 Bacillus subtilis 1423 -11531446 7500952424 yqfl (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:3947) (re:4759) (di:complement) BSUB0014 Z99117 g2634970 Bacillus subtilis 1423 -11531446 6500727588 hypothetical protein:hypothetical 30.3 kd protein in glys-dnag/dnae intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfL yqfL Bacillus subtilis 1423 -11531446

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805718	5239	27395	462	153

Description

6500727589 hypothetical protein:similar to hypothetical proteins (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqzB yqzB Bacillus subtilis 1423 -11531447 7000692715 yqzb conserved hypothetical protein yqzb (db:pir2.dat) A69969 A69969 Bacillus subtilis 1423 -11531447 6000691218 yqzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:208975) (re:209613) (di:complement) BSUB0013 Z99116 g2634957 Bacillus subtilis 1423 -11531447 7500963800 yqzb (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:4785) (re:5423) (di:complement) BSUB0014 Z99117 g2634971 Bacillus subtilis 1423 -11531447

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805720	5240	27396	726	241

Description

6500727590 yqfi:yqxn hypothetical protein:hypothetical 29.3 kd protein in bex-dnag/dnae intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqxN yqxN Bacillus subtilis 1423 -11531448 116037 yqxn:yqfi (de:(orf3)) (db:swissprot) YQXN_BACSU P42095 BACILLUS SUBTILIS 1423 -11531448 7000688502 yqxn conserved hypothetical protein yqxn (db:pir2.dat) H69968 H69968 Bacillus subtilis 1423 -11531448 216071 yqfi (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:109891) (re:110658) (di:direct) BACJH642 D84432 g1303827 Bacillus subtilis 1423 -11531448 6000685789 yqxn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:alternate gene name: yqfi; similar to hypothetical) (le:212962) (re:213729) (di:complement) BSUB0013 Z99116 g2634960 Bacillus subtilis 1423 -11531448 7500952579 yqxn (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:alternate gene name: yqfi; similar to hypothetical) (le:8772) (re:9539) (di:complement) BSUB0014 Z99117 g2634974 Bacillus subtilis 1423 -11531448 5000689686 (de:(yqxn) (pn:hypothetical 29:hypothetical protein in bex 3"region:orf3:fragment) (gn:yqfi) (gtcfc:13.07) (ec:) (yqxn_bacsu) (keggfc:11.2) (bsorffc:8.0.0) (db:gtc-bacillus subtilis)) yqxN yqxN Bacillus subtilis 1423 10057763

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805728	5241	27397	1182	393

Description

5000689288 hypothetical protein:hypothetical 17.8 kd protein in phoh-dgka intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfG yqfG Bacillus subtilis 1423 -11531449 115876 yqfg (de:hypothetical 17.8 kd protein in phoh-dgka intergenic region) (db:swissprot) YQFG_BACSU P46347 BACILLUS SUBTILIS 1423 -11531449 7000688377 yqfg conserved hypothetical protein yqfg (db:pir2.dat) F69953 F69953 Bacillus subtilis 1423 -11531449 216067 yqfg (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:107324) (re:107797) (di:direct) BACJH642 D84432 g1303823 Bacillus subtilis 1423 -11531449 6000685685 yqfg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (nt:similar to hypothetical proteins) (le:215823) (re:216296) (di:complement) BSUB0013 Z99116 g2634964 Bacillus subtilis 1423 -11531449 7500952423 yqfg (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:11633) (re:12106) (di:complement) BSUB0014 Z99117 g2634978 Bacillus subtilis 1423 -11531449 6500727591 hypothetical protein:hypothetical 17.8 kd protein in phoh-dgka intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfG yqfG Bacillus subtilis 1423 -11531449

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805732	5242	27398	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805742	5243	27399	543	181

Description

5000689287 hypothetical protein:hypothetical 79.2 kd protein in phoh-dgka intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfF yqfF Bacillus subtilis 1423 -11531450 115875 yqff (de:hypothetical 79.2 kd protein in phoh-dgka intergenic region) (db:swissprot) YQFF_BACSU P46344 BACILLUS SUBTILIS 1423 -11531450 7000688376 yqff hypothetical protein yqff (db:pir2.dat) E69953 E69953 Bacillus subtilis 1423 -11531450 216066 yqff (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:105188) (re:107323) (di:direct) BACJH642 D84432 g1303822 Bacillus subtilis 1423 -11531450 6000685683 yqff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.) (le:216297) (re:218432) (di:complement) BSUB0013 Z99116 g2634965 Bacillus subtilis 1423 -11531450 7500952422 yqff (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:12107) (re:14242) (di:complement) BSUB0014 Z99117 g2634979 Bacillus subtilis 1423 -11531450 6500727592 hypothetical protein:hypothetical 79.2 kd protein in phoh-dgka intergenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfF yqfF Bacillus subtilis 1423 -11531450

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805751	5244	27400	267	88

Description

5000689286 hypothetical protein:hypothetical 45.7 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfD yqfD Bacillus subtilis 1423 -11531451 115873 yqfd (de:hypothetical 45.7 kd protein in rpsu-phoh interegenic region) (db:swissprot) YQFD_BACSU P54469 BACILLUS SUBTILIS 1423 -11531451 7000688374 yqfd conserved hypothetical protein yqfd (db:pir2.dat) D69953 D69953 Bacillus subtilis 1423 -11531451 216064 yqfd (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:102957) (re:104153) (di:direct) BACJH642 D84432 g1303820 Bacillus subtilis 1423 -11531451 7500952420 yqfd (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins) (le:15277) (re:16473) (di:complement) BSUB0014 Z99117 g2634981 Bacillus subtilis 1423 -11531451 6500727593 hypothetical protein:hypothetical 45.7 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfD yqfD Bacillus subtilis 1423 -11531451

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805758	5245	27401	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805759	5246	27402	351	116

Description

GTC ORF with score 145 to: (sr:plasmid ptrab4) (db:genpept-bct1) (de:agrobacterium vitis plasmid ptrab4 putative lysr-type protein(ttua), putative tartrate transport protein (ttub), putativetartrate dehydrogenase (ttuc), putative hydroxypyruvate ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805760	5247	27403	306	101

Description

5000689285 hypothetical protein:hypothetical 10.8 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfC yqfC Bacillus subtilis 1423 -11531452 115872 yqfc (de:hypothetical 10.8 kd protein in rpsu-phoh interegenic region) (db:swissprot) YQFC_BACSU P54468 BACILLUS SUBTILIS 1423 -11531452 7000688373 yqfc hypothetical protein yqfc (db:pir2.dat) C69953 C69953 Bacillus subtilis 1423 -11531452 216063 yqfc (sr:bacillus subtilis (strain:jh642(trpc2 phea1)) dna) (db:genpept-bct1) (de:bacillus subtilis dna, 283 kb region containing skin element.) (le:102657) (re:102938) (di:direct) BACJH642 D84432 g1303819 Bacillus subtilis 1423 -11531452 7500952419 yqfc (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (le:16492) (re:16773) (di:complement) BSUB0014 Z99117 g2634982 Bacillus subtilis 1423 -11531452 6500727594 hypothetical protein:hypothetical 10.8 kd protein in rpsu-phoh interegenic region (gtcfc:14.1) (keggfc:14.2) (bsorffc:8.1.1) (db:gtc-bacillus subtilis) yqfC yqfC Bacillus subtilis 1423 -11531452

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501805770	5248	27404	183	60

Description

Hypothetical protein